

? ds

Set	Items	Description
S1	1305	TAU AND PHOSPHORYL? AND (MONOCLONAL OR MAB)
S2	599	RD S1 (unique items)
S3	304	S2 AND PY<1996
S4	111	S3 AND PY<1993
S5	234	E3-E9
S6	805	E1-E11
S7	148	E3-E11
S8	1128	S5 OR S6 OR S7
S9	77	S8 AND TAU AND (MONOCLONAL OR MAB)
S10	33	RD S9 (unique items)

? logoff y

20may02 08:29:42 User226352 Session D629.3

WEST[Help](#)[Logout](#)[Interrupt](#)[Main Menu](#)[Search Form](#)[Posting Counts](#)[Show S Numbers](#)[Edit S Numbers](#)[Preferences](#)[Cases](#)**Search Results -**

Terms	Documents
tau and phosphorylat? and (monoclonal or mab) and Alzheimer?	7

Database: US Patents Full-Text Database ▲
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins ▼

Search: L3 ▲ ▼ Refine Search

Recall Text Clear

Search History

DATE: Monday, May 20, 2002 [Printable Copy](#) [Create Case](#)

Set Name Query

side by side

Hit Count Set Name

result set

DB=USPT; PLUR=YES; OP=AND

<u>L3</u>	tau and phosphorylat? and (monoclonal or mab) and Alzheimer?	7	<u>L3</u>
<u>L2</u>	tau and phosphoryl? and (monoclonal ro mab) and Alzheimer?	0	<u>L2</u>
<u>L1</u>	tau and phosphory? and (monoclonal or mab)	8	<u>L1</u>

66969

From: Duffy, Patricia
Sent: Monday, May 20, 2002 9:47 AM
To: STIC-Biotech/ChemLib
Subject: Sequence Search 09/734,281
Importance: High

In re: 09/734,281

Please search SEQ ID NOs:1 and 2.
Please include an interference search.
Please print out top 40 hits in each category.

Thank you.

Patricia A. Duffy
Art Unit 1645
Office CM-1, 8D05
Mailbox CM-1, 8E12
Phone 703-305-7555

Mary Hale - Supervisor, Info. Branch
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 2
Structures: _____
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Full text: _____
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VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
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Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: May 21, 2002, 11:10:10 ; Search time 51.55 seconds
(without alignments)
19.392 Million cell updates/sec

Title: US-09-734-281-1

Perfect score: 50

Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database :

A_Geneseq_032802:*

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- 3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
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- 13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
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- 19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	9	14	AA198557
2	50	100.0	12	14	AA198235
3	50	100.0	12	14	AA197554
4	50	100.0	12	18	AA194857
5	50	100.0	12	21	AA191390
6	50	100.0	14	21	AA191959
7	50	100.0	34	15	AA191330
8	50	100.0	34	18	AA194875
9	50	100.0	67	15	AA198837
10	50	100.0	78	22	AA195640
11	50	100.0	106	17	AA192516

12	50	100.0	112	16	AA176937	PHF-tau (143-254)
13	50	100.0	351	21	AA152200	Human Tau protein.
14	50	100.0	352	10	AA191294	Paired helical fil.
15	50	100.0	352	14	AA192708	Human tau-protein.
16	50	100.0	352	19	AA192048	Human microtubule
17	50	100.0	390	17	AA190583	Truncated human ta
18	50	100.0	441	15	AA195810	Human tau protein.
19	50	100.0	441	17	AA195810	Human tau protein.
20	50	100.0	441	18	AA195810	Human tau protein.
21	50	100.0	441	21	AA191386	Human paired helix
22	43	86.0	13	13	AA192823	Phosphopeptide as
23	43	86.0	13	18	AA194860	Human tau protein
24	43	86.0	13	18	AA194858	Human tau protein
25	40	80.0	263	18	AA192945	Oerskovia xanthine
26	40	80.0	435	18	AA192945	Oerskovia xanthine
27	39	78.0	7	14	AA193823	Alzheimer paired h
28	39	78.0	7	14	AA193752	Phosphorylated tau
29	39	78.0	263	22	AA191714	Novel signal trans
30	39	78.0	376	22	AA190057	Human protein seq
31	39	78.0	424	21	AA194838	Human ORFX ORF1602
32	39	78.0	424	21	AA194838	Human protein seq
33	39	78.0	424	22	AA192727	Human EXMAD-5 seq
34	38	76.0	98	22	AA190562	Human polypeptide
35	37	74.0	284	22	AA192734	Novel human diago
36	37	74.0	335	13	AA192506	Soluble human IL-5
37	37	74.0	335	14	AA193369	shIL-5R-alpha. Sy
38	37	74.0	350	22	AA193217	Human polypeptide,
39	37	74.0	351	22	AA193217	Chicken zyxine fra
40	37	74.0	353	13	AA192831	AHSV protein. Afr
41	37	74.0	395	22	AA193380	Human polypeptide
42	37	74.0	396	13	AA192216	Sequence of human
43	37	74.0	396	13	AA192216	Human neurotensin
44	37	74.0	418	17	AA198562	Non-endogenous hum
45	37	74.0	418	22	AA195671	Sequence of human
46	37	74.0	420	13	AA192215	Human interleukin-
47	37	74.0	420	13	AA192219	Human IL-5 recepto
48	37	74.0	420	19	AA192842	Human polypeptide,
49	37	74.0	421	13	AA192506	Human brain proteo
50	37	74.0	464	22	AA193631	Novel human diago
51	37	74.0	494	22	AA191165	Chicken zyxine. G
52	37	74.0	539	21	AA197747	Human brain Neurog
53	37	74.0	542	22	AA192316	
54	37	74.0	542	22	AA192304	
55	37	74.0	545	18	AA192867	

ALIGNMENTS

RESULT 1

AA1936557
ID AA1936557 standard; peptide; 9 AA.

XX AA1936557;

XX AC

XX AC

DT 10-AUG-1993 (first entry)

XX

DE Peptide sequence for abnormally phosphorylated tau protein.

XX

KW Alzheimer's disease; Down's syndrome; Pick's disease; monoclonal;

KW antibody; detection; SSPE; antigen.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 3

FT /note= "may be phosphorylated"

FT Misc-difference 6

FT /note= "may be phosphorylated"

XX

PN W09308302-A.

XX

PD 29-APR-1993.

Wed May 22 11:04:22 2002

(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;
 PI Steiner B;
 XX WPI; 1993-197050/24.

XX Tau protein epitope(s), specific antibodies and protein kinase(s)
 PT - used in the prevention, diagnosis and treatment of Alzheimer's
 PT disease

XX Claim 5; Page 89; 148pp; English.
 XX This is one of 26 preferred epitopes which occur in a phosphorylated
 CC state in tau protein from Alzheimer paired helical filaments. The
 CC epitopes all include phosphorylatable serine residues in Ser-Pro
 CC motifs, Ile-Gly-Ser motifs or Cys-Gly-Ser motifs and/or
 CC phosphorylatable threonine residues in Thr-Pro motifs. The pattern
 CC of tau protein phosphorylation differs between Alzheimer's and
 CC non-Alzheimer's individuals. Knowledge of the phosphorylated
 CC epitopes and antibodies which recognise them may be useful in
 CC diagnosis, treatment and prevention of Alzheimer's Disease. The
 CC protein kinases present in mammalian brain which phosphorylate the
 CC different epitopes are also claimed but no sequences are given.

XX Sequence 12 AA;

XX Query Match 100.0%; Score 50; DB 14; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 0.14;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 YSSPGSPGT 9
 XX | | | | | | | | | |
 XX Db 1 ysspgspgt 9

XX RESULT 3

XX AAR37554
 XX ID AAR37554 standard; peptide; 12 AA.

XX AC AAR37554;

XX DT 07-OCT-1993 (first entry)

XX DE Phosphorylated tau protein epitope.

XX KW Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
 XX KW treatment; formation; inhibition; inhibitor.

XX OS Homo sapiens.

XX PN EP544942-A.

XX PD 09-JUN-1993.

XX PF 06-DEC-1991; 91EP-0120974.

XX PR 06-DEC-1991; 91EP-0120974.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow EM, Steiner B;
 XX WPI; 1993-183841/23.

XX Phosphorylated tau protein epitope associated with Alzheimer's
 PT disease - is used as protein kinase inhibitor for treatment and
 PT diagnosis

XX Claim 4; Page 16; 34pp; English.

XX The sequence is that of an epitope of tau protein which specifically

XX PF 17-OCT-1992; 92WO-EP02392.

XX PR 25-OCT-1991; 91EP-0402871.

XX PA (INNO-) INNOGENETICS NV SA.

XX Mandelkow E, Mercken M, Van DE VOORDE A, Vandermeeren M;
 PI Vanmechelen E;

XX WPI; 1993-152493/18.

XX Monoclonal antibodies binding abnormal micro-tubule-associated
 PT tau-protein - for diagnosing neurological disorders e.g.
 PT Alzheimer's disease, Downs syndrome, Picks disease, etc.

XX Claim 8; Page 36; 47pp; English.

XX The peptide is able to form an immunogenic complex with a
 CC monoclonal antibody contg. a phosphorylated epitope of an antigen
 CC belonging to human abnormally phosphorylated tau protein which can be
 CC obtd. from a brain homogenate isolated from the cerebral cortex of a
 CC patient having Alzheimer's disease. The monoclonal antibody is able
 CC to specifically detect only abnormally phosphorylated tau protein and
 CC not react with normal tau protein, and thus may be used in the detection
 CC or diagnosis of neurological diseases, e.g. Alzheimer's disease, Down's
 CC syndrome, Pick's disease or SSPE.
 CC See also AAR36556.

XX Sequence 9 AA;

XX Query Match 100.0%; Score 50; DB 14; Length 9;

XX Best Local Similarity 100.0%; Pred. NO. 6.4e-05;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 YSSPGSPGT 9
 XX | | | | | | | | | |
 XX Db 1 ysspgspgt 9

XX RESULT 2

XX AAR38235
 XX ID AAR38235 standard; peptide; 12 AA.

XX AC AAR38235;

XX DT 08-OCT-1993 (first entry)

XX DE Alzheimer paired helical filament tau protein epitope 197-208.

XX KW Alzheimer tau protein; phosphorylation-dependent; PHF;
 XX KW neuronal microtubule; mitogen activated protein kinase; MAP kinase.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Modified-site 3..4 /label= Phosphorylation_motif

XX FT Modified-site 6..7 /label= Phosphorylation_motif

XX FT Modified-site 9..10 /label= Phosphorylation_motif

XX WO9311231-A.

XX PD 10-JUN-1993.

XX PF 07-DEC-1992; 92WO-EP02829.

XX PR 06-DEC-1991; 91EP-0120974.

XX PR 16-NOV-1992; 92EP-0119551.

CC occurs in a phosphorylated state in tau protein from Alzheimer's
 CC paired helical fragments. It may be used as part of a method for the
 CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
 CC also be used in an in vitro model for the study of the generation of
 CC the Alzheimer state of proteins and the testing of substances which
 CC prevent the conversion of normal to Alzheimer tau protein. The
 CC epitope occurs at residues 197-208 of human tau protein.
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 50; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 YSSPGSPGT 9
 DB 1 YSSPGSPGT 9

RESULT 4
 AAW34857
 ID AAW34857 standard; peptide; 12 AA.
 AC AAW34857;
 XX
 DT 27-MAR-1998 (first entry)
 XX Human tau protein fragment.
 DE
 XX
 KW Antibody; phosphorylated tau protein; paired helical filament;
 KW detection; Alzheimer's disease; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6 /note= "phosphoserine"
 ET
 XX WO9734145-A1.
 XX 18-SEP-1997.
 XX
 XX 13-MAR-1997; 97WO-JP00804.
 XX
 PR 13-MAR-1996; 96JP-0056090.
 XX
 PA (MITU) MITSUBISHI CHEM CORP.
 XX
 XX Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
 XX WPI; 1997-470978/43.
 DR
 XX
 PT Antibody prepared using a partial peptide containing part of
 PT phosphorylated tau protein - used for detecting Alzheimer's disease
 XX
 PS Example; Page 28; 48pp; Japanese.
 XX
 CC An antibody, prepared using a partial peptide containing the
 CC phosphorylated residue of the phosphorylated tau protein, e.g. the
 CC present sequence, in a paired helical filament, can be used to
 CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 CC protein in brain extracts or tissue fragments.
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 50; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 YSSPGSPGT 9
 DB 1 YSSPGSPGT 9

Db 4 ysspgspgt 12
 RESULT 5
 AAY81390
 ID AAY81390 standard; protein; 12 AA.
 XX
 AC AAY81390;
 XX
 DT 19-JUN-2000 (first entry)
 XX Human phosphorylated tau protein derived peptide fragment, PS199.
 DE
 XX
 KW Phosphorylated tau protein; human; paired helical filament; fragment;
 KW polyclonal antibody; Alzheimer's disease; cerebrospinal fluid; CSF;
 KW diagnosis; detection.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6 /note= "Phosphorylated"
 FT
 XX JP2000034300-A.
 XX
 PD 02-FEB-2000.
 XX
 PF 17-JUL-1998; 98JP-0204040.
 XX
 PR 17-JUL-1998; 98JP-0204040.
 XX
 PA (MITU) MITSUBISHI CHEM CORP.
 XX
 DR WPI; 2000-285529/25.
 XX
 PT Anti-phosphated tau protein antibody - for the detection of Alzheimer
 PT disease
 XX
 PS Claim 4; Page 4; 12pp; Japanese.
 XX
 CC The invention relates to an antibody against a phosphorylated tau
 CC protein (AAY81386), which is a component of the paired helical filament
 CC found in the plaques associated with Alzheimer's disease. A
 CC phosphorylated tau protein fragment selected from peptides
 CC AAY81387-Y81390 is conjugated to keyhole limpet haemocyanin (KLH), and
 CC used to raise polyclonal antibodies in a rabbit. The antibodies of the
 CC invention are specific for phosphorylated tau protein and may be used to
 CC detect phosphorylated tau protein in the cerebrospinal fluid (CSF) of a
 CC patient suspected of having Alzheimer's disease. Use of the antibodies of
 CC the invention provides specific diagnosis of Alzheimer's disease.
 CC Sequences AAY81387-Y81390 represent phosphorylated peptides derived from
 CC tau protein used to raise anti-phosphorylated tau antibodies. The
 CC N-terminal residue is not part of the full-length tau protein, but
 CC facilitates KLH conjugation.
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 50; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 YSSPGSPGT 9
 DB 4 ysspgspgt 12

RESULT 6
 AAB21959
 ID AAB21959 standard; Peptide; 14 AA.
 XX
 AC AAB21959;

```

Qy      1 ysspgspgt 9
        |||||
Db      2 ysspspgt 10

RESULT 7
AA061330
ID  AAR61330 standard; Protein; 34 AA.
XX  AAR61330;
AC  AAR61330;
XX  XX
XX  XX
XX  24-APR-1995 (first entry)
XX  Peptide phosphorylated by human tau-protein kinase.
XX  Tau-protein kinase I enzyme; TPK-I; Phosphorylated peptide.
XX  XX
XX  Synthetic.
XX  OS
XX  EP616032-A.
XX  PN
XX  XX
XX  21-SEP-1994.
XX  PD
XX  01-MAR-1994; 94EP-0103057.
XX  PF
XX  02-MAR-1993; 93JP-0041160.
XX  PR
XX  22-MAR-1993; 93JP-0085143.
XX  PR
XX  02-AUG-1993; 93JP-0191246.
XX  XX
XX  (TAKA/) TAKASHIMA A.
XX  (MITU ) MITSUBISHI KASEI CORP.
XX  PA
XX  PA
XX  Hoshino T, Imahori K, Saito K, Sato S, Shiratsuchi A;
XX  Takashima A;
XX  PI
XX  WPI; 1994-287181/36.
XX  XX
XX  Newly isolated tau-protein kinase I enzyme - with specificity for
XX  tau-protein providing means for prevention and treatment of
XX  Alzheimer's disease
XX  XX
XX  Example 4; Page 25; 30pp; English.
XX  XX
XX  AAR61330 is a peptide which has been phosphorylated by human
XX  tau-protein kinase (AAR61326).
XX  CC
XX  CC
XX  Sequence 34 AA;
XX  SQ

Query Match 100.0%; Score 50; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Gaps 0;
Matches 9; Conservative 0; Indels 0; Mismatches 0;

Qy      1 YSSPGSPGT 9
        |||||
Db      7 ysspspgt 15

RESULT 8
AAW34875
ID  AAW34875 standard; peptide; 34 AA.
XX  XX
XX  AAW34875;
XX  XX
XX  XX
XX  27-MAR-1998 (first entry)
XX  XX
XX  Human tau protein fragment.
XX  DE
XX  Antibody; phosphorylated tau protein; paired helical filament;
XX  KW detection; Alzheimer's disease; human.
XX  KW
XX  XX
XX  Homo sapiens.
XX  OS

```

XX WO9734145-A1.
 XX 18-SEP-1997.
 XX PF 13-MAR-1997; 97NO-JP00804.
 XX PR 13-MAR-1996; 96JP-0056090.
 XX PA (MITU) MITSUBISHI CHEM CORP.
 XX PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
 XX WPI; 1997-470978/43.
 XX DR Antibody prepared using a partial peptide containing part of
 XX PT phosphorylated tau protein - used for detecting Alzheimer's disease
 XX PS Example; Pages 36-37; 48pp; Japanese.
 XX CC An antibody, prepared using a partial peptide containing the
 XX CC phosphorylated residue of the phosphorylated tau protein, e.g. the
 XX CC present sequence, in a paired helical filament, can be used to
 XX CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 XX CC protein in brain extracts or tissue fragments.
 XX SQ Sequence 34 AA;

Query Match 100.0%; Score 50; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSPGSGPCT 9
 DB 7 YSPGSGPCT 15
 |||||

RESULT 9
 AAR59837
 ID AAR59837 standard; peptide; 67 AA.
 AC AAR59837;
 DT 04-MAR-1995 (first entry)
 DE Sequence of human microtubule-associated protein tau.
 KW Tau protein; brain; cerebral cortex; hybridoma ECACC 92100853;
 KW Alzheimer's disease; monoclonal antibody; paired helical filament.
 XX Homo sapiens.
 XX WO9413795-A.
 XX PD 23-JUN-1994.
 XX PF 10-DEC-1993; 93WO-EP03499.
 XX PR 14-DEC-1992; 92EP-0403403.
 XX PA (INNO-) INNOGENETICS NV SA.
 XX PI Mercken M, Van De Voorde A, Vandermeeren M, Vanmechelen E;
 XX WPI; 1994-234211/28.
 XX CC Monoclonal antibody reactive with tau protein - used to develop
 XX CC prods. for detection of brain diseases involving tau or paired
 XX CC helical filaments esp. Alzheimer's disease
 XX PS Claim 6; Page 38; 52pp; English.

CC Paired helical filament (PHF) tau was partially purified from
 CC postmortem tissue, consisting mostly of grey matter from the frontal
 CC and temporal cortex obtd. from Alzheimer patients. The tissue (5-10g)
 CC was homogenised with 10 vols of cold buffer (10mM Tris, 1mM EGTA,
 CC 0.8M NaCl, 10% sucrose, pH 7.4). After centrifugation for 20 mins at
 CC 4 degrees C, the supernatant was adjusted to 1% (wt/vol) N-
 CC lauroylsarcosine and 1% (vol/vol) 2-mercaptoethanol and incubated
 CC while rotating on a mixer for 2.5 hrs at 37 degrees C. The mixt. was
 CC centrifuged at 108,000 g for 35 mins at 20 degrees C. The PHF-tau
 CC contg. pellet was washed with PBS and resuspended in 1ml of the same
 CC buffer. Hybridomas which produced MAb's reactive with tau protein
 CC were obtd. from the spleen cells of Balb/C mice primed s.c. with
 CC partially purified PHF. A MAb which forms an immunological complex
 CC with a human tau protein of sequence in AAR59837 is secreted by the
 CC hybridoma deposited at ECACC on Oct. 8 1992 under No. 92100853.
 XX SQ Sequence 67 AA;

Query Match 100.0%; Score 50; DB 15; Length 67;
 Best Local Similarity 100.0%; Pred. No. 0.74;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSPGSGPCT 9
 DB 43 YSPGSGPCT 51
 |||||

RESULT 10
 AAB85640
 ID AAB85640 standard; peptide; 78 AA.
 AC AAB85640;
 DT 29-OCT-2001 (first entry)
 DE Tau peptide region (residues 155-232).
 KW Tauopathy; phospho-tau (181); neurological marker; monoclonal antibody;
 KW HT7; AT270; neurotropic; neuroprotective; cerobroprotective; epitope.
 XX Homo sapiens.
 XX WO200155725-A2.
 XX PD 02-AUG-2001.
 XX PF 18-JAN-2001; 2001WO-EP00560.
 XX PR 24-JAN-2000; 2000EP-0870008.
 XX PR 27-JAN-2000; 2000US-0178391.
 XX PR 22-NOV-2000; 2000EP-0870280.
 XX PA (INNO-) INNOGENETICS NV.
 XX PI Vanmechelen E, Vanderstichele H;
 XX WPI; 2001-476242/51.
 XX DR Determining the ratio of phospho-tau / total tau is useful for
 XX PT diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease,
 XX PT versus a non tauopathy -
 XX PS Example 1; Fig 1; 71pp; English.
 XX CC The invention provides a method of diagnosis of tauopathies in an
 XX CC individual that comprises determining the ratio of phospho-tau (181)/
 XX CC total tau. Tau and phospho tau are useful as neurological markers for the
 XX CC manufacture of a diagnostic kit for the diagnosis of a tauopathy and/or
 XX CC the differential diagnosis of a tauopathy versus a non tauopathy. A
 XX CC phospho-peptide liable to form an immunological complex with monoclonal
 XX CC antibody HT7 and MAb AT270 comprising at least the minimal epitope of HT7
 XX CC or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy

CC and/or for the differential diagnosis of a tauopathy versus a non
 CC tauopathy. The kit is useful for the diagnosis of Alzheimer's disease,
 CC pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal
 CC dementia with Parkinsonism linked to chromosome 17, Creutzfeldt Jacob
 CC disease, stroke and/or neurotoxicity in patients with leukemia. The
 CC phosphopeptide kits and methods are useful for therapeutic monitoring and
 CC for determining the effectiveness of a treatment. The present sequence
 CC represents a tau peptide fragment.

XX Sequence 78 AA;

Query Match 100.0%; Score 50; DB 22; Length 78;
 Best Local Similarity 100.0%; Pred. No. 0.86;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 43 YSSPGSPGT 51

RESULT 11

AAR92516
 ID AAR92516 standard; peptide; 106 AA.

XX AC AAR92516;

XX DT 20-SEP-1996 (first entry)

XX DE Microtubule-associated tau protein epitope corresp. to pos. 146-251.

XX KW Epitope; microtubule-associated protein; tau; phosphorylation; subclass;
 KW paired helical fibre; neurofibrillary tangle; dementia; neurological;
 KW Alzheimer's disease; monoclonal antibody; brain; pathology.

XX OS Synthetic.

XX PN WO9604309-A1.

XX PD 15-FEB-1996.

XX PF 31-JUL-1995; 95WO-EP03032.

XX PR 29-JUL-1994; 94EP-0870131.

XX PA (INNO-) INNOGENETICS NV.

XX PI Van DE VOORDE A, Vanmechelen E;

XX DR WPI; 1996-129338/13.

XX PT Monoclonal antibodies specific for phosphorylated tau - for improved
 PT detection and diagnosis of e.g. Alzheimer's Disease

XX PS Claim 2; Page 32; 42pp; English.

XX CC This is the amino acid of an epitope derived from the microtubule-
 CC associated tau protein. The phosphorylated subclass of tau protein
 CC from which this epitope originates, forms a major part of the paired
 CC helical fibres which make up neurofibrillary tangles seen in patients
 CC suffering from dementia e.g. Alzheimer's disease. The epitope is esp.
 CC isolated from patients who have recently died from Alzheimer's disease.
 CC It is used to generate monoclonal antibodies for the in vitro detection
 CC or diagnosis of brain/neurological diseases such as Alzheimer's disease
 CC or other diseases where neurofibrillary tangles are a pathological
 CC symptom.

XX Sequence 106 AA;

Query Match 100.0%; Score 50; DB 17; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 52 YSSPGSPGT 60

RESULT 12

AAR76937
 ID AAR76937 standard; Peptide; 112 AA.

XX AC AAR76937;

XX DT 04-DEC-1995 (first entry)

XX DE PHF-tau (143-254) peptide.

XX KW PHF-tau; paired helical filament tau protein; monoclonal antibody;
 KW MAB; phosphorylation; neurological disease; Alzheimer disease;
 KW cerebrospinal fluid.

XX OS Homo sapiens.

XX PN WO9517429-A.

XX PD 29-JUN-1995.

XX PF 14-DEC-1994; 94WO-EP04145.

XX PR 21-DEC-1993; 93EP-0403133.

XX PA (INNO-) INNOGENETICS NV.

XX PI Van De Voorde A, Vandermeeren M, Vanmechelen E;

XX DR WPI; 1995-240616/31.

XX PT Novel monoclonal antibodies specific for abnormally phosphorylated
 PT paired helical filament tau protein (PHF-Tau) - useful for post
 PT mortem or in vitro detection of neurological diseases eg. Alzheimer's
 PT disease

XX PS Claim 1; Page 44; 57pp; English.

XX CC Novel MABs AT180 and AT270 (ECACC 92122204, 93070774) form
 CC immunological complexes with a phosphorylated epitope, given in
 CC AAR76937, of abnormally phosphorylated tau protein (PHF-tau). The
 CC MABs are used to specifically detect PHF-tau in cerebrospinal fluid.

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 50; DB 16; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 55 YSSPGSPGT 63

RESULT 13

AA15200
 ID AA15200 standard; Protein; 351 AA.

XX AC AA15200;

XX DT 28-FEB-2000 (first entry)

XX DE Human Tau protein.

XX KW Human Tau gene; neurofibrillary tangle formation; abnormal tau filament;
 KW brain; mutation; phosphorylation; isoform ratio; diagnosis; tauopathy;
 KW treatment; neurodegenerative disorder; Fronto-Temporal Dementia;

KW Familial Multiple System Tauopathy with presenile Dementia; MSTD;
 KW Pick's Disease; Progressive Supranuclear Palsy; PSP; Alzheimer's Disease;
 KW Corticobasal Degeneration; CD; Prion Protein Cerebral Amyloid Angiopathy;
 KW cognitive disorder.

OS Homo sapiens.

Key Location/Qualifiers
 FT Protein
 FT 1..351
 FT /label= Tau_protein
 FT /note= "Microtubule related protein"

XX WO962548-A1.

XX PD 09-DEC-1999.

XX PF 28-MAY-1999; 99WO-US12036.

XX PR 01-JUN-1998; 98US-0087557.

XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX PI Ghetti B, Spillantini MG, Murrell JR, Goedert M, Farlow MR;
 XX PI Klug A;

XX DR WPI; 2000-086858/07.

XX DR N-PSDB; AAZ29262.

XX PT Diagnosing a tauopathy, especially a Fronto-Temporal Dementia -
 XX PS Disclosure; Page 85; 90pp; English.

XX The present amino acid sequence is a form of human Tau protein.
 CC There are six tau isoforms, expressed in the normal adult brain with a
 CC slight preponderance of those with 3 repeats over those with 4 repeats.
 CC Mutations in the tau gene affects phosphorylation and leads to formation
 CC of neurofibrillary tangles and alters the tau isoform ratio. The
 CC increased ratio of 4:3 repeat and abnormal tau filaments is closely
 CC related to neurodegenerative disorders. This sequence can be used for
 CC diagnosis and treatment of tauopathies, like Fronto-Temporal Dementia,
 CC Familial Multiple System Tauopathy with presenile Dementia (MSTD),
 CC Pick's Disease, Progressive Supranuclear Palsy (PSP), Corticobasal
 CC Degeneration (CD) or Alzheimer's Disease. A composition that decreases
 CC the ratio of 4:3 repeat tau isomers, along with an agent for treatment
 CC of a cognitive disorder, is useful for treating a tauopathy. It may also
 CC be useful in diagnosis of Prion Protein Cerebral Amyloid Angiopathy and
 CC other prion protein associated disease characterized by abnormal tau
 CC filament formation.

XX SQ Sequence 351 AA;

Query Match 100.0%; Score 50; DB 21; Length 351;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 139 ysspgspgt 147
 |||||

RESULT 14

AAP91294

ID AAP91294 standard; protein; 352 AA.

XX AC AAP91294;

XX DT 18-DEC-1989 (first entry)

XX DE Paired helical filament (PHF) core protein.

XX KW Paired helical filament (PHF) core protein; Alzheimer's disease;
 KW neurofibrillary tangles.

XX OS Homo sapiens.
 XX PN WO903993-A.
 XX PD 05-MAY-1989.
 XX PF 19-OCT-1988; 88WO-GB00867.
 XX PR 19-OCT-1987; 87GB-0024412.
 XX PA (MEDI) MEDICAL RESEARCH COUNCIL.
 XX XX Wischik CM, Milstein C, Klug A;
 XX DR WPI; 1989-150854/20.
 XX PT Paired helical filament core protein - used for providing reagents
 PT sensitive to neurofibrillary tangles used for diagnosing Alzheimer's
 PT disease.
 XX PS Disclosure; fig 1; 29pp; English.
 XX CC Paired helical filament core protein was sequenced from DNA obtained
 CC from brain tissue contg. Alzheimer neurofibrillary tangles. The protein
 CC can be used to make MAB's to the PHF core or nucleotide probes, used to
 CC diagnose Alzheimer's disease. The protein sequence QIVYKP (AAs 218-223)
 CC was used to design the probes.
 CC See also AAN91707.
 XX SQ Sequence 352 AA;

Query Match 100.0%; Score 50; DB 10; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 139 ysspgspgt 147
 |||||

RESULT 15

AA32708

ID AAR32708 standard; protein; 352 AA.

XX AC AAR32708;

XX DT 15-JUN-1993 (first entry)

XX DE Human tau-protein.

XX KW Alzheimer's disease; diagnosis; subtyping; monitoring; assay.
 XX OS Homo sapiens.

XX PN WO9303369-A.

XX PD 18-FEB-1993.

XX PF 03-AUG-1992; 92WO-US06382.

XX PR 01-AUG-1991; 91US-0738778.

XX PA (VOOR/) VOORHEIS P H.

XX PI Voorheis PH;

XX DR WPI; 1993-076670/09.

XX DR N-PSDB; AAQ37305.

XX PT Method for diagnosing, subtyping and monitoring Alzheimer's
 PT disease - by assaying a sample of body fluid for the presence of a

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PT tau-peptide using an anti-tau antibody

XX Disclosure; Fig 1; 43pp; English.

XX The sequence is that one form of human tau protein (from Goedert et al., PNAS USA 85: 4051-4055) which was used for the prodn. of anti-tau peptide antibodies. These are used as part of a method for diagnosing, subtyping or monitoring Alzheimer's disease by assaying a sample of body fluid for the presence of a tau-peptide using an anti-tau antibody or the presence of an anti-tau-peptide autoantibody. The methods can be used for confirming a clinical diagnosis of Alzheimer's disease and in following the course of the disease and treatment.

XX Sequence 352 AA;

Query Match 100.0%; Score 50; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
Db 139 yspgspgt 147
|||||

RESULT 16
AAY20248
ID AAY20248 standard; Protein; 352 AA.
XX AC AAY20248;
XX 22-JUL-1999 (first entry)
XX Human microtubule associated protein Tau wild type fragment.
XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M; neurofilament-F; presenilin I; presenilin II; cellular tumour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A.
XX Homo sapiens.
XX WO9845322-A2.
XX 15-OCT-1998.
XX 02-APR-1998; 98WO-IB00705.
XX 10-APR-1997; 97US-0043163.
XX (UYUT-) RIJKSUNIV UTRECHT.
XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
XX (UYRO-) UNIV ROTTERDAM ERASMUS.
XX Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX WPI: 1998-609901/51.
XX N-PSDB; AAX75754.
XX Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA
XX Disclosure; Figure 3; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the use of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A.

XX Sequence 352 AA;

Query Match 100.0%; Score 50; DB 19; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
Db 139 yspgspgt 147
|||||

RESULT 17
AAW05283
ID AAW05283 standard; Protein; 390 AA.
XX AC AAW05283;
XX 20-DEC-1996 (first entry)
XX Truncated human tau protein.
XX Tau protein; inhibition; modulation; prophylaxis; treatment; Alzheimer's disease; motor neurone disease; Lewy body disease; progressive supranuclear palsy; Pick's disease.
XX Homo sapiens.
XX WO9630766-A1.
XX 03-OCT-1996.
XX 25-MAR-1996; 96WO-EP01307.
XX 27-MAR-1995; 95GB-0006197.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
XX WPI: 1996-455570/45.
XX Assay for inhibitors of tau-tau interaction - used for identifying cpds., partic. phenothiazine cpds., for treating pathological tau-tau or neuro-filament aggregation
XX Claim 11; 97pp; English.
XX Detecting an agent which modulates or inhibits tau-tau protein association comprises contacting two tau proteins, distinct from each other yet capable of binding to the other and where one of the tau proteins is labelled, in the presence of the agent suspected of being capable of modulating or inhibiting tau-tau interaction.

CC Agents identified as being modulators or inhibitors of tau-tau
 CC interaction may be used for the prophylaxis and treatment of
 CC Alzheimer's disease, motor neurone disease, Lewy body disease,
 CC Pick's disease or progressive supranuclear palsy. This sequence of
 CC the human tau protein is truncated at amino acid residue 390. The
 CC full length protein is given in AAW05282.
 XX
 SQ Sequence 390 AA;

Query Match 100.0%; Score 50; DB 17; Length 390;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSPGSPCT 9
 Db 197 YSSPGSPGT 205
 |||||

RESULT 18
 AAR5810
 ID AAR5810 standard; protein; 441 AA.
 XX
 AC AAR5810;
 XX
 DT 27-MAR-1995 (first entry)
 DE Human tau protein.
 XX
 KW Tau; cerebrospinal fluid; immunoassay; antibody; detection;
 KW diagnosis; central nervous system; CNS; cytopathies; cytopathy;
 XX Alzheimer's disease.
 OS Homo sapiens.
 XX
 PN WO9418560-A.
 XX
 PD 18-AUG-1994.
 XX
 PF 10-FEB-1994; 94WO-JP00196.
 XX
 PR 12-FEB-1993; 93JP-0046133.
 XX
 PA (TEIJ) TEIJIN LTD.
 XX
 PI Etsuji H, Hosoda K, Kobayashi S, Kubota T, Mori H;
 PI Nakamoto T;
 XX
 DR WPI; 1994-279910/34.
 XX

Sandwich immunoassay of tau protein in cerebrospinal fluid - for
 diagnosis of Alzheimer's disease and other CNS cytopathies
 Claim 1; Page 16-18; 36pp; Japanese.
 CC
 CC Detection of the human tau protein (or fragments of it) in samples
 CC of cerebrospinal fluid enables the diagnosis of central nervous
 CC system cytopathies such as Alzheimer's disease. Detection is
 CC performed using labelled antibodies which recognise sites within the
 CC region defined by the amino acid residues 251-441. The antibodies
 CC are preferably polyclonal.
 XX
 SQ Sequence 441 AA;

Query Match 100.0%; Score 50; DB 15; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSPGSPCT 9
 Db 197 YSSPGSPGT 205
 |||||

RESULT 19
 AAW05282
 ID AAW05282 standard; Protein; 441 AA.
 XX
 AC AAW05282;
 XX
 DT 20-DEC-1996 (first entry)
 DE Human tau protein.
 XX
 KW Tau protein; inhibition; modulation; prophylaxis; treatment;
 KW Alzheimer's disease; motor neurone disease; Lewy body disease;
 KW progressive supranuclear palsy; Pick's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9630766-A1.
 XX
 PD 03-OCT-1996.
 XX
 PF 25-MAR-1996; 96WO-EP01307.
 XX
 PR 27-MAR-1995; 95GB-0006197.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
 XX
 DR WPI; 1996-455570/45.
 DR N-PSDB; AAT39591.
 XX
 PT Assay for inhibitors of tau-tau interaction - used for identifying
 PT cpds., partic. phenothiazine cpds., for treating pathological
 PT tau-tau or neuro:fibril aggregation
 XX
 PS Example 2; Page 53-54; 97pp; English.
 CC
 CC Detecting an agent which modulates or inhibits tau-tau protein
 CC association comprises contacting two tau proteins, distinct from
 CC each other yet capable of binding to the other and where one of the
 CC tau proteins is labelled, in the presence of the agent suspected of
 CC being capable of modulating or inhibiting tau-tau interaction.
 CC Agents identified as being modulators or inhibitors of tau-tau
 CC interaction may be used for the prophylaxis and treatment of
 CC Alzheimer's disease, motor neurone disease, Lewy body disease,
 CC Pick's disease or progressive supranuclear palsy.
 XX
 SQ Sequence 441 AA;

Query Match 100.0%; Score 50; DB 17; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSPGSPCT 9
 Db 197 YSSPGSPGT 205
 |||||

RESULT 20
 AAW34856
 ID AAW34856 standard; protein; 441 AA.
 XX
 AC AAW34856;
 XX
 DT 27-MAR-1998 (first entry)
 DE Human tau protein.
 XX
 KW Antibody; phosphorylated tau protein; paired helical filament;
 KW detection; Alzheimer's disease; human.
 XX

OS Homo sapiens.
 PN WO9734145-A1.
 XX 18-SEP-1997.
 PD
 XX 13-MAR-1997; 97WO-JP00804.
 PF
 XX 13-MAR-1996; 96JP-0056090.
 PR
 XX (MITU) MITSUBISHI CHEM CORP.
 PA
 FI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
 XX WPI; 1997-470978/43.
 DR
 XX Antibody prepared using a partial peptide containing part of
 PT phosphorylated tau protein - used for detecting Alzheimer's disease
 PT
 XX Claim 2; Pages 25-27; 48pp; Japanese.
 PS
 XX An antibody, prepared using a partial peptide containing the
 CC phosphorylated residue of the phosphorylated tau protein, e.g. the
 CC present sequence, in a paired helical filament, can be used to
 CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 CC protein in brain extracts or tissue fragments.
 CC
 XX Sequence 441 AA;
 SQ

Query Match 100.0%; Score 50; DB 18; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSPGSPGT 9
 DB 197 ysspgspgt 205
 I|||||

RESULT 21
 AAY81386
 ID AAY81386 standard; protein; 441 AA.
 XX
 AC AAY81386;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Human paired helical filament phosphorylated tau protein.
 XX
 KW phosphorylated tau protein; human; paired helical filament;
 KW polyclonal antibody; Alzheimer's disease; cerebrospinal fluid; CSF;
 KW diagnosis; detection.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 199 /note= "Phosphorylated"
 FT Modified-site 231 /note= "Phosphorylated"
 FT Modified-site 235 /note= "Phosphorylated"
 FT
 FT JP2000034300-A.
 XX
 PN
 XX 02-FEB-2000.
 PD
 XX 17-JUL-1998; 98JP-0204040.
 PF
 XX 17-JUL-1998; 98JP-0204040.
 PR
 XX (MITU) MITSUBISHI CHEM CORP.
 XX
 PA

DR WPI; 2000-285529/25.
 XX Anti-phosphated tau protein antibody - for the detection of Alzheimer
 PT disease
 PT
 XX Claim 1; Page 8-9; 12pp; Japanese.
 PS
 XX The invention relates to an antibody against a phosphorylated tau
 CC protein (AAY81386), which is a component of the paired helical filament
 CC found in the plaques associated with Alzheimer's disease. A
 CC phosphorylated tau protein fragment selected from peptides
 CC AAY81387-Y81390 is conjugated to keyhole limpet haemocyanin (KLH), and
 CC used to raise polyclonal antibodies in a rabbit. The antibodies of the
 CC invention are specific for phosphorylated tau protein and may be used to
 CC detect phosphorylated tau protein in the cerebrospinal fluid (CSF) of a
 CC patient suspected of having Alzheimer's disease. Use of the antibodies of
 CC the invention provides specific diagnosis of Alzheimer's disease. The
 CC present sequence represents phosphorylated tau protein.
 XX
 XX Sequence 441 AA;
 SQ

Query Match 100.0%; Score 50; DB 21; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSPGSPGT 9
 DB 197 ysspgspgt 205
 I|||||

RESULT 22
 AAR28237
 ID AAR28237 standard; peptide; 13 AA.
 XX
 AC AAR28237;
 XX
 DT 18-MAR-1993 (first entry)
 XX
 DE Phosphopeptide as Alzheimers's disease detection antigen.
 XX
 KW AD; antigen; antibody; paired helical filament; PHF; brain.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 6 /note= "at least one of Ser6 and Thr9 is modified
 FT by PO(OH)"
 FT Modified-site 9 /note= "at least one of Ser6 and Thr9 is modified
 FT by PO(OH)"
 FT Modified-site 13 /note= "the C-terminal is amidated"
 FT
 FT JP04270299-A.
 XX
 PN
 XX 25-SEP-1992.
 PD
 XX 25-FEB-1991; 91JP-0146476.
 PF
 XX 25-FEB-1991; 91JP-0146476.
 PR
 XX (MITU) MITSUBISHI KASEI CORP.
 XX
 PA WPI; 1992-369427/45.
 XX
 DR New phosphopeptide(s) - useful as antigen for detection of
 XX Alzheimer's disease
 PT
 XX Claim 1; Page 2; 4pp; Japanese.
 PS
 XX The C-terminal of the peptide is amidated.
 XX
 CC

CC The phosphopeptide is useful as antigen for preparing antibody
 CC against paired helical filaments (PHF) present in brain of patients
 CC with Alzheimer's disease.
 XX
 SQ Sequence 13 AA;

Query Match 86.0%; Score 43; DB 13; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSPGSPGT 9
 Db 2 sspgspgt 9
 |||||

RESULT 23
 AAW34860
 ID AAW34860 standard; peptide; 13 AA.
 XX
 AC AAW34860;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Human tau protein fragment.
 XX
 KW Antibody; phosphorylated tau protein; paired helical filament;
 KW detection; Alzheimer's disease; human.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT Modified-site 3
 FT Modified-site 6 /note= "phosphoserine"
 FT Modified-site 6 /note= "phosphoserine"
 FT
 PN WO9734145-A1.
 XX
 PD 18-SEP-1997.

PF 13-MAR-1997; 97WO-JP00804.
 XX
 PR 13-MAR-1996; 96JP-0056090.
 XX
 PA (MITU) MITSUBISHI CHEM CORP.

PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
 DR WPI; 1997-470978/43.

PT Antibody prepared using a partial peptide containing part of
 PT phosphorylated tau protein - used for detecting Alzheimer's disease
 XX
 PS Example; Page 29; 48pp; Japanese.

CC An antibody, prepared using a partial peptide containing the
 CC phosphorylated residue of the phosphorylated tau protein, e.g. the
 CC present sequence, in a paired helical filament, can be used to
 CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 CC protein in brain extracts or tissue fragments.
 XX
 SQ Sequence 13 AA;

Query Match 86.0%; Score 43; DB 18; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSPGSPGT 9
 Db 2 sspgspgt 9
 |||||

RESULT 24
 AAW34858
 ID AAW34858 standard; peptide; 13 AA.
 XX
 AC AAW34858;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Human tau protein fragment.
 XX
 KW Antibody; phosphorylated tau protein; paired helical filament;
 KW detection; Alzheimer's disease; human.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT Modified-site 6
 FT Modified-site 6 /note= "phosphoserine"
 FT
 PN WO9734145-A1.
 XX
 PD 18-SEP-1997.
 XX
 PF 13-MAR-1997; 97WO-JP00804.
 XX
 PR 13-MAR-1996; 96JP-0056090.
 XX
 PA (MITU) MITSUBISHI CHEM CORP.

PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
 DR WPI; 1997-470978/43.
 XX
 PT Antibody prepared using a partial peptide containing part of
 PT phosphorylated tau protein - used for detecting Alzheimer's disease
 XX
 PS Example; Page 28; 48pp; Japanese.
 XX
 CC An antibody, prepared using a partial peptide containing the
 CC phosphorylated residue of the phosphorylated tau protein, e.g. the
 CC present sequence, in a paired helical filament, can be used to
 CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 CC protein in brain extracts or tissue fragments.
 XX
 SQ Sequence 13 AA;

Query Match 86.0%; Score 43; DB 18; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 Db 2 sspgspgt 9
 |||||

RESULT 25
 AAW29455
 ID AAW29455 standard; Protein; 263 AA.
 XX
 AC AAW29455;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Oerskovia xanthineolytica mature beta-1,3-glucanase.

Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
 fungal cell wall; intracellular product; purification; protoplast.
 XX
 OS Oerskovia xanthineolytica LMG109 (DSM 10297).
 XX
 FH Key Location/Qualifiers

us-09-734-281-1.rag

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XX FH Key Location/Qualifiers
FT FT 1..52
FT FT /label= sig_peptide
FT FT 53..435
FT FT /label= Mat_protein
FT FT 304..435
FT FT /label= Mannose-binding_domain
XX PN WO9739114-A1.
XX PN 23-OCT-1997.
XX PD
XX PF 14-APR-1997; 97WO-DK00160.
XX PR 23-AUG-1996; 96DK-0000885.
XX PR 12-APR-1996; 96DK-0000427.
XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Diers I, Ferrer P, Halkier T, Hedegaard L;
XX PI WPI; 1997-526451/48.
XX DR N-PSDB; AAT89156.
XX CC New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia
XX CC xanthineolytica, used particularly for the lysis of microbial cells
XX CC for obtaining desirable products
XX PS Example 2; Page 35-36; 64pp; English.
XX CC This polypeptide comprises a novel Oerskovia xanthineolytica (OX)
XX CC enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino
XX CC acid sequence was deduced from an isolated genomic DNA sequence
XX CC (see AAT89155). Claimed DNA constructs that encode the novel BG (see
XX CC also AAW29456 for corrected sequence), a mannose binding domain (see
XX CC AAW29458) or a full-length enzyme, i.e. BG with mannose binding
XX CC domain (see AAW29456), can be used to produce recombinant BG
XX CC polypeptides, with or without a mannose binding domain, in fungal
XX CC or bacterial host cells. BG polypeptides are used for the
XX CC degradation or modification of beta-glucan containing material,
XX CC especially for the gentle lysis of microbial cell walls, thereby
XX CC enabling recovery of desirable intracellular products with a
XX CC reduced amount of contaminants. They can also be used for the
XX CC production of e.g. pigments, colourants, flavourants, yeast
XX CC extracts, pharmaceuticals, food or feed compositions, and to
XX CC prepare protoplasts for use in fusion, transformation and cloning
XX CC studies.
XX CC Sequence 263 AA;
XX SQ
XX Query Match 80.0%; Score 40; DB 18; Length 263;
XX Best Local Similarity 87.5%; Pred. No. 1e+02;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 2 SSPGSPGT 9
XX Db 244 sspgpnpgt 251
XX RESULT 26
XX AAW29456
XX ID AAW29456 standard; Protein; 435 AA.
XX AC AAW29456;
XX AC
XX DT 14-APR-1998 (first entry)
XX DE Oerskovia xanthineolytica beta-1,3-glucanase.
XX DE
XX DE Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
XX KW fungal cell wall; intracellular product; purification; protoplast.
XX KW Oerskovia xanthineolytica LIG109 (DSM 10297).
XX OS
XX Query Match 80.0%; Score 40; DB 18; Length 435;
XX Best Local Similarity 87.5%; Pred. No. 1.6e+02;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 2 SSPGSPGT 9
XX Db 297 sspgpnpgt 304
XX RESULT 27
XX AAR38233
XX ID AAR38233 standard; peptide; 7 AA.
XX AC AAR38233;
XX AC
XX DT 08-OCT-1993 (first entry)
XX DE Alzheimer paired helical filament tau protein epitope 197-203.
XX DE
XX DE Alzheimer tau protein; phosphorylation-dependent; PHF;
XX KW neuronal microtubule; mitogen activated protein kinase; MAP kinase.
XX KW

```

XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Modified-site 3..4 /label= Phosphorylation_motif
 FT Modified-site 6..7 /label= Phosphorylation_motif
 XX FT
 PN WQ9311231-A.
 XX PD
 XX PD 10-JUN-1993.
 XX PF
 XX PF 07-DEC-1992; 92WO-EP02829.
 XX PR
 XX PR 06-DEC-1991; 91EP-0120974.
 XX PR 16-NOV-1992; 92EP-0119551.
 XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;
 XX PI Steiner B;
 XX DR WPI; 1993-197050/24.
 XX PT Tau protein epitope(s), specific antibodies and protein kinase(s)
 PT - used in the prevention, diagnosis and treatment of Alzheimer's
 PT disease
 XX PS
 PS Claim 5; Page 89; 148pp; English.
 CC This is one of 26 preferred epitopes which occur in a phosphorylated
 CC state in tau protein from Alzheimer paired helical filaments. The
 CC epitopes all include phosphorylatable serine residues in Ser-Pro
 CC motifs, ile-gly-Ser motifs or Cys-Gly-Ser motifs and/or
 CC phosphorylatable threonine residues in Thr-Pro motifs. The pattern
 CC of tau protein phosphorylation differs between Alzheimer's and
 CC non-Alzheimer's individuals. Knowledge of the phosphorylated
 CC epitopes and antibodies which recognise them may be useful in
 CC diagnosis, treatment and prevention of Alzheimer's Disease. The
 CC protein kinases present in mammalian brain which phosphorylate the
 CC different epitopes are also claimed but no sequences are given.
 XX SQ Sequence 7 AA;

Query Match 78.0%; Score 39; DB 14; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSPGSP 7
 |||||
 Db 1 yspgsp 7

RESULT 28
 AAR37552
 ID AAR37552 standard; peptide; 7 AA.
 XX AC
 AC AAR37552;

DT 07-OCT-1993 (first entry)

XX Phosphorylated tau protein epitope.

DE Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
 KW treatment; formation; inhibition; inhibitor.
 XX OS Homo sapiens.

XX EP544942-A.
 XX PN
 XX PD 09-JUN-1993.

XX 06-DEC-1991; 91EP-0120974.
 PF 06-DEC-1991; 91EP-0120974.
 XX PR
 XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow EM, Steiner B;
 XX PI WPI; 1993-183841/23.
 XX DR
 XX DR phosphorylated tau protein epitope associated with Alzheimer's
 PT disease - is used as protein kinase inhibitor for treatment and
 PT diagnosis
 XX PS
 PS Claim 4; Page 16; 34pp; English.
 XX CC The sequence is that of an epitope of tau protein which specifically
 CC occurs in a phosphorylated state in tau protein from Alzheimer's
 CC paired helical fragments. It may be used as part of a method for the
 CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
 CC also be used in an in vitro model for the study of the generation of
 CC the Alzheimer state of proteins and the testing of substances which
 CC prevent the conversion of normal to Alzheimer tau protein. The
 CC epitope occurs at residues 197-203 of human tau protein.
 XX SQ Sequence 7 AA;

Query Match 78.0%; Score 39; DB 14; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSPGSP 7
 |||||
 Db 1 yspgsp 7

RESULT 29
 AAU17141
 ID AAU17141 standard; Protein; 263 AA.
 XX AC
 AC AAU17141;
 XX DT
 DT 07-NOV-2001 (first entry)
 XX DE
 DE Novel signal transduction pathway protein, Seq ID 706.
 XX KW
 KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;
 KW organ transplant rejection; infection; hepatitis C; blood disorder;
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW chromosomal abnormality; Down syndrome; Ischaemia; renal disorder;
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 KW reproductive system; gastrointestinal; liver disorder; AIDS;
 XX XX acquired immune deficiency syndrome.
 OS Homo sapiens.
 XX PN
 PN WO200154733-A1.
 XX XX
 XX PD 02-AUG-2001.
 XX PF
 PF 17-JAN-2001; 2001WO-US01312.
 XX PR
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.

us-09-734-281-1.l.rag

Wed May 22 11:04:22 2002

PR	18-APR-2000;	2000US-0198123.	PR	20-OCT-2000;	2000US-0240960.
PR	19-MAY-2000;	2000US-0205515.	PR	20-OCT-2000;	2000US-0241221.
PR	07-JUN-2000;	2000US-0209467.	PR	20-OCT-2000;	2000US-0241785.
PR	28-JUN-2000;	2000US-0214886.	PR	20-OCT-2000;	2000US-0241787.
PR	30-JUN-2000;	2000US-0215135.	PR	20-OCT-2000;	2000US-0241808.
PR	07-JUL-2000;	2000US-0216647.	PR	20-OCT-2000;	2000US-0241809.
PR	07-JUL-2000;	2000US-0216880.	PR	20-OCT-2000;	2000US-0241826.
PR	11-JUL-2000;	2000US-0217487.	PR	01-NOV-2000;	2000US-0244617.
PR	11-JUL-2000;	2000US-0217496.	PR	08-NOV-2000;	2000US-0244674.
PR	14-JUL-2000;	2000US-0218230.	PR	08-NOV-2000;	2000US-0246475.
PR	26-JUL-2000;	2000US-0220963.	PR	08-NOV-2000;	2000US-0246476.
PR	26-JUL-2000;	2000US-0220964.	PR	08-NOV-2000;	2000US-0246477.
PR	14-AUG-2000;	2000US-0224518.	PR	08-NOV-2000;	2000US-0246478.
PR	14-AUG-2000;	2000US-0224519.	PR	08-NOV-2000;	2000US-0246523.
PR	14-AUG-2000;	2000US-0225213.	PR	08-NOV-2000;	2000US-0246524.
PR	14-AUG-2000;	2000US-0225214.	PR	08-NOV-2000;	2000US-0246525.
PR	14-AUG-2000;	2000US-0225266.	PR	08-NOV-2000;	2000US-0246526.
PR	14-AUG-2000;	2000US-0225267.	PR	08-NOV-2000;	2000US-0246527.
PR	14-AUG-2000;	2000US-0225268.	PR	08-NOV-2000;	2000US-0246528.
PR	14-AUG-2000;	2000US-0225270.	PR	08-NOV-2000;	2000US-0246532.
PR	14-AUG-2000;	2000US-0225447.	PR	08-NOV-2000;	2000US-0246609.
PR	14-AUG-2000;	2000US-0225577.	PR	08-NOV-2000;	2000US-0246610.
PR	14-AUG-2000;	2000US-0225758.	PR	08-NOV-2000;	2000US-0246611.
PR	14-AUG-2000;	2000US-0225759.	PR	08-NOV-2000;	2000US-0246613.
PR	14-AUG-2000;	2000US-0226279.	PR	08-NOV-2000;	2000US-0249207.
PR	18-AUG-2000;	2000US-0226681.	PR	17-NOV-2000;	2000US-0249208.
PR	22-AUG-2000;	2000US-0226868.	PR	17-NOV-2000;	2000US-0249209.
PR	22-AUG-2000;	2000US-0227182.	PR	17-NOV-2000;	2000US-0249210.
PR	23-AUG-2000;	2000US-0227009.	PR	17-NOV-2000;	2000US-0249211.
PR	30-AUG-2000;	2000US-0228924.	PR	17-NOV-2000;	2000US-0249212.
PR	01-SEP-2000;	2000US-0229287.	PR	17-NOV-2000;	2000US-0249213.
PR	01-SEP-2000;	2000US-0229343.	PR	17-NOV-2000;	2000US-0249214.
PR	01-SEP-2000;	2000US-0229344.	PR	17-NOV-2000;	2000US-0249215.
PR	01-SEP-2000;	2000US-0229345.	PR	17-NOV-2000;	2000US-0249216.
PR	05-SEP-2000;	2000US-0229509.	PR	17-NOV-2000;	2000US-0249217.
PR	05-SEP-2000;	2000US-0229513.	PR	17-NOV-2000;	2000US-0249218.
PR	06-SEP-2000;	2000US-0230437.	PR	17-NOV-2000;	2000US-0249244.
PR	06-SEP-2000;	2000US-0230438.	PR	17-NOV-2000;	2000US-0249245.
PR	08-SEP-2000;	2000US-0231242.	PR	17-NOV-2000;	2000US-0249264.
PR	08-SEP-2000;	2000US-0231243.	PR	17-NOV-2000;	2000US-0249265.
PR	08-SEP-2000;	2000US-0231244.	PR	17-NOV-2000;	2000US-0249266.
PR	08-SEP-2000;	2000US-0231413.	PR	17-NOV-2000;	2000US-0249297.
PR	08-SEP-2000;	2000US-0231414.	PR	17-NOV-2000;	2000US-0249299.
PR	08-SEP-2000;	2000US-0232080.	PR	17-NOV-2000;	2000US-0249300.
PR	08-SEP-2000;	2000US-0232081.	PR	01-DEC-2000;	2000US-0250160.
PR	12-SEP-2000;	2000US-0232081.	PR	01-DEC-2000;	2000US-0250391.
PR	12-SEP-2000;	2000US-0232397.	PR	05-DEC-2000;	2000US-0251030.
PR	14-SEP-2000;	2000US-0232398.	PR	05-DEC-2000;	2000US-0251988.
PR	14-SEP-2000;	2000US-0232399.	PR	05-DEC-2000;	2000US-0256719.
PR	14-SEP-2000;	2000US-0232400.	PR	06-DEC-2000;	2000US-0251479.
PR	14-SEP-2000;	2000US-0232401.	PR	08-DEC-2000;	2000US-0251856.
PR	14-SEP-2000;	2000US-0233063.	PR	08-DEC-2000;	2000US-0251868.
PR	14-SEP-2000;	2000US-0233084.	PR	08-DEC-2000;	2000US-0251869.
PR	14-SEP-2000;	2000US-0233085.	PR	08-DEC-2000;	2000US-0251989.
PR	21-SEP-2000;	2000US-0234223.	PR	08-DEC-2000;	2000US-0251990.
PR	21-SEP-2000;	2000US-0234274.	PR	11-DEC-2000;	2000US-0254097.
PR	25-SEP-2000;	2000US-0234997.	PR	05-JAN-2001;	2001US-0259678.
PR	25-SEP-2000;	2000US-0235484.	XX		
PR	26-SEP-2000;	2000US-0235834.	PA		
PR	27-SEP-2000;	2000US-0235836.			
PR	29-SEP-2000;	2000US-0236327.			
PR	29-SEP-2000;	2000US-0236367.			
PR	29-SEP-2000;	2000US-0236368.			
PR	29-SEP-2000;	2000US-0236369.			
PR	29-SEP-2000;	2000US-0236370.			
PR	02-OCT-2000;	2000US-0236802.			
PR	02-OCT-2000;	2000US-0237037.			
PR	02-OCT-2000;	2000US-0237038.			
PR	02-OCT-2000;	2000US-0237039.			
PR	02-OCT-2000;	2000US-0237040.			
PR	13-OCT-2000;	2000US-0239935.			
PR	13-OCT-2000;	2000US-0239937.			

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;
WPI; 2001-465460/50.
N-PSDB; AAS27058.

Novel polypeptides useful for diagnosing, treating, preventing and/or
prognosing disorders related to the proteins, including cancers, immune
disorders and neuronal disorders -

Claim 1; SEQ ID No 706; 880pp; English.

The invention relates to novel isolated polypeptides (I), and
polynucleotides (II). (I), (II) and the antibody to (I) are useful for

CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B-cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction
 CC pathway protein, amino acid sequences of the invention.
 XX

Query Match 78.0%; Score 39; DB 22; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPT 9
 Db 180 spgspt 186
 |||||

RESULT 30

AA080057
 ID AA080057 standard; Protein; 376 AA.

AC AA080057;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3703.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

PN W0200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;

PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wehrman T, Goodrich R;

XX WPI: 2001-476283/51.

DR N-PSDB; AAK53190.

XX Nucleic acids encoding polypeptides with cytokine-like activities,

PT

PT useful in diagnosis and gene therapy -
 XX Claim 20; Page 415; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC actin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX Sequence 376 AA;

Query Match 78.0%; Score 39; DB 22; Length 376;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPT 9

Db 358 spgspt 364
 |||||

RESULT 31

AA041838
 ID AAB41838 standard; Protein; 424 AA.

XX AAB41838;

DT 08-FEB-2001 (first entry)

DE Human ORF1602 polypeptide sequence SEQ ID NO:3204.

KW Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antineoplastic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antineoplastic disease; coagulation;
 KW thrombosis; contraceptive.

OS Homo sapiens.

PN W0200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08621.

PR 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

PA (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX

Wed May 22 11:04:22 2002

us-09-734-281-1.l.rag

DR WPI; 2000-602362/57.
 XX N-PSDB; AAC76047.
 XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 XX Claim 11; Page 2417-2418; 5507pp; English.
 XX
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
 CC antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
 CC osteoprotective; anticonvulsant; antiarthritic; immunosuppressant;
 CC osteoparalytic; cardiatic; thrombolytic; coagulant; vasotropic;
 CC immunostimulant; cardiant; dermatological; immunosuppressive;
 CC antidiabetic; hypotensive; antitubercular; antiviral; antifungal; antirheumatic;
 CC antiinflammatory; antibacterial; antitumor; antiparasitic; antiparasitic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 XX Sequence 424 AA;

Query Match 78.0%; Score 39; DB 21; Length 424;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 Db 341 spgspgt 347
 |||||

RESULT 32
 AAM79073
 ID AAM79073 standard; Protein: 424 AA.
 XX
 XX AAM79073;
 XX
 XX 06-NOV-2001 (first entry)
 DT Human protein SEQ ID NO 1735.
 DE
 DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 XX Homo sapiens.
 OS
 XX WO200157190-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 05-FEB-2001; 2001WO-US04098.
 PF
 XX 03-FEB-2000; 2000US-0496914.
 PR
 XX 27-APR-2000; 2000US-0560875.
 PR
 XX 20-JUN-2000; 2000US-0598075.
 PR
 XX 19-JUL-2000; 2000US-0620325.
 PR
 XX 01-SEP-2000; 2000US-0654936.
 PR
 XX 15-SEP-2000; 2000US-0663561.
 PR
 XX 20-OCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.
 (HYSE-) HYSEQ INC.
 Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAK52200.
 XX
 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 XX Claim 20; Page 4070-4071; 6221pp; English.
 XX
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides have various cytokine-like activities,
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX
 XX Sequence 424 AA;

Query Match 78.0%; Score 39; DB 22; Length 424;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 Db 341 spgspgt 347
 |||||

RESULT 33
 AAB27227
 ID AAB27227 standard; Protein: 424 AA.
 XX
 XX AAB27227;
 XX
 XX 27-MAR-2001 (first entry)
 DT Human EXMAD-5 SEQ ID NO: 5.
 DE
 DE Extracellular matrix and adhesion-associated protein; EXMAD; cancer;
 KW inflammation; reproductive disorder; cardiovascular disorder;
 KW immune disorder; musculoskeletal disorder; developmental disorder;
 KW gastrointestinal disorder; cell proliferation disorder.
 XX
 XX Homo sapiens.
 OS
 XX WO2000068380-A2.
 PN
 XX 16-NOV-2000.
 PD
 XX 10-MAY-2000; 2000WO-US12811.
 PF
 XX 11-MAY-1999; 99US-0133643.
 PR
 XX 23-AUG-1999; 99US-0150409.
 PR
 XX (INCY-) INCYTE GENOMICS INC.
 PA Bandman O, Hillman JL, Tang YT, Lal P, Yue H, Baughn MR, Lu DAM;
 XX Azimzai Y;
 PI

XX WPI: 2001-007395/01.
 DR N-PSDB; AAC66894.
 XX
 PT Isolated polynucleotide encoding extracellular matrix or
 PT adhesion-associated protein (EXMAD) useful for diagnosing, treating, or
 PT preventing disorders associated with expression of EXMAD such as
 PT proliferative, immune and genetic disorders -
 XX
 PS Claim 1: Page 92-93; 129pp; English.
 XX
 CC The present invention provides the protein and coding sequences for 25
 CC novel extracellular matrix and adhesion-associated proteins (EXMADS).
 CC These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-5,
 CC EXMAD-6, EXMAD-7, EXMAD-8, EXMAD-9, EXMAD-10, EXMAD-11, EXMAD-12,
 CC EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-18, EXMAD-19,
 CC EXMAD-20, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24 and EXMAD-25. They are
 CC useful in the prevention and treatment of cancers, cell proliferation,
 CC cardiovascular, reproductive, immune, musculoskeletal, developmental and
 CC gastrointestinal disorders and inflammation.
 XX
 SQ Sequence 424 AA;
 CC
 Query Match 78.0%; Score 39; DB 22; Length 424;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SPGSPCT 9
 DB 341 SPGSPGT 347
 |||||
 RESULT 34
 AAO05662
 ID AAO05662 standard; Protein: 98 AA.
 XX
 AC AAO05662;
 XX
 DT 06-NOV-2001 (first entry)
 DE Human polypeptide SEQ ID NO 19554.
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 XX
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-514838/56.
 DR N-PSDB; AAI85593.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 19554; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and

CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence 98 AA;
 CC
 Query Match 76.0%; Score 38; DB 22; Length 98;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SPGSPG 8
 DB 79 SPGSPG 85
 |||||
 RESULT 35
 ABG27348
 ID ABG27348 standard; Protein: 284 AA.
 XX
 AC ABG27348;
 XX
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #27339.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 XX
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS91535.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 57707; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABC30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 284 AA;

Query Match 74.0%; Score 37; DB 22; Length 284;

Best Local Similarity 75.0%; Pred. No. 3.2e+02; 0;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YSSPGSPG 8
 : : |||||

Db 56 fgspspg 63

RESULT 36

AAR25063
 ID AAR25063 standard; Protein; 335 AA.

AC AAR25063;

DT 10-DEC-1992 (first entry)

DE Soluble human IL-5 receptor alpha chain.

KW Soluble interleukin-5; chronic asthma; eosinophilia;
 screening antagonists; ss.

OS Homo sapiens.

PN EP492214-A.

PP 01-JUL-1992.

PF 06-DEC-1991; 91EP-0120951.

PR 27-DEC-1990; 90EP-0811030.

PR 30-APR-1991; 91EP-0810327.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Devos R, Fiers W, Plaetinck G, Tavernier J, Van Der Hayden J;

DR WPI; 1992-218502/27.

DR N-PSDB; AAQ25789.

XX Recombinant alpha chain of human interleukin-5 receptor - and DNA
 PT encoding it, for treatment of interleukin-5 mediated disorders
 PT such as chronic asthma

PS Claim 7; Fig 1; 15pp; English.

XX This amino acid sequence was deduced from the nucleotide sequence,
 CC isolated as detailed in AAQ25789. Recombinant IL-5 alpha chain can be
 CC used as an IL-5 antagonist in chronic asthma or other disease
 CC states with demonstrated eosinophilia. It may also be used either
 CC alone or with the beta chain of the whole IL-5 receptor as a tool
 CC for screening for IL-5 antagonists. See also AAQ25790-2, AAQ30767,8
 CC AAR25064.

XX Sequence 335 AA;

Query Match 74.0%; Score 37; DB 13; Length 335;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YSSPGSPGT 9
 : : |||||

Db 119 happgspt 127

RESULT 37

AAR33699
 ID AAR33699 standard; Protein; 335 AA.

AC AAR33699;

DT 09-JUL-1993 (first entry)

DE shIL-5R-alpha.

KW Probe; murine; interleukin-5; IL-5; receptor; IL-5R; IL-5R-alpha; IgG;
 chain; human; hIL-5R; constant domain; heavy; light; immunoglobulin;
 IGA; IgM; IgE; chimeric protein; antagonist; asthma; half-life.

OS Synthetic.

PN EP533006-A.

PP 24-MAR-1993.

PP 05-SEP-1992; 92EP-0115246.

PR 18-SEP-1991; 91EP-0810738.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Devos R, Fiers W, Tavernier J;

DR WPI; 1993-095341/12.

DR N-PSDB; AAQ38440.

XX Deoxyribonucleic acid sequence for chimeric polypeptide prodn. -
 PT comprises parts coding fragment of alpha and/or beta chain of
 PT human interleukin-5 receptor and heavy or light chain of
 PT immunoglobulin, for chronic asthma treatment

PS Disclosure; Fig 1; 17pp; English.

XX The sequence given represents soluble human interleukin-5 (IL-5)
 CC receptor (IL-5R)-alpha chain. This sequence was used in the
 CC construction of a chimeric human IL-5R-alpha-IgG1 molecule. Chimeric
 CC proteins such as this can be used as IL-5 antagonists in the treatment
 CC of diseases, esp. chronic asthma. The chimeric proteins have an
 CC increased half-life in vivo compared to hIL-5R. See also AAQ38433-40.

XX Sequence 335 AA;

Query Match 74.0%; Score 37; DB 14; Length 335;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YSSPGSPGT 9
 : : |||||

Db 119 happgspt 127

RESULT 38

AAM93217
 ID AAM93217 standard; Protein; 350 AA.

AC AAM93217;

DT 06-NOV-2001 (first entry)

XX DE Human polypeptide, SEQ ID NO: 2622.
 XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX OS Homo sapiens.
 XX PN EP1130094-A2.
 XX PD 05-SEP-2001.
 XX PF 07-JUL-2000; 2000EP-0114089.
 XX PR 08-JUL-1999; 99JP-0194486.
 XX PR 11-JAN-2000; 2000JP-0118774.
 XX PR 02-MAY-2000; 2000JP-0183765.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX DR WPI: 2001-524255/58.
 XX DR N-PSDB; AAK94126.
 XX PT 830 Primers useful for synthesizing full length cDNA clones and their
 XX PT use in genetic manipulation -
 XX PS Claim 8; SEQ ID NO 2622; 1380pp + sequence listing; English.
 XX CC The invention relates to primers for synthesizing full length cDNA
 XX CC clones. 830 cDNA molecules encoding a human protein have been
 XX CC isolated and nucleotide sequences of 5' and 3'-ends of the cDNA
 XX CC molecules have been determined. Primers for synthesizing the full length
 XX CC cDNA are useful for clarifying the function of the protein encoded by
 XX CC the cDNA. The full length clones were obtained by construction of full
 XX CC length enriched cDNA libraries that were synthesised by the oligo-capping
 XX CC method. The primers enable the production of the full length cDNA easily
 XX CC without any special methods. The present sequence is a polypeptide
 XX CC encoded by a full length human cDNA of the invention.
 XX CC Note: The sequence data for this patent did not form part of the printed
 XX CC specification, but was obtained in CD-ROM format directly from EPO.
 XX SQ Sequence 350 AA;

Query Match 74.0%; Score 37; DB 22; Length 350;
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 Db 249 ftspgpggt 257

RESULT 39

AAM52310
 ID AAM52310 standard; Protein; 351 AA.
 XX AC AAM52310;
 XX DT 18-JAN-2002 (first entry)
 XX DE Chicken zyxine fragment.
 XX KW Actin polymerisation; Ena/VASP; vasodilator-stimulated phosphoprotein;
 XX KW metastatic cancer; parasitic infection; cytotoxic; Chicken; zyxine.
 XX OS Gallus gallus.
 XX PN WO200171356-A2.
 XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-FR00843.
 XX PR 22-MAR-2000; 2000FR-0003637.
 XX XX (CNRS) CENT NAT RECH SCI.
 XX PA (CURI-) INST CURIE.
 XX XX Fradelizi J, Friederich E, Golsteyn RM, Louvard D, Noireaux V;
 XX PI Sykes C;
 XX WPI: 2001-639148/73.
 XX DR N-PSDB; AAI71780.
 XX PT Identifying modulators of actin polymerization, potentially useful for
 XX PT treating tumor metastasis and parasitic infection, using proteins that
 XX PT contain Ena/VASP binding sites -
 XX PS Claim 16; Pages 77-78; 109pp; French.
 XX CC The present invention relates to a method for identifying modulators of
 XX CC actin polymerisation. The method involves using proteins that contain at
 XX CC least one binding motif for proteins of the Ena/VASP
 XX CC (vasodilator-stimulated phosphoprotein) family in the preparation of
 XX CC reagents for identification/screening of molecules that modulate
 XX CC formation of the actin cytoskeleton. The proteins used in the method
 XX CC (i.e. the proteins with binding motif(s) for Ena/VASP proteins) do not
 XX CC bind to the Arp2/3 protein complex. The modulators identified by the
 XX CC method are potentially useful for treating disorders of actin
 XX CC polymerisation, e.g. metastatic cancer or parasitic infection; and as
 XX CC cytotoxic agents. The present sequence one such protein with binding
 XX CC motif(s) for Ena/VASP proteins, which was used in the method of the
 XX CC present invention.
 XX SQ Sequence 351 AA;

Query Match 74.0%; Score 37; DB 22; Length 351;
 Best Local Similarity 75.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 Db 2 aspgtpgt 9

RESULT 40

AAR28314
 ID AAR28314 standard; Protein; 353 AA.
 XX AC AAR28314;
 XX DT 24-MAR-1993 (first entry)
 XX DE AHSV protein.
 XX KW African horse sickness virus; diagnosis; S7.
 XX OS African horse sickness virus serotype 7.
 XX PN EP515235-A.
 XX PD 25-NOV-1992.
 XX PF 26-MAY-1992; 92EP-0304734.
 XX PR 23-MAY-1991; 91GB-0011111.
 XX PR 14-JUN-1991; 91GB-0012875.
 XX XX (NAIN-) INST NACIONAL INVESTIGACIONES AGRARIAS.
 XX PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
 XX PI Roy P, Sanchez-Vizcaino Rodrique, JM;

us-09-734-281-1.rag

Wed May 22 11:04:22 2002

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XX WPI; 1992-391791/48.
DR N-PSDB; AAQ30130.
XX
XX DNA coding for African horse sickness virus protein - used for
PT diagnosis, and producing polypeptide(s) for use in diagnosis and
PT vaccines
XX
XX Claim 9; Fig 1: 29pp; English.
XX
XX African horse sickness virus serotype 7 clones were identified by
CC colony hybridisation and Northern blot analysis. A full length clone
CC contained fragments at the 5' and 3' ends of the sequence which are
CC characteristic of orbivirus RNA segments. The DNA fragment may be
CC inserted into an expression system and used in assays for detecting
CC AHSV RNA and as primers in amplification processes.
XX
XX Sequence 353 AA;
SQ
Query Match 74.0%; Score 37; DB 13; Length 353;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SSPGSPGT 9
Db 204 sapgapgt 211

```

Search completed: May 21, 2002, 11:18:07
Job time: 477 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2002, 11:15:45 ; Search time 26.77 Seconds
(without alignments)
32.305 Million cell updates/sec

Title: US-09-734-281-1

Perfect score: 50

Sequence: 1 YSSPGSPCT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	316	1 ORHUT2	microtubule-associ
2	50	100.0	341	2 B28820	microtubule-associ
3	50	100.0	364	2 A28820	microtubule-associ
4	50	100.0	374	2 S46264	microtubule-associ
5	50	100.0	402	1 ORB02	microtubule-associ
6	50	100.0	432	2 JS0306	microtubule-associ
7	50	100.0	441	1 ORHUT1	microtubule-associ
8	50	100.0	448	1 ORB01	microtubule-associ
9	50	100.0	686	2 A38235	microtubule-associ
10	50	100.0	733	2 A45301	microtubule-associ
11	39	78.0	150	2 T35638	hypothetical prote
12	39	78.0	272	2 T36270	probable expressio
13	39	78.0	2232	2 T34434	hypothetical prote
14	38	76.0	710	2 S72497	oligopeptide trans
15	38	76.0	756	1 A55943	1-phosphatidylinos
16	38	76.0	1345	2 T29090	surface layer-asso
17	38	76.0	3122	2 T17202	DNA-directed DNA p
18	37	74.0	168	2 B8066	protein R52.4 [imp
19	37	74.0	302	2 T40490	probable 26s prote
20	37	74.0	335	2 A40267	interleukin-5 rece
21	37	74.0	353	1 JQ1946	core protein vp7 -
22	37	74.0	372	2 AE3191	conserved hypothet
23	37	74.0	393	2 S16844	titin - rabbit (fr
24	37	74.0	415	1 W2WLEP	E2 protein - Europ
25	37	74.0	418	2 S29506	neurotensin recept
26	37	74.0	420	2 S21052	interleukin-5 rece
27	37	74.0	515	2 H75589	aldehyde dehydroge
28	37	74.0	542	2 A44358	zyxin - chicken
29	37	74.0	847	1 A53800	mixed-lineage prot

30	37	74.0	963	2 T19140	hypothetical prote
31	37	74.0	1387	2 JC5502	G-protein signalin
32	37	74.0	1986	2 S28353	probable polyketid
33	37	74.0	2623	2 T09456	intrinsic factor-B
34	37	74.0	26926	1 S20901	titin - rabbit (fr
35	37	74.0	26926	1 S20901	titin - rabbit (fr
36	36	72.0	119	2 T17003	titin, cardiac mus
37	36	72.0	305	2 S41860	dormancy-associate
38	36	72.0	323	2 A55983	gene Nkx-1.1 prote
39	36	72.0	329	2 T32783	microtubule-associ
40	36	72.0	351	2 A75621	hypothetical prote
41	36	72.0	381	2 S51375	ToxS-related prote
42	36	72.0	425	2 F97437	microtubule-associ
43	36	72.0	425	2 A12655	phosphoribosylamin
44	36	72.0	438	2 C86271	phosphoribosylamin
45	36	72.0	472	2 I67793	F12F23.21 protein
46	36	72.0	501	2 D64453	microtubule-associ
47	36	72.0	506	2 H83396	biotin carboxylase
48	36	72.0	511	2 S10527	probable aldehyde
49	36	72.0	603	2 S51461	endoglucanase B pr
50	36	72.0	680	2 S31216	BUD8 protein - yea
51	36	72.0	729	2 E70803	collagen alpha 1(X
52	36	72.0	914	2 S18942	hypothetical prote
53	36	72.0	1321	2 T00382	hypothetical prote
54	36	72.0	1824	1 ORHUT	microtubule-associ
55	36	72.0	1825	2 S13507	microtubule-associ

ALIGNMENTS

RESULT 1

ORHUT2
Microtubule-associated protein tau, fetal (clone p18) - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 02-Sep-1997
C:Accession: PNO001
R:Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A:Title: The microtubule binding domain of tau protein.
A:Reference number: JN0009; MUID:90180482
A:Accession: PNO001
A:Molecule type: mRNA
A:Residues: 1-316 <LEP>
A>Note: this sequence differs from a previously reported fetal tau protein sequence
C:Genetics:
A:Gene: GDB:MAPT; MTBT1
A:Cross-references: GDB:119434; OMIM:157140
A:Map position: 17q21-17q21
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bind
F:158-188/Domain: MAP2/tau repeat homology <WT1>
F:189-219/Domain: MAP2/tau repeat homology <WT2>
F:220-251/Domain: MAP2/tau repeat homology <WT3>

Query Match 100.0%; Score 50; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.59; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 YSSPGSPCT 9

Db 103 YSSPGSPCT 111

RESULT 2

B28820
Microtubule-associated protein tau type 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: B28820
R:Lee, G.; Cowan, N.; Kirschner, M.
Science 239, 285-288, 1988

A:Title: The primary structure and heterogeneity of tau protein from mouse brain.

A:Reference number: A94298; MUID:88099510

A:Accession: B28620

A:Molecule type: mRNA

A:Residues: 1-341 <LEE>

A:Cross-references: GB:M18775; NID:g201114; PIDN:AAA0165.1; PID:g201115

A:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; tandem repeat

F:183-213/Domain: MAP2/tau repeat homology <MT1>

F:214-244/Domain: MAP2/tau repeat homology <MT2>

F:245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 100.0%; Score 50; DB 2; Length 341;

Best Local Similarity 100.0%; Pred. No. 0.64;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

DB 128 YSSPGSPGT 136

RESULT 3

A28820

Microtubule-associated protein tau type 1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C:Accession: A28820

R:Lee, G.; Cowan, N.; Kirschner, M.

Science 239, 285-288, 1988

A:Title: The primary structure and heterogeneity of tau protein from mouse brain.

A:Reference number: A94298; MUID:88099510

A:Accession: A28820

A:Molecule type: mRNA

A:Residues: 1-364 <LEE>

A:Cross-references: GB:M18776; NID:g201116; PIDN:AAA0166.1; PID:g201117

A:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; tandem repeat

F:183-213/Domain: MAP2/tau repeat homology <MT1>

F:214-244/Domain: MAP2/tau repeat homology <MT2>

F:245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 100.0%; Score 50; DB 2; Length 364;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

DB 128 YSSPGSPGT 136

RESULT 4

S46264

Microtubule-associated protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 13-Aug-1999

C:Accession: S46264

R:Sadoc, E.; Marx, R.; Barg, J.; Behar, L.; Ginzburg, I.

J. Mol. Biol. 241, 325-331, 1994

A:Title: Complete sequence of 3'-untranslated region of tau from rat central nervous sys

A:Reference number: S46264; MUID:94334997

A:Accession: S46264

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <SAD>

A:Cross-references: ENBL:X79321; NID:g517393; PIDN:CAA55889.1; PID:g517394

A:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

F:185-215/Domain: MAP2/tau repeat homology <MT1>

F:216-246/Domain: MAP2/tau repeat homology <MT2>

F:247-277/Domain: MAP2/tau repeat homology <MT3>

~F:278-309/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 0.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

DB 130 YSSPGSPGT 138

RESULT 5

QB072

Microtubule-associated protein tau, form 3 - bovine

N:Contains: microtubule-associated protein tau, form 4; microtubule-associated protein

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 31-Mar-1996

C:Accession: B31939; A48885; A28173

R:Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.

Mol. Cell. Biol. 9, 1381-1388, 1989

A:Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bli

A:Reference number: A31939; MUID:89261765

A:Accession: E31939

A:Molecule type: mRNA

A:Residues: 1-402 <HIM>

A:Cross-references: GB:M26157; GB:M26158

R:Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.

J. Biol. Chem. 268, 23512-23518, 1993

A:Title: Brain proline-directed protein kinase phosphorylates tau on sites that ar

A:Reference number: A48885; MUID:94043150

A:Accession: A48885

A:Molecule type: Protein

A:Residues: 'X', 157-162, 'X', 164-165, 'X', 167-170; 192-195, 'X', 197-201, 'X', 358-364, 'X'

A:Note: sequence modified after extraction from NCBI backbone

R:Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.

J. Biol. Chem. 263, 7703-7707, 1988

A:Title: Microtubule-binding domain of Tau proteins.

A:Reference number: A28173; MUID:88227970

A:Accession: A28173

A:Molecule type: Protein

A:Residues: 159-172, 'X', 174-177 <AIZ>

A:Experimental source: brain

A:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repe

F:1-402/Product: microtubule-associated protein tau, form 3 #status predicted <B74>

F:101-402/Product: microtubule-associated protein tau, form 4 #status predicted <B74>

F:159-177/Region: microtubule binding #status experimental

F:213-243/Domain: MAP2/tau repeat homology <MT1>

F:244-274/Domain: MAP2/tau repeat homology <MT2>

F:275-305/Domain: MAP2/tau repeat homology <MT3>

F:306-337/Domain: MAP2/tau repeat homology <MT4>

F:156,163,196,202,365/Binding site: phosphate (Thr) (covalent) (by proline-directed

F:166/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #statu

Query Match 100.0%; Score 50; DB 1; Length 402;

Best Local Similarity 100.0%; Pred. No. 0.75;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

DB 158 YSSPGSPGT 166

RESULT 6

JS0306

Microtubule-associated protein tau - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993

C:Accession: JS0306; A33574

R:Kosik, K.S.; Orecchio, L.D.; Bakalis, S.; Neve, R.L.

Neuron 2, 1389-1397, 1989

A:Title: Developmentally regulated expression of specific tau sequences.
A:Reference number: JS0306; MUID:90180457

A:Accession: JS0306
A:Molecule type: mRNA
A:Residues: 1-432 <KAN>
A:Note: the sequence shown is from adult rat brain
A:Note: the partial sequence from fetal rat brain is lacking residues 266-296; the fetal
A:Note: both fetal and adult forms were found in the paired helical filaments character
R:Kanai, Y.; Takemura, R.; Oshima, T.; Mori, H.; Ihara, Y.; Yanagisawa, M.; Masaki, T.;
J. Cell Biol. 109, 1173-1184, 1989
A:Title: Expression of multiple tau isoforms and microtubule bundle formation in fibrobl
A:Reference number: A33574; MUID:89359509
A:Accession: A33574
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-432 <KAN>
A:Note: a variant lacking residues 63-91 was also found
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; Alzheimer's disease; calmodulin binding; microtubule b
F:243-273/Domain: MAP2/tau repeat homology <MT1>
F:274-304/Domain: MAP2/tau repeat homology <MT2>
F:305-335/Domain: MAP2/tau repeat homology <MT3>
F:336-367/Domain: MAP2/tau repeat homology <MT4>
F:282-313/Disulfide bonds: #status experimental
F:347/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 50; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
|||||||
Db 188 YSSPGSPGT 196

RESULT 7

QRBOT1
A:Title: microtubule-associated protein tau, long splice form - human
N:Alternate names: microtubule-binding protein tau; neurofibrillary tangle protein pair
C:Contains: microtubule-associated protein tau type II; microtubule-associated protein t
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C:Accession: JS0370; A30217; JN0009; S03796; S26665; S26662; S17302; A43444; A27
R:Goedert, M.; Spillantini, M.G.; Jakes, R.; Rutherford, D.; Crowther, R.A.
Neuron 3, 519-526, 1989
A:Title: Multiple isoforms of human microtubule-associated protein tau: sequences and lo
A:Reference number: JS0370; MUID:90380393
A:Accession: JS0370
A:Molecule type: mRNA
A:Residues: 1-441 <GOE>
A:Note: six isoforms are found; the clone htau40 sequence is shown. Residues 45-73, 74-1
R:Goedert, M.; Wischik, C.M.; Crowther, R.A.; Walker, J.E.; Klug, A.
Proc. Natl. Acad. Sci. U.S.A. 85, 4051-4055, 1988
A:Title: Cloning and sequencing of the cDNA encoding a core protein of the paired helica
A:Reference number: A30217; MUID:88234557
A:Accession: A30217
A:Molecule type: mRNA
A:Residues: 1-44,103-274,306-441 <GO2>
A:Cross-references: GB:J03778; NID:9338684; PIDN:AAA60615.1; PID:9338685
R:Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A:Title: The microtubule binding domain of tau protein.
A:Reference number: JN0009; MUID:90180482
A:Accession: JN0009
A:Molecule type: mRNA
A:Residues: 1-44,103-274,306-441 <LEE>
R:Goedert, M.; Spillantini, M.G.; Potler, M.C.; Ulrich, J.; Crowther, R.A.
EMBO J. 8, 393-399, 1989
A:Title: Cloning and sequencing of the cDNA encoding an isoform of microtubule-associate
A:Reference number: S03796; MUID:89251564
A:Accession: S03796

A:Molecule type: mRNA
A:Residues: 1-44,103-441 <GO3>
A:Cross-references: EMBL:X14474; NID:936724; PIDN:CAA32636.1; PID:936725
R:Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A:Title: Structure and novel exons of the human tau gene.
A:Reference number: S26665
A:Accession: S26662; MUID:93041757
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 144-185 <AND>
A:Cross-references: EMBL:X61372; NID:936718; PID:936719
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1999
A:Accession: S26666
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 187-274 <AN2>
A:Cross-references: EMBL:X61374; NID:936722; PID:936723
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A:Accession: S26662
A:Molecule type: DNA
A:Residues: 371-441 <ANW>
A:Cross-references: EMBL:X61373
R:Jakes, R.; Novak, M.; Davison, M.; Wischik, C.M.
EMBO J. 10, 2725-2729, 1991
A:Title: Identification of 3- and 4-repeat tau isoforms within the PHF in Alzheimer's
A:Reference number: S17302; MUID:92007714
A:Accession: S17302
A>Status: preliminary
A:Molecule type: protein
A:Residues: 268-274,306-395 <JAR>
R:Hasegawa, M.; Morishima-Kawashima, M.; Takio, K.; Suzuki, K.; Titani, K.; Ihara, Y.
J. Biol. Chem. 267, 17047-17054, 1992
A:Title: Protein sequence and mass spectrometric analyses of tau in the Alzheimer's
A:Reference number: A43444; MUID:92381012
A:Accession: A43444
A:Molecule type: protein
A:Residues: 2-73,103-130;151-180;191-254;260-269;275-290;299-317;322-340;344-347;354
A:Experimental source: Alzheimer's disease brain
A:Note: sequence extracted from NCBI backbone (NCBIP:112039)
C:Comment: This heterogeneous protein, which is found predominantly in cells of the
o the core protein of the paired helical filament of Alzheimer's disease.
C:Genetics:
A:Gene: GDB:MAPT
A:Map position: 17q21-17q21
A:Cross-references: GDB:119434; OMIM:157140
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bindi
F:1-441/Product: microtubule-associated protein tau, long splice form #status predict
F:1-274,306-441/Product: microtubule-associated protein tau (clone htau39) #status pr
F:1-73,103-441/Product: microtubule-associated protein tau (clone htau34) #status pr
F:1-73,103-274,306-441/Product: microtubule-associated protein tau (clone htau37) #st
F:1-44,103-274,306-441/Product: microtubule-associated protein tau, fecal #status pre
F:1-44,103-441/Product: microtubule-associated protein tau type II #status predicted
F:252-282/Domain: MAP2/tau repeat homology <MT1>
F:283-313/Domain: MAP2/tau repeat homology <MT2>
F:314-344/Domain: MAP2/tau repeat homology <MT3>
F:345-376/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
|||||||
Db 197 YSSPGSPGT 205

RESULT 8

QRBOT1
A:Title: microtubule-associated protein tau, form 1 - bovine
N:Contains: microtubule-associated protein tau, form 2

C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
 C:Accession: A31939; A33914; S04005; A48885; A28173; T83734
 R:Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
 Mol. Cell. Biol. 9, 1381-1388, 1989
 A:Title: Tau consists of a set of proteins with repeated C-terminal microtubule-binding
 A:Reference number: A31939; MUID:89261765

A:Accession: A31939
 A:Molecule type: mRNA
 A:Residues: 1-448 <HTM>
 A:Cross-references: GB:M26157; NID:g514913; PIDN:AAA30770.1; PID:g514914
 R:Iqbal, K.; Grundke-Iqbal, I.; Smith, A.J.; George, L.; Tung, Y.C.; Zaidi, T.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5646-5650, 1989
 A:Title: Identification and localization of a tau-peptide to paired helical filaments of
 A:Reference number: A33914; MUID:89315854
 A:Accession: A33914
 A:Molecule type: protein
 A:Residues: 26, 'A', 30-38, 'IG', 41, 'AP', 44, 'LK' <IQB>
 A:Experimental source: brain
 A:Note: 40-Pro was also found
 R:Iqbal, K.; Smith, A.J.; Zaidi, T.; Grundke-Iqbal, I.
 FEBS Lett. 248, 87-91, 1989
 A:Title: Microtubule-associated protein tau. Identification of a novel peptide from bovi
 A:Reference number: S04005; MUID:89252057

A:Accession: S04005
 A:Molecule type: protein
 A:Residues: 28, 'A', 30-38, 'IG', 41, 'AP', 44, 'LK' <IQ2>
 A:Experimental source: brain
 A:Note: 40-Pro was also found
 R:Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
 J. Biol. Chem. 268, 23512-23518, 1993
 A:Title: Brain proline-directed protein kinase phosphorylates tau on sites that are abn
 A:Reference number: A48885; MUID:94043150
 A:Accession: A48885
 A:Molecule type: protein
 A:Residues: 'X', 203-208, 'X', 210-211, 'X', 213-216; 238-241, 'X', 243-247, 'X', 404-410, 'X', 412
 A:Experimental source: brain
 A:Note: sequence modified after extraction from NCBI backbone
 R:Alizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
 J. Biol. Chem. 263, 7703-7707, 1988
 A:Title: Microtubule-binding domain of Tau proteins.
 A:Reference number: A28173; MUID:88227970

A:Accession: A28173
 A:Molecule type: protein
 A:Residues: 205-218, 'X', 220-223 <AIZ>
 A:Experimental source: brain
 C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C:Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
 F:1-448/Product: microtubule-associated protein tau, form 1 #status predicted <BP43>
 F:1-174,193-448/Product: microtubule-associated protein tau, form 2 #status predicted <B
 F:205-223/Region: microtubule binding #status experimental
 F:259-289/Domain: MAP2/tau repeat homology <MT1>
 F:290-320/Domain: MAP2/tau repeat homology <MT2>
 F:321-351/Domain: MAP2/tau repeat homology <MT3>
 F:352-383/Domain: MAP2/tau repeat homology <MT4>
 F:202,209,242,248,411/Binding site: phosphate (Ser) (covalent) (by proline-directed kin
 F:212/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status expe

Query Match 100.0%; Score 50; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 0.84;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 |||||
 Db 204 YSSPGSPGT 212

RESULT 9
 A38235
 microtubule-associated protein, 110K tau - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999

C:Accession: A38235

R:Goedert, M.; Spillantini, M.G.; Crowther, R.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 1983-1987, 1992

A:Title: Cloning of a big tau microtubule-associated protein characteristic of the

A:Reference number: A38235; MUID:92179305

A:Accession: A38235

A:Molecule type: mRNA

A:Residues: 1-686 <GOE>

A:Cross-references: GB:M84156; NID:g207157; PIDN:AAA42204.1; PID:g207158

A:Note: sequence extracted from NCBI backbone (NCBIN:87358, NCBI:P:87359)

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; tandem repeat

F:497-527/Domain: MAP2/tau repeat homology <MT1>

F:528-558/Domain: MAP2/tau repeat homology <MT2>

F:559-589/Domain: MAP2/tau repeat homology <MT3>

F:590-621/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 2; Length 686;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

|||||

Db 442 YSSPGSPGT 450

RESULT 10

A45301

microtubule-associated protein tau - mouse

A:Alternate names: microtubule binding protein tau

C:Species: Mus musculus (house mouse)

C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 13-Aug-1999

C:Accession: A45301; S31658

R:Couchie, D.; Mavilia, C.; Georgieff, I.S.; Liem, R.K.; Shelanski, M.L.; Nunez, J.

Proc. Natl. Acad. Sci. U.S.A. 89, 4378-4381, 1992

A:Title: Primary structure of high molecular weight tau present in the peripheral

A:Reference number: A45301; MUID:92262443

A:Accession: A45301

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-733 <COU>

A:Note: this sequence is inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:102045, NCBI:P:102046)

R:Kenner, L.; Forstner, M.; Hutter, H.; Hoefler, G.; Kurzbauer, R.; Zatloukal, K.;

submitted to the EMBL Data Library, May 1992

A:Description: First observation of mRNA for a tau-protein from murine liver and k

A:Reference number: S31658

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-529-651 <KEN>

A:Cross-references: EMBL:Z12133; NID:g54263; PIDN:CAA78121.1; PID:g388534

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: microtubule binding; tandem repeat

F:544-574/Domain: MAP2/tau repeat homology <MT1>

F:575-605/Domain: MAP2/tau repeat homology <MT2>

F:606-636/Domain: MAP2/tau repeat homology <MT3>

F:637-668/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 2; Length 733;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

|||||

Db 489 YSSPGSPGT 497

RESULT 11

T35638

hypothetical protein SC6G9.42c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C:Accession: T35638
 R:Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A:Reference number: Z21584
 A:Accession: T35638
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-150 <SEE>
 A:Cross-references: EMBL:AL079356; PIDN:CAB45633.1; GSPDB:GN000070; SCOEDB:SC6G9.42c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC6G9.42c

Query Match 78.0%; Score 39; DB 2; Length 150;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 SSPGSPGT 9
 Db 3 SSPGKPGT 10
 |||||

RESULT 12
 T36770
 probable expression regulator - Streptomyces coelicolor (fragment)
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T36770
 R:Saunders, D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, July 1999
 A:Reference number: Z21613
 A:Accession: T36770
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-272 <SAU>
 A:Cross-references: EMBL:AL096849; PIDN:CAB50963.1; GSPDB:GN000070; SCOEDB:SCI11.37c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SCI11.37c

Query Match 78.0%; Score 39; DB 2; Length 272;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YSSPGSPGT 9
 Db 170 YAPPGAPGT 178
 |||||

RESULT 13
 T34434
 hypothetical protein K06A9.1a - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T34434
 R:Geisler, C.; Gattung, S.
 submitted to the EMBL Data Library, December 1996
 A:Description: The sequence of C. elegans cosmid K06A9.
 A:Reference number: Z21525
 A:Accession: T34434
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-2232 <GEI>
 A:Cross-references: EMBL:U80846; PIDN:AACT0890.1; GSPDB:GN000028; CESP:K06A9.1a
 A:Experimental source: strain Bristol N2; clone K06A9
 C:Genetics:
 A:Gene: CESP:K06A9.1a
 A:Map position: X
 A:Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075/1

Query Match 78.0%; Score 39; DB 2; Length 2232;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 Db 886 SPGSPGT 892
 |||||
 RESULT 14
 S72497
 oligopeptide transport protein Pept1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
 C:Accession: S72497; S68161
 R: Miyamoto, K.I.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: S72497
 A:Accession: S72497
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-710 <MIY>
 A:Cross-references: EMBL:D50664; NID:g1384098; PIDN:BAA09318.1; PID:g1212746
 R: Miyamoto, K.; Shiraga, T.; Morita, K.; Yamamoto, H.; Haga, H.; Taketani, Y.; Tamai, K.
 Blochim. Biophys. Acta 1305, 34-38, 1996
 A:Title: Sequence, tissue distribution and developmental changes in rat intestinal C

A:Reference number: S68161; MUID:96180982
 A:Accession: S68161
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-258 'E' 260-278, 'MV' 281-710 <MI2>
 A:Cross-references: GB:D50664
 C:Genetics:
 A:Gene: Pept1
 C:Superfamily: peptide transport protein Pept1
 C:Keywords: oligopeptide transport; transmembrane protein; transport protein

Query Match 76.0%; Score 38; DB 2; Length 710;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSPGSPG 8
 Db 441 SSPGSPG 447
 |||||

RESULT 15
 A55943
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 [val]
 N:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide
 C:Species: Homo sapiens (man)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: A55943
 R:Cheng, H.F.; Jiang, M.J.; Chen, C.L.; Liu, S.M.; Wong, L.P.; Lomasney, J.W.; King, J. Biol. Chem. 270, 5495-5505, 1995
 A:Title: Cloning and identification of amino acid residues of human phospholipase C
 A:Reference number: A55943; MUID:95197554
 A:Accession: A55943
 A:Molecule type: mRNA
 A:Residues: 1-756 <CHE>
 A:Cross-references: GB:U09117; NID:9483919; PIDN:AAA73567.1; PID:g483920
 A:Experimental source: aortic smooth muscle
 C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphosphate
 C:Genetics:
 A:Gene: GDB:PLCD1
 A:Cross-references: GDB:6075994
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phosphodiesterase domain Y homology; calmodulin repeat homology; pleckstrin repeat homology
 C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; si F:19-128/Domain: pleckstrin repeat homology <PLK>

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F;140-172/Domain: calmodulin repeat homology <EF1>
 F;176-208/Domain: calmodulin repeat homology <EF2>
 F;298-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
 F;491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
 F;614-724/Domain: protein kinase C2 region homology <KC2>

Query Match 76.0%; Score 38; DB 1; Length 756;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
 :|||||
 Db 507 FSSPGTPG 514

RESULT 16
 T29090
 surface layer-associated STABLE proteinase - Staphylothermus marinus
 N:Alternate names: hyperthermostable proteinase
 C:Species: Staphylothermus marinus

C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
 C:Accession: T29090

R:Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.

Curr. Biol. 6, 739-749, 1996

A:Title: A hyperthermostable protease of the subtilisin family bound to the surface layer

A:Reference number: 220559; MUID:96385442

A:Accession: T29090

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1345 <MAY>

A:Cross-references: EMBL:U57968; NID:g1374755; PID:g1374756; PIDN:AAB02323.1

A:Experimental source: strain F1

C:Function:

A:Description: probably serves an exodigestive function related to the organism's energy

A:Note: stoichiometric S-layer component

Query Match 76.0%; Score 38; DB 2; Length 1345;
 Best Local Similarity 77.8%; Pred. No. 2.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPG 9
 :|||||
 Db 596 YSSNGAPGT 604

RESULT 17
 T17202
 DNA-directed DNA polymerase (EC 2.7.7.7) zeta chain - mouse
 C:Species: Mus musculus (house mouse)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17202

R:Van Sloun, P.P.H.; Romeijn, R.J.; Eeken, J.C.J.

Mutat. Res. 433, 109-116, 1999

A:Title: Molecular cloning, expression and chromosomal localisation of the mouse Rev31

A:Reference number: 218720; MUID:99202265

A:Accession: T17202

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-3122 <VAN>

A:Cross-references: EMBL:AF083464; NID:g4079830; PID:g4079831; PIDN:AAC98785.1

A:Experimental source: strain 129/Ola; testis

C:Genetics:

A:Map position: 10

C:Keywords: nucleotidyltransferase

Query Match 76.0%; Score 38; DB 2; Length 3122;
 Best Local Similarity 87.5%; Pred. No. 5.4e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8

Db 2108 YSSPDSPG 2115
 :|||||

RESULT 18

B88066

protein R52.4 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: B88066

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999

A:Accession: B88066

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-168 <STO>

A:Cross-references: GB:chr_II; PIDN:AB71062.1; PID:g2429536; GSPDB:GN00020; CESP:R

C:Genetics:

A:Gene: R52.4

A:Map position: 2

Query Match 74.0%; Score 37; DB 2; Length 168;
 Best Local Similarity 75.0%; Pred. No. 43;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||||
 Db 40 TTPGSPGT 47

RESULT 19

T40490

probable 26s proteasome regulatory subunit - fission yeast (Schizosaccharomyces po

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: T40490

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft

submitted to the EMBL Data Library, February 1998

A:Reference number: Z21910

A:Accession: T40490

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-302 <WOO>

A:Cross-references: EMBL:AL021730; PIDN:CAA16829.1; GSPDB:GN000067; SPDB:SPBC4C3.0

A:Experimental source: strain 972h-; cosmid c4C3

C:Genetics:

A:Gene: SPDB:SPBC4C3.07

A:Map position: 2

C:Superfamily: mov-34 protein

Query Match 74.0%; Score 37; DB 2; Length 302;
 Best Local Similarity 66.7%; Pred. No. 77;
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YSSPGSPGT 9
 :|||||
 Db 123 YASPAEPT 131

RESULT 20

A40267

interleukin-5 receptor alpha chain precursor - human

C:Species: Homo sapiens (man)

C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999

C:Accession: A40267

R:Tavernier, J.; Devos, R.; Cornells, S.; Tuijens, T.; Van der Heyden, J.; Fiers,

Cell 66, 1175-1184, 1991

A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
A:Reference number: A40267; MUID:92005669
A:Accession: A40267
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <TAV>
A:CROSS-references: GB:M75914; NID:gl86387; PIDN:AAA36110.1; PID:gl86388
C:Keywords: cytokine receptor; transmembrane protein

Query Match 74.0%; Score 37; DB 2; Length 335;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 119 HAPGSPGT 127

RESULT 21

JQ1946
core protein VP7 - African horse sickness virus (serotype 4, strain Spane)
C:Species: African horse sickness virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jun-2000
A:Accession: JQ1946
R:ROY, P.; Hirasawa, T.; Fernandez, M.; Blinov, V.M.; Sanchez-Vixcain Rodrique, J.M.
J. Gen. Virol. 72, 1237-1241, 1991
A:Title: The complete sequence of the group-specific antigen, VP7, of African horse sickn
A:Reference number: JQ1946; MUID:91259049
A:Accession: JQ1946

A:Molecule type: genomic RNA
A:Residues: 1-353 <ROY>
A:CROSS-references: GB:D12533; NID:g221010; PIDN:BAA02096.1; PID:g221011
C:Genetics:
A:Map position: segment 7
C:Superfamily: bluetongue virus core protein VP7
C:Keywords: core protein

Query Match 74.0%; Score 37; DB 1; Length 353;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
DB 204 SAPGAPGT 211

RESULT 22

AE3191
conserved hypothetical protein Atu5258 [imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AE3191
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AE3191

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-372 <KUR>

A:CROSS-references: GB:AE008687; PIDN:AAL45947.1; PID:gl7743697; GSPDB:GN00188
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu5258
A:Genome: plasmid

Query Match 74.0%; Score 37; DB 2; Length 372;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 146 YHQPSPGS 154

RESULT 23

S16844
titin - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
A:Accession: S16844
R:Fritz, J.D.; Greaser, M.L.; Wolff, J.A.
Nucleic Acids Res. 19, 3747, 1991
A:Title: A novel 3' extension technique using random primers in RNA-PCR.
A:Reference number: S16844; MUID:91305130
A:Accession: S16844

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-393 <FRI>
A:CROSS-references: EMBL:X59596; NID:gl722; PIDN:CAA42165.1; PID:gl723
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1991
C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology;

Query Match 74.0%; Score 37; DB 2; Length 393;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 55 YKPGPGGT 63

RESULT 24

W2WLEP
E2 protein - European elk papillomavirus
C:Species: European elk papillomavirus
C:Date: 31-Mar-1999 #sequence_revision 31-Mar-1989 #text_change 11-May-2000
C:Accession: D29499; D94457; D94506
R:Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U.
Gene 50, 195-205, 1986
A:Title: Organization and expression of the transforming region from the European ell
A:Reference number: A91567; MUID:87219878
A:Accession: D29499

A:Molecule type: DNA
A:Residues: 1-415 <AHO>
A:CROSS-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
R:Eriksson, A.
unpublished results 1987, cited by GenBank
A:Reference number: A94457
A:Accession: D94457
A:Molecule type: DNA
A:Residues: 1-415 <ERI>
A:CROSS-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
R:Pettersson, U.
submitted to GenBank, August 1987

A:Reference number: A94506
A:Accession: D94506
A:Molecule type: DNA

A:Residues: 1-415 <PET>
A:CROSS-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
C:Superfamily: papillomavirus E2 protein
C:Keywords: early protein

Query Match 74.0%; Score 37; DB 1; Length 415;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Wed May 22 11:04:28 2002

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A:Residues: 1-128,'I',130-395,'I' <MUW>
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
R:Murata, Y.
submitted to the EMBL Data Library, September 1991
A:Reference number: S78107
A:Accession: S78107
A:Molecule type: mRNA
A:Residues: 1-128,'I',130-332,'K' <MU4>
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane pr
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>
F:345-365/Domain: transmembrane #status predicted <TM>
F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 74.0%; Score 37; DB 2; Length 420;
Best Local Similarity 66.7%; Pred. No. 1.le+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YSSPGSPGT 9
Db 119 HAPGSPGT 127

RESULT 27
H75589
aldehyde dehydrogenase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: H75589
R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
A:Reference number: A75250; MUID:20036896
A:Accession: H75589
A:Molecule type: DNA
A:Residues: 1-515 <WH>
A:Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12436.1; PID:g
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0348
A:Map position: 2
C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Query Match 74.0%; Score 37; DB 2; Length 515;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSPGSPGT 9
Db 13 YANPGTGS 21

RESULT 28
A44358
zyxin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Jun-1993 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000
C:Accession: A44358; S30506
R:Sadler, I.; Crawford, A.W.; Michelsen, J.W.; Beckerle, M.C.
J. Cell Biol. 119, 1573-1587, 1992
A:Title: Zyxin and cCRP: two interactive LIM domain proteins associated with the
A:Reference number: A44358; MUID:93107157
A:Accession: A44358
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-542 <SAD>
A:Cross-references: EMBL:X69190; NID:g63897; PIDN:CAA48936.1; PID:g63898

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QY 1 YSSPGSPGT 9
Db 268 YSAPSPGS 276

RESULT 25
S29506
neurotensin receptor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C:Accession: S29506
R:Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad, M.; Gully, D.; le
FEBS Lett. 317, 139-142, 1993
A:Title: Cloning and expression of a complementary DNA encoding a high affinity human ne
A:Reference number: S29506; MUID:93154505
A:Accession: S29506
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <VIT>
A:Cross-references: EMBL:X70070; NID:g35020; PIDN:CAA49675.1; PID:g35021
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 74.0%; Score 37; DB 2; Length 418;
Best Local Similarity 75.0%; Pred. No. 1.le+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSPGSPGT 9
Db 6 SAPGTPGT 13

RESULT 26
S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored is
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C:Accession: S21052; S21050; S21053; A46175; S78106; S78107
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.
A:Reference number: S21050; MUID:92121815
A:Accession: S21052
A:Molecule type: DNA
A:Residues: 1-420 <MUR>
A:Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A:Experimental source: clone lambda h5R.12
A:Accession: S21050
A:Molecule type: DNA
A:Residues: 1-395,'I' <MU2>
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A:Experimental source: clone lambda h5R.27
A:Accession: S21053
A:Molecule type: mRNA
A:Residues: 1-332,'K' <MU3>
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A:Experimental source: clone lambda h5R.25
R:Ravener, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the human
A:Reference number: A46175; MUID:92357767
A:Accession: A46175
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 333-420 <TAV>
A:Experimental source: HL-60 cells and eosinophils
A:Note: sequence extracted from NCBI Backbone (NCBIN:116243, NCBI:116244)
R:Murata, Y.
submitted to the EMBL Data Library, July 1991
A:Reference number: S78106
A:Accession: S78106
A:Molecule type: DNA

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A:Note: sequence extracted from NCBI backbone (NCBIN:121172, NCBIIP:121174)
 A:Note: this sequence may be one segment of several
 C:Superfamily: LIM metal-binding repeat homology
 F:352-404/Domain: LIM metal-binding repeat homology <LIM1>
 F:412-463/Domain: LIM metal-binding repeat homology <LIM2>
 F:472-533/Domain: LIM metal-binding repeat homology <LIM3>

Query Match 74.0%; Score 37; DB 2; Length 542;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||:|
 Db 2 ASPTCTPCT 9

RESULT 29
 A53800
 mixed-lineage protein kinase (EC 2.7.1.1-) 3 - human
 N:Alternate names: protein kinase PKI; protein kinase SPRK
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A53800; I58395
 R:Galio, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
 J. Biol. Chem. 269, 15092-15100, 1994
 A:Title: Identification and characterization of SPRK, a novel src-homology 3 domain-cont
 A:Reference number: A53800; MUID:94253068
 A:Accession: A53800
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-847 <GAL>
 A:CROSS-references: GB:U07747; NID:q464027; PIDN:AAAL9647.1; PID:q464028
 R:Ing, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassar, N.J.
 Oncogene 9, 1745-1750, 1994
 A:Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domain
 A:Reference number: I58395; MUID:94239754
 A:Accession: I58395
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-847 <RES>
 A:CROSS-references: GB:L32976; NID:q488295; PIDN:AAA59859.1; PID:q488296
 C:Genetics:
 A:Gene: GDB:MLK3; PTK1; SPRK
 A:CROSS-references: GDB:I34755; OMIM:600050
 A:Map position: 11q13.1-11q13.3
 C:Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
 F:48-100/Domain: SH3 homology <SH3>
 F:115-383/Domain: protein kinase homology <KIN>
 F:123-131/Region: protein kinase ATP-binding motif
 F:403-424/Region: leucine zipper motif
 F:438-459/Region: leucine zipper motif
 F:468-482/Region: basic

Query Match 74.0%; Score 37; DB 1; Length 847;
 Best Local Similarity 75.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||:|
 Db 748 SAPGTPCT 755

RESULT 30
 T19140
 hypothetical protein C09G5.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19140
 R:Palmer, S.
 submitted to the EMBL Data Library, November 1994

A:Reference number: Z19080
 A:Accession: T19140
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-963 <WIL>
 A:CROSS-references: EMBL:Z46791; PIDN:CAA86755.1; GSPDB:GN00020; CESP:C09G5.6
 A:Experimental source: clone C09G5
 C:Genetics:
 A:Gene: CESP:C09G5.6
 A:Map position: 2
 A:Introns: 48/3; 862/3; 898/1

Query Match 74.0%; Score 37; DB 2; Length 963;
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||:|
 Db 559 SAPGAPCT 566

RESULT 31
 JC5502
 G-protein signaling regulator 12 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
 C:Accession: JC5502
 R:Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, D.P.
 Biochem. Biophys. Res. Commun. 233, 770-777, 1997
 A:Title: Molecular cloning and expression analysis of rat Rgs12 and Rgs14.
 A:Reference number: JC5502; MUID:97312490
 A:Accession: JC5502
 A:Molecule type: mRNA
 A:Residues: 1-1387 <SNO>
 A:CROSS-references: GB:U92280; NID:q2088557; PIDN:AAC53176.1; PID:q2088558
 C:Comment: This protein functions as GTPase activating protein. It interacts with
 F:18-80/Domain: rhoGAP-like #status predicted <RHO>
 F:712-761/Domain: GH1 #status predicted <GH1>
 F:765-800/Domain: GH2 #status predicted <GH2>
 F:804-828/Domain: GH3 #status predicted <GH3>
 F:1204-1220/Region: conserved #status predicted
 F:1266-1295/Region: coiled heptad repeat (S-P-X-S-A)

Query Match 74.0%; Score 37; DB 2; Length 1387;
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
 :|||:|
 Db 1296 HSTPGPPGT 1304

RESULT 32
 S28353
 probable polyketide synthase - Emericella nidulans
 C:Species: Emericella nidulans, Aspergillus nidulans
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-May-2000
 C:Accession: S28353
 R:Mayorga, M.E.; Timberlake, W.E.
 Mol. Gen. Genet. 235, 205-212, 1992
 A:Title: The developmentally regulated Aspergillus nidulans wa gene encodes a polypep
 A:Reference number: S28353; MUID:93101122
 A:Accession: S28353
 A:Molecule type: DNA
 A:Residues: 1-1986 <NAY>
 A:CROSS-references: EMBL:X65866; NID:g55508; PID:g55509
 C:Genetics:
 A:Gene: wa
 A:Introns: 96/2; 193/3; 1336/3; 1588/3
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier pr
 C:Keywords: carrier protein

F:397-805/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F:911-1199/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
 F:1648-1718/Domain: acyl carrier protein homology <ACP>
 F:1766-1840/Domain: acyl carrier protein homology <ACPL>

Query Match 74.0%; Score 37; DB 2; Length 1986;
 Best Local Similarity 87.5%; Pred. No. 5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
 ||| |||
 Db 1749 SSPASPGT 1756

RESULT 33

T09456
 Intrinsic factor-B12 receptor Cubillin precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T09456
 R:Kozayaki, R.; Kristiansen, M.; Silhahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.
 Blood 91, 3593-3600, 1998
 A:Title: The human intrinsic factor-vitamin B12 receptor, cubillin: Molecular characterization.
 A:Reference number: Z16677; MUID:98241400
 A:Accession: T09456
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-3623 <KOZ>
 A:Cross-references: EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3929529
 C:Genetics:
 A:Map position: 10p12
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 C:Keywords: receptor; vitamin B12 uptake
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
 F:436-467/Domain: EGF homology <EGF>

Query Match 74.0%; Score 37; DB 2; Length 3623;
 Best Local Similarity 66.7%; Pred. No. 9.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSPGSPGT 9
 :||| |||
 Db 3522 FTSPGPGT 3530

RESULT 34

S20901
 titin - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
 C:Accession: S20901; I46520
 R:Labeit, S.; Gautel, M.; Lakey, J.
 EMBO J. 11, 1711-1716, 1992
 A:Title: Towards a molecular understanding of titin.
 A:Reference number: S20897; MUID:92258380
 A:Accession: S20901
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-6805 <LAB>
 A:Cross-references: EMBL:X64696
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
 R:Labeit, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U.;
 Nature 345, 273-276, 1990
 A:Title: A regular pattern of two types of 100-residue motif in the sequence of titin.
 A:Reference number: I46520; MUID:90238553
 A:Accession: I46520
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 4235-5250 <LA2>

A:Cross-references: EMBL:X17329; NID:g1756; PIDN:CAA35207.1; PID:g930251
 C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology
 C:Keywords: muscle

Query Match 74.0%; Score 37; DB 2; Length 6805;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YSPGSPGT 9
 | || |||
 Db 5282 YKEPGPGT 5290

RESULT 35

I38344
 titin, cardiac muscle [validated] - human
 N:Alternate names: connectin
 N:Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
 C:Species: Homo sapiens (man)
 C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
 C:Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393
 R:Labeit, S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A:Reference number: A57430; MUID:96026330
 A:Accession: I38344
 A:Status: nucleic acid sequence not shown; translation not shown; translated from
 A:Molecule type: mRNA
 A:Residues: 1-26926 <LAB1>
 A:Cross-references: EMBL:X90568; NID:g1017424; PID:g1017425
 R:Musco, G.; Triatziolos, C.; Schuck, P.; Pastore, A.
 Biochemistry 34, 553-561, 1995
 A:Title: Dissecting titin into its structural motifs: identification of an alpha-helical
 A:Reference number: I38345; MUID:95119041
 A:Accession: I38345
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1977-2014 <MUS>
 A:Cross-references: EMBL:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580
 A:Note: conformation and properties are reported for a synthetic peptide corresponding
 R:Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
 EMBO J. 11, 1711-1716, 1992
 A:Title: Towards a molecular understanding of titin.
 A:Reference number: S20897; MUID:92258380
 A:Accession: S20898
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 13597-14200, 'I', 14202-14696 <LAB2>
 A:Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
 A:Accession: S20897
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 16330-16382, 'S', 16384-16756, 'F', 16758-16860 <LAB3>
 A:Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191
 A:Accession: S20899
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 'P', 22278-22431, 'R', 22433-22448, 'G', 22450-22453, 'Q', 22455-22480, 'TR', 'L',
 R:Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.
 J. Mol. Biol. 256, 556-563, 1996
 A:Title: Genomic organization of M line titin and its tissue-specific expression
 A:Reference number: S63665; MUID:96177761
 A:Accession: S63665
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 26729-26825 <KOL>
 A:Cross-references: EMBL:X92412; NID:gl236761
 R:Gautel, M.; Leonard, K.; Labeit, S.
 EMBO J. 12, 3827-3834, 1993
 A:Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differ
 A:Reference number: S37393; MUID:94008990

A:Accession: S37393
A:Molecule type: mRNA
A:Residues: 26831-26926 <GAU>
R:Improtro, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A:Reference number: A66736; PDB:1TIT
A:Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
R:Fuhl, M.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66201; PDB:1NCT
A:Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
C:Genetics:
A:Gene: GDB:TIN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q32
C:Function:
C:Description: structural protein forming filaments in striated muscle
C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; glyco-
C:Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glycyl-
structural protein
F:24752-25008/Domain: protein kinase homology <KIN>
F:84_177_905_2276_2378_2439_2481_2563_2669_2763_2896_F388
F:88_11066_11488_11515_11635_11949_12170_12478_12526_12645_12875_13001_13036_13295_13540_13888_predicted
F:16780_16976_17579_17602_17667_17681_17845_17899_18121_18188_18209_18336_18670_18680_18742_1900_21935_22295_22627_22897_23024_23318_23883_24012_24177_24290_24447_24642_24818_25190_25619_25650_25651_25652_25653_25654_25655_25656_25657_25658_25659_25660_25661_25662_25663_25664_25665_25666_25667_25668_25669_25670_25671_26178_26184_26190/Binding site: Phosphate (Ser) (covalent) %status experimental

```

Query Match          74.0%;      Score 37;  DB 1;  Length 26936;
Best Local Similarity 66.7%;      Pred. NO. 6.7e+03;
Matches 6;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

QY      1  YSSPGSPGT 9
          |  |  |  |  |  |
Db 16923 YKEPGPGT 16931

```

RESULT 36
T17003
dormancy-associated protein [similarity] - apple tree
C:Species: Malus domestica (apple tree)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C:Accession: T17003
R:Lee, S.A.; Gardner, R.C.; Lay-See, M.
Plant Physiol. 103, 1017, 1993
A:Title: An apple gene highly expressed in fruit.
A:Reference number: Z18646; MUID:94294548
A:Accession: T17003
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-119 <LE>
A:Cross-references: EMBL:L15194; NID:g439878; PIDN:AA71194.1; PID:g439879
A:Experimental source: cultivar Golden Delicious; fruit cortical

```

Query Match          72.0%;   Score 36;   DB 2;   Length 119;
Best Local Similarity 85.7%;   Pred. No. 44;
Matches 6;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;
Qy      3   SPCSPGPT 9
         ||| |||
Db      51   SPCPTGPT 57

```

RESULT 37
S41860 gene Nkx-1.1 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C:Accession: S41860
R:Schubert, F.R.; Gruss, P.
submitted to the EMBL Data Library, October 1993

A;Description: Expression of the novel Murine homeobox gene Nkx-1.1 in the developing
A;Reference number: S41860
A;Accession: S41860
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <SCH>
A;Cross-references: EMBL:X75384; NTD:9453171; PID:CAA53153.1; PID:9453172
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;157-213/Domain: homeobox homology <HGX>

```

Query Match      72.0%; Score 36; DB 2; Length 305;
Best Local Similarity 75.0%; pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 SSPGSPGT 9
        :|||||:
Db      134 ASPGSPGS 141

```

```

RESULT      38
A55983      microtubule-associated protein MAP2 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Jan-1996 #sequence_revision
C:Accession: A55983; A47011; A33734
R:Coffey, R.L.; Joly, J.C.; Cain, B.D.; Purlich, D.L.
Biochemistry 33, 13199-13207, 1994
A:Title: Exploring the microtubule-binding region of bovine microtubule-associated
A:Reference number: A55983; MUID:95034751

```

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-323 <Cof>
A:Cross-references: GB:S74035
R:Dingus, J.; Obar, R.A.; Hyams, J.S.; Goedert, M.; Vallee, R.B.
J. Biol. Chem. 266, 18854-18860, 1991
A:Title: Use of a heat-stable microtubule-associated protein class-specific antibody
A:Reference number: A41011; MUID:92011652
A:Accession: A41011
A:Molecule type: protein
A:Residues: 227-258 <DIN>
R:Joly, J.C.; Flynn, G.; Purich, D.L.
J. Cell Biol. 109, 3289-3294, 1989
A:Title: The microtubule-binding fragment of microtubule-associated protein-2: localization
A:Reference number: A33734; MUID:90037224
A:Accession: A33734
A:Status: preliminary
A:Molecule type: protein
A:Residues: 121-139 <JOL>
C:Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C:Keywords: microtubule binding; tandem repeat
F:165-195/Domain: MAP2/tau repeat homology <MT1>
F:227-258/Domain: MAP2/tau repeat homology <MT2>

```

Query Match      72.0%; Score 36; DB 2; Length 323;
Best Local Similarity 72.7%;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY      1 YSS--PGSPGT 9
Db       105 YSSRTGPTGPT 115
         ||| |||||

```

RESULT 39
T32783
hypothetical protein C50D2.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C:Accession: T32783
R:Sammons, L.; Wohldmann, P.; Bauer, C.

Wed May 22 11:04:28 2002

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C50D2.

A:Reference number: Z21224

A:Accession: T32783

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-329 <SAM>

A:Cross-references: EMBL:AF040642; PIDN:AB94952.1; GSPDB:GN00020; CESP:C50D2.4

A:Experimental source: strain Bristol N2; clone C50D2

C:Genetics:

A:Gene: CESP:C50D2.4

A:Map position: 2

A:Introns: 27/1; 59/3; 76/3; 237/1

C:Superfamily: unassigned collagens

Query Match 72.0%; Score 36; DB 2; Length 329;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPCT 9
|||:|
Db 160 SPGNPCT 166

RESULT 40

A75621

Tors-related protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: A75621

R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: A75621

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-351 <WHI>

A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12581.1; PID:g6460877; TIGR:DRB00

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRB0027

A:Map position: megaplasmid

A:Genome: plasmid

A:Note: plasmid MP1

Query Match 72.0%; Score 36; DB 2; Length 351;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPCT 9
|||:|
Db 95 YSTAGTCT 103

Search completed: May 21, 2002, 11:19:10
Job time: 205 sec

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: May 21, 2002, 11:18:40 ; Search time 13.48 seconds
(without alignments)
25.851 Million cell updates/sec

Title: US-09-734-281-1

Perfect score: 50

Sequence: 1 YSPGSPGT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	382	1 TAU_PAPHA	Q9myx8 papio hamad
2	50	100.0	402	1 TAU_CAPHI	O02828 capra hircu
3	50	100.0	447	1 TAU_BOVIN	P29172 bos taurus
4	50	100.0	458	1 TAU_MACMU	P57786 macaca mula-
5	50	100.0	732	1 TAU_MOUSE	P10637 mus musculu
6	50	100.0	751	1 TAU_RAT	P19332 rattus norv
7	50	100.0	757	1 TAU_HUMAN	O42773 cryptococcu
8	39	78.0	639	1 P2B1_CRYNE	P51574 rattus norv
9	38	76.0	710	1 PET1_RAT	O61178 homo sapien
10	38	76.0	756	1 PID1_HUMAN	O61493 mus musculu
11	38	76.0	3122	1 DP04_MOUSE	O19002 felis silve
12	37	74.0	164	1 CDN1_FELCA	O9eqn3 mus musculu
13	37	74.0	387	1 TI22_MOUSE	P11329 european el
14	37	74.0	395	1 TI22_HUMAN	P30989 homo sapien
15	37	74.0	415	1 VE2_PAPVE	O01344 homo sapien
16	37	74.0	418	1 NTR1_HUMAN	Q9fy99 deinoceccu
17	37	74.0	420	1 ILSR_HUMAN	O04584 gallus gall
18	37	74.0	515	1 DHAL_DEIRA	Q09457 caenorhabd
19	37	74.0	542	1 ZYX_CHICK	O08774 rattus norv
20	37	74.0	963	1 YQ36_CAEEL	Q03149 emericella
21	37	74.0	1387	1 RGSC_RAT	P42580 mus musculu
22	37	74.0	1986	1 WA_EMENT	Q58626 mechanococc
23	36	72.0	305	1 SAX1_MOUSE	P18126 pseudomonas
24	36	72.0	501	1 PYCA_METJA	P41698 saccharomyc
25	36	72.0	511	1 GUNB_PSEFL	Q05306 mus musculu
26	36	72.0	603	1 BUD8_YEAST	Q9-kb9 streptomyc
27	36	72.0	680	1 CA1A_MOUSE	P11137 homo sapien
28	36	72.0	1171	1 TR12_STRCO	P20357 mus musculu
29	36	72.0	1827	1 MAP2_HUMAN	P15146 rattus norv
30	36	72.0	1828	1 MAP2_MOUSE	P39689 mus musculu
31	36	72.0	1861	1 MAP2_RAT	P49684 rattus norv
32	35	70.0	159	1 CDN1_MOUSE	
33	35	70.0	386	1 UR2R_RAT	

ALIGNMENTS

RESULT 1

ID	TAU_PAPHA	STANDARD	PRT	382 AA
AC	Q9MYX8			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	Microtubule-associated protein tau (Neurofibrillary tangle protein)			
DE	(Paired helical filament-tau) (PHF-tau).			
GN	MAPT OR TAU.			
OS	Papio hamadryas (Hamadryas baboon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OX	Cercopithecoidea; Papio.			
RP	[J]			
RA	SEQUENCE FROM N.A.			
RA	Wang X.L., Wang J., Schultz C., Hubbard G.B.;			
CC	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
CC	- - FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND MAINTENANCE OF NEURONAL			
CC	BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL			
CC	POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-			
CC	TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT			
CC	TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS			
CC	PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE			
CC	DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME (BY SIMILARITY).			
CC	- - SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE			
CC	CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS (BY			
CC	SIMILARITY).			
CC	- - TISSUE SPECIFICITY: EXPRESSED IN NEURONS.			
CC	- - DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN.			
CC	- - PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN			
CC	S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDKP: CDC2,			
CC	CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN			
CC	MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY			
CC	MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).			
CC	- - SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			

P21183 mus musculu
Q92407 aspergillus
O16671 homo sapien
P21647 klebsiella
P06436 herpes simp
P10211 herpes simp
P08665 herpes simp
P21405 southern be
P08121 mus musculu
P53420 homo sapien
O920Y8 rattus norv
P19998 oryctolagus
P11338 homo sapien
P13505 meleagris g
P39039 mus musculu
P49874 sus scrofa
O04959 mycobacteri
P11414 cricetus
O43237 homo sapien
P45413 klebsiella
Q9uew3 homo sapien
P25918 mus musculu

34 35 70.0 415 1 IL5R_MOUSE
35 35 70.0 495 1 HKKG_ASPNG
36 35 70.0 573 1 AMH2_HUMAN
37 35 70.0 828 1 MRKC_KLEPN
38 35 70.0 903 1 VGLB_HSV1P
39 35 70.0 904 1 VGLB_HSV1P
40 35 70.0 904 1 VGLB_HSV1P
41 35 70.0 956 1 RPO_SBMV
42 35 70.0 1464 1 CAL3_MOUSE
43 35 70.0 1690 1 CA44_HUMAN
44 35 70.0 1835 1 CCAI_RAT
45 34 68.0 114 1 ET3_RABIT
46 34 68.0 238 1 ET3_HUMAN
47 34 68.0 239 1 CALD_MEUGA
48 34 68.0 239 1 MABA_MOUSE
49 34 68.0 249 1 PSPA_PIG
50 34 68.0 298 1 34KD_MYCPA
51 34 68.0 467 1 RPBI_CRIGR
52 34 68.0 492 1 DYJ2_HUMAN
53 34 68.0 508 1 CILA_KLEPN
54 34 68.0 520 1 MRCO_HUMAN
55 34 68.0 547 1 CD19_MOUSE

Wed May 22 11:04:29 2002

CC EMBL; AF281310; AAF97596.1; -
CC InterPro; IPR002955; Tau_protein.
CC InterPro; IPR001084; Tubulin-bind.
CC Pfam; PF00418; tubulin-binding; 4.
CC PRINTS; PR01261; TAUPROTEIN.
CC PROSITE; PS00229; TAU_MAP; 4.
KW Microtubules; Cytoskeleton; Repeat; Acetylation; Phosphorylation.
FT INIT_MET 0
FT REPEAT 185 215 TAU/MAP MOTIF 1.
FT REPEAT 216 246 TAU/MAP MOTIF 2.
FT REPEAT 247 277 TAU/MAP MOTIF 3.
FT REPEAT 278 309 TAU/MAP MOTIF 4.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT DISULFID 232 263 BY SIMILARITY.
SQ SEQUENCE 382 AA; 39879 MW; D2D15A53AA00B8E7 CRC64;

Query Match 100.08; Score 50; DB 1; Length 382;
Best Local Similarity 100.08; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 138 YSSPGSPGT 146
|||||

RESULT 2
TAU_CAPHI
ID TAU_CAPHI STANDARD; PRT; 402 AA.
AC 002828;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE (Paired helical filament-tau) (PHF-tau).
GN MAPT OR TAU.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC TISSUE=Brain cortex;
RX MEDLINE=97012131; PubMed=8858947;
RA Nelson P.T., Stefansson K., Gulcher J., Saper C.B.;
RT "Molecular evolution of tau protein: implications for Alzheimer's disease.";
RL J. Neurochem. 67:1622-1632(1996).
CC -|- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION. CC -|- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS. CC -|- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; TAU-A (SHOWN HERE) AND TAU-B; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF TWO EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS THE ADDITIONAL TAU/MAP REPEAT. CC -|- TISSUE SPECIFICITY: EXPRESSED IN NEURONS. CC -|- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS. CC -|- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2, CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY). CC

CC -|- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
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CC EMBL; S83347; AAB50785.1; -
CC InterPro; IPR002955; Tau_protein.
CC InterPro; IPR001084; Tubulin-bind.
CC Pfam; PF00418; tubulin-binding; 4.
CC PRINTS; PR01261; TAUPROTEIN.
CC PROSITE; PS00229; TAU_MAP; 4.
KW Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation; Phosphorylation.
FT INIT_MET 0
FT REPEAT 205 235 TAU/MAP MOTIF 1.
FT REPEAT 236 266 TAU/MAP MOTIF 2.
FT REPEAT 267 297 TAU/MAP MOTIF 3.
FT REPEAT 298 329 TAU/MAP MOTIF 4.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT DISULFID 252 283 BY SIMILARITY.
FT VARSPLIC 33 61 MISSING (IN ISOFORM TAU-B).
FT VARSPLIC 236 266 MISSING (IN ISOFORM TAU-B).
SQ SEQUENCE 402 AA; 41716 MW; 3B523B684E9F8AEF CRC64;

Query Match 100.08; Score 50; DB 1; Length 402;
Best Local Similarity 100.08; Pred. No. 0.32; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 158 YSSPGSPGT 166
|||||

RESULT 3
TAU_BOVIN
ID TAU_BOVIN STANDARD; PRT; 447 AA.
AC P29172; P29173; Q28185; Q28186; Q28187; Q28188; Q28189; Q28190;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE (Paired helical filament-tau) (PHF-tau).
GN MAPT OR TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS TAU-A; TAU-B; TAU-G AND TAU-H).
RC TISSUE=Brain;
RX MEDLINE=89261765; PubMed=2498649;
RA Himmler A., Drechsel D., Kirschner M.W., Martin D.W. Jr.;
RT "Tau consists of a set of proteins with repeated C-terminal microtubule-binding domains and variable N-terminal domains.";
RL Mol. Cell. Biol. 9:1381-1388(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS TAU-A TO TAU-F AND TAU-I TO TAU-T).
RC TISSUE=Brain;
RX MEDLINE=89261766; PubMed=2498650;
RA Himmler A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts generate a protein family.";
RL Mol. Cell. Biol. 9:1389-1396(1989).
RN [3]
RP GLYCOSYLATION.
RX MEDLINE=97067111; PubMed=8910513;

RA Arnold C.S., Johnson G.V.W., Cole R.N., Dong D.L.-Y., Lee M.,
RT "The microtubule-associated protein tau is extensively modified with
RL J. Biol. Chem. 271:28741-28744 (1996).
CC - FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
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CC DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC - SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC - ALTERNATIVE PRODUCTS: AT LEAST 20 ISOFORMS; TAU-A/PBT43112 (SHOWN
CC HERE), TAU-B/PBT43-12, TAU-C, TAU-D, TAU-E, TAU-F, TAU-G/PBT4,
CC TAU-H/PBT7, TAU-I, TAU-J, TAU-K, TAU-L, TAU-M, TAU-N, TAU-O, TAU-
CC P, TAU-Q, TAU-R, TAU-S AND TAU-T; ARE PRODUCED BY ALTERNATIVE
CC SPLICING. THEY DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE
CC OF UP TO 6 OF THE 14 EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS
CC THE ADDITIONAL TAU/MAP REPEAT. TAU-A CDNA HAS BEEN CONSTRUCTED
CC FROM TWO OVERLAPPING CDNAS BY THE AUTHORS OF REF.1. TAU-G AND TAU-
CC H SEQUENCES BEGIN WITH EXON 6 OR A PART OF IT (EXON 6 IS MISSING
CC IN ISOFORMS THAT BEGIN WITH EXON 1). 3 DIFFERENT C-TERMINI ARE
CC OBTAINED EITHER BY THE RETENTION OR THE SPLICING OF INTRON 13/14
CC (2 DIFFERENT 5' SPLICING DONORS).
CC - TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC - INDUCTION: DURING NEURITE OUTGROWTH.
CC - DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC - PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
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CC MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC - PTM: O-LINKED N-ACETYLGLUCOSAMINATION AT MORE THAN 4 SITES PER
CC PROTEIN. SITE-SPECIFIC OR STOICHIOMETRIC CHANGES IN GLYCOSYLATION
CC MAY MODULATE TAU FUNCTION AND ALSO PLAY A ROLE IN PHF'S FORMATION.
CC - SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
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DR EMBL; L35346; AAA51609.1; JOINED.
DR EMBL; L35347; AAA51609.1; JOINED.
DR EMBL; L35348; AAA51609

CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.

RP SEQUENCE FROM N.A. (ISOFORMS TAU-B AND TAU-C)
RC TISSUE=Brain;

SEQUENCE 458 AA; 47841 MW; 00DE03DBA3000300 CACCA

RP SEQUENCE FROM N.A. (ISOFORMS TAU-B AND TAU-C)
RC TISSUE=Brain;

RX MEDLINE=88099510; PubMed=3122323;
 RA Lee G., Cowan N.J., Kirschner M.;
 RT "The primary structure and heterogeneity of tau protein from mouse
 RL brain."; Science 239:285-288(1988).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM B).
 RC STRAIN=ICR; TISSUE=Brain;
 RX MEDLINE=93182802; PubMed=7877441;
 RA Sawa A., Oyama F., Matsushita M., Ihara Y.;
 RT "Molecular diversity at the carboxyl terminus of human and rat tau."; Brain Res. Mol. Brain Res. 27:111-117(1994).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=94005827; PubMed=8402267;
 RA Couchie D., Gache Y., Mavilia C., Guilleminot J., Bridoux A.-M.,
 RA Nunez J.;
 RT "High molecular weight tau proteins and acquisition of neuronal
 RL polarity in peripheral nervous system."; C. R. Acad. Sci., III, Sci. Vie 316:404-409(1993).
 CC -1- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
 CC BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
 CC POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
 CC TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
 CC TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
 CC DETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
 CC DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
 CC ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
 CC ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
 CC -1- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
 CC CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; PMS-TAU (SHOWN HERE),
 CC TAU-A, TAU-B, TAU-C, TAU-D AND TAU-E; ARE PRODUCED BY ALTERNATIVE
 CC SPLICING. THEY DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE
 CC OF UP TO 5 OF THE 14 EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS
 CC THE ADDITIONAL TAU/MAP REPEAT. TWO DIFFERENT C-TERMINI ARE
 CC OBTAINED EITHER BY THE RETENTION OR THE SPLICING OF INTRON 13/14.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONS AND AT A LOWER LEVEL IN
 CC THE LIVER AND KIDNEY. PMS-TAU IS EXPRESSED IN THE PERIPHERAL
 CC NERVOUS SYSTEM WHILE THE OTHERS ARE EXPRESSED IN THE CENTRAL
 CC NERVOUS SYSTEM.
 CC -1- DEVELOPMENTAL STAGE: SHORTER FORMS OR LOW MOLECULAR WEIGHT TAU
 CC (LMW-TAU) ARE GENERALLY EXPRESSED AT EARLY DEVELOPMENT STAGES AND
 CC LONGER FORMS OR HIGH MOLECULAR WEIGHT TAU (HMW-TAU) IN THE ADULT
 CC BRAIN.
 CC -1- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
 CC CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
 CC -1- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
 CC S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
 CC CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
 CC MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
 CC MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
 CC -1- DISEASE: MAY BE INVOLVED IN THE PATHOGENESIS OF CYTOPLASMIC
 CC INCLUSIONS (AS MALLORY BODIES) IN LIVERS OF MICE CHRONICALLY
 CC INTOXICATED WITH GRISOFLUVIN OR DDC (3,5-DIETHOXYCARBONYL-2,4-
 CC DIHYDROCOLLIDINE), A MODEL FOR HUMAN ALCOHOLIC HEPATITIS.
 CC ALTERATION OF TAU (ABNORMAL PHOSPHORYLATION AND CROSSLINKING)
 CC COULD CONTRIBUTE TO MALLORY BODIES FORMATION AND DISTURBANCE OF
 CC MICROTUBULE FUNCTION IN ALCOHOLIC LIVER DISEASE.
 CC -1- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
 CC -----
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 DR EMBL; U12914; AAA58343.1; -;
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DR EMBL; M93266; -; NOT_ANNOTATED_CDS.
 DR EMBL; M18775; AAA40165.1; -;
 DR EMBL; M18776; AAA40166.1; -;
 DR EMBL; D30627; BAA18878.1; -;
 DR PIR; A28820; A28820.
 DR PIR; B28820; B28820.
 DR MGD; MGI:97180; Mapt.
 DR InterPro; IPR002955; Tau_protein.
 DR InterPro; IPR001084; Tubulin-bind.
 DR Pfam; PF00418; tubulin-binding; 7.
 DR PRINTS; PRO1261; TAUPROTEIN.
 DR PROSITE; PS00229; TAU MAP; 3.
 KW Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
 KW Phosphorylation.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT REPEAT 535 565 TAU/MAP MOTIF 1.
 FT REPEAT 566 596 TAU/MAP MOTIF 2.
 FT REPEAT 597 627 TAU/MAP MOTIF 3.
 FT REPEAT 628 659 TAU/MAP MOTIF 4.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT DISULFID 582 613 BY SIMILARITY.
 FT VARSPLIC 33 90 MISSING (IN ISOFORM TAU-B, ISOFORM TAU-C,
 FT VARSPLIC 91 112 MISSING (IN ISOFORM TAU-E).
 FT VARSPLIC 113 349 MISSING (IN ISOFORM TAU-B, ISOFORM TAU-C,
 FT VARSPLIC 367 432 MISSING (IN ISOFORM TAU-D AND ISOFORM TAU-E).
 FT VARSPLIC 566 596 MISSING (IN ISOFORM TAU-B AND ISOFORM TAU-E).
 FT VARSPLIC 732 732 L -> KAALLSQWVNSHDLATITDGL (IN
 FT CONFLICT 2 2 D -> N (IN REF. 1).
 FT CONFLICT 8 8 D -> N (IN REF. 1).
 FT CONFLICT 527 527 P -> T (IN REF. 2; CAA78121).
 FT CONFLICT 671 671 E -> Q (IN REF. 1).
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 Best Local Similarity 100.0%; Pred. No. 0.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSPGSPGT 9
 Db 488 YSSPGSPGT 496
 |||||
 RESULT 6
 TAU_RAT
 ID TAU_RAT STANDARD; PRT; 751 AA.
 AC P19332; O63567; O9QW06; O63567;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Microtubule-associated protein tau (Neurofibrillary tangle protein)
 DE (Paired helical filament-tau) (PHF-tau).
 DE MAPT OR MTAPT OR TAU.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM TAU-B).
 RC TISSUE=Phenochromocytoma;
 RX MEDLINE=92179305; PubMed=1542696;
 RA Goedert M., Spillantini M.G., Crowther R.A.;
 RT "Cloning of a big tau microtubule-associated protein characteristic of
 RL the peripheral nervous system."; Proc. Natl. Acad. Sci. U.S.A. 89:1983-1987(1992).
 RN [2]

- DT 16-OCT-2001 (Rel. 40, Last sequence update)
- DT 01-MAR-2002 (Rel. 41, Last annotation update)
- DE Microtubule-associated protein tau (Neurofibrillary tangle protein)
- DE (Paired helical filament-tau) (PHF-tau).
- GN MAPT OR MTBT1 OR TAU.
- OS Homo sapiens (Human).
- OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
- OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
- OX NCBI_TaxID=9606;
- RN [1]
- RP SEQUENCE FROM N.A. (ISOFORMS PNS-TAU; TAU-A AND TAU-F).
- RA Andreadis A.;
- RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
- RL [2]
- RP SEQUENCE FROM N.A. (ISOFORM TAU-A).
- RC TISSUE=Brain;
- RX MEDLINE=88234557; PubMed=3131773;
- RA Goedert M., Wischik C., Crowther R., Walker J., Klug A.;
- RT "Cloning and sequencing of the cDNA encoding a core protein of the
- RT paired helical filament of Alzheimer disease: identification as the
- RT microtubule-associated protein tau.";
- RL Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
- RN [3]
- RP SEQUENCE FROM N.A. (ISOFORMS TAU-B; TAU-C; TAU-E AND TAU-F).
- RC TISSUE=Brain;
- RX MEDLINE=90380393; PubMed=2484340;
- RA Goedert M., Spillantini M.G., Jakes R., Rutherford D., Crowther R.A.;
- RT "Multiple isoforms of human microtubule-associated protein tau:
- RT sequences and localization in neurofibrillary tangles of Alzheimer's
- RT disease.";
- RL Neuron 3:519-526(1989).
- RN [4]
- RP SEQUENCE FROM N.A. (ISOFORM TAU-D).
- RC TISSUE=Brain;
- RX MEDLINE=89251564; PubMed=2498079;
- RA Goedert M., Spillantini M.G., Foltier M.C., Ulrich J., Crowther R.A.;
- RT "Cloning and sequencing of the cDNA encoding an isoform of
- RT microtubule-associated protein tau containing four tandem repeats:
- RT differential expression of tau protein mRNAs in human brain.";
- RL EMBO J. 8:393-399(1989).
- RN [5]
- RP SEQUENCE FROM N.A. (ISOFORMS TAU-A AND FETAL-TAU).
- RC TISSUE=Fetal brain;
- RX MEDLINE=90180482; PubMed=2516729;
- RA Lee G., Neve R.L., Kosik K.S.;
- RT "The microtubule binding domain of tau protein.";
- RL Neuron 2:1615-1624(1989).
- RN [6]
- RP SEQUENCE FROM N.A. (ISOFORM TAU-F), AND ALTERNATIVE SPLICING.
- RX MEDLINE=93041757; PubMed=1420178;
- RA Andreadis A., Brown W.M., Kosik K.S.;
- RT "Structure and novel exons of the human tau gene.";
- RL Biochemistry 31:10626-10633(1992).
- RN [7]
- RP SEQUENCE OF 591-621 FROM N.A.
- RC TISSUE=Brain;
- RX MEDLINE=89193714; PubMed=2495000;
- RA Mori H., Hamada Y., Kawaguchi M., Honda T., Kondo J., Ihara Y.;
- RT "A distinct form of tau is selectively incorporated into Alzheimer's
- RT paired helical filaments.";
- RL Biochem. Biophys. Res. Commun. 159:1221-1226(1989).
- RN [8]
- RP SEQUENCE OF 1-72; 102-380; 467-496; 507-570; 576-582; 591-606;
- RP 615-633; 638-656; 660-663; 670-699 AND 702-757.
- RC TISSUE=Brain;
- RX MEDLINE=92381012; PubMed=1512244;
- RA Hasegawa M., Morishima-Kawashima M., Takio K., Suzuki M., Titani K.,
- RA Ihara Y.;
- RT "Protein sequence and mass spectrometric analyses of tau in the
- RT Alzheimer's disease brain.";
- RL J. Biol. Chem. 267:17047-17054(1992).
- RN [9]
- RP SEQUENCE OF 576-583; 607-610; 615-627; 638-647 AND 670-685,
- RP PHOSPHORYLATION, AND MUTAGENESIS.
- RX MEDLINE=95221434; PubMed=7706316;
- RA Drewes G., Trinczek B., Illenberger S., Biernat J., Schmitt-Ulms G.,
- RA Meyer H.E., Mandelkow E.-M., Mandelkow E.;
- RT "Microtubule-associated protein/microtubule affinity-regulating kinase
- RT (p10mark). A novel protein kinase that regulates tau-microtubule
- RT interactions and dynamic instability by phosphorylation at the
- RT Alzheimer-specific site serine 262.";
- RL J. Biol. Chem. 270:7679-7688(1995).
- RN [10]
- RP REVIEW.
- RX MEDLINE=91320377; PubMed=1713721;
- RA Goedert M., Crowther R.A., Garner C.C.;
- RT "Molecular characterization of microtubule-associated proteins tau and
- RT MAP2.";
- RL Trends Neurosci. 14:193-199(1991).
- RN [11]
- RP SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
- RX MEDLINE=20283597; PubMed=10747907;
- RA Maas T., Eidenmueller J., Brandt R.;
- RT "Interaction of tau with the neural membrane cortex is regulated by
- RT phosphorylation at sites that are modified in paired helical
- RT filaments.";
- RL J. Biol. Chem. 275:15733-15740(2000).
- RN [12]
- RP PHOSPHORYLATION, AND MUTAGENESIS.
- RX MEDLINE=98413833; PubMed=9735171;
- RA Sengupta A., Kabat J., Novak M., Wu Q., Grundke-Iqbal I., Iqbal K.;
- RT "Phosphorylation of tau at both Thr 231 and Ser 262 is required for
- RT maximal inhibition of its binding to microtubules.";
- RL Arch. Biochem. Biophys. 357:299-309(1998).
- RN [13]
- RP PHOSPHORYLATION, AND MUTAGENESIS.
- RX MEDLINE=98278959; PubMed=9614189;
- RA Illenberger S., Zheng-Fischer Q., Preuss U., Stamer K., Baumann K.,
- RA Trinczek B., Biernat J., Godemann R., Mandelkow E.-M., Mandelkow E.;
- RT "The endogenous and cell cycle-dependent phosphorylation of tau
- RT protein in living cells: implications for Alzheimer's disease.";
- RL Mol. Biol. Cell 9:1495-1512(1998).
- RN [14]
- RP GLYCATION.
- RX MEDLINE=97465580; PubMed=9326300;
- RA Nacharaju P., Ko L., Yen S.H.;
- RT "Characterization of in vitro glycation sites of tau.";
- RL J. Neurochem. 69:1709-1719(1997).
- RN [15]
- RP REVIEW ON VARIANTS.
- RX MEDLINE=20437008; PubMed=10899436;
- RA Goedert M., Spillantini M.G.;
- RT "Tau mutations in frontotemporal dementia FTDP-17 and their relevance
- RT for Alzheimer's disease.";
- RL Biochim. Biophys. Acta 1502:110-121(2000).
- RN [16]
- RP VARIANT FTDP17 M-653, AND VARIANTS N-284; A-288; Y-440 AND P-446.
- RX MEDLINE=98291804; PubMed=9629852;
- RA Poorkaj P., Bird T.D., Wijsman E., Nemens E., Garruto R.M.,
- RA Anderson L., Bird T.D., Wijsman E., Wiederholt W.C., Raskind M.,
- RA Schellenberg G.D.;
- RT "Tau is a candidate gene for chromosome 17 frontotemporal dementia.";
- RL Ann. Neurol. 43:815-825(1998).
- RN [17]
- RP ERRATUM.
- RX MEDLINE=98409513; PubMed=9736786;
- RA Dumanchin C., Camuzat A., Campion D., Verpillat P., Hannequin D.,
- RA Dubois B., Saugier-Verber P., Martin C., Penet C., Charbonnier F.,
- RA Agid Y., Frebourg T., Brice A.;
- RT "Segregation of a missense mutation in the microtubule-associated

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RT protein tau gene with familial frontotemporal dementia and
RL parkinsonism.; 7:1825-1829(1998).
RN [19]
RP VARIANTS FTDP17 VAL-588; LEU-617 AND TRP-722.
RX MEDLINE=98303385; PubMed=9641683;
RA Hutton M., Lendon C.L., Rizzu P., Baker M., Froelich S., Houlden H.,
RA Pickering-Brown S., Chakraverty S., Isaacs A., Grover A., Hackett J.,
RA Adamson J., Lincoln S., Dickson D., Davies P., Petersen R.C.,
RA Stevens M., de Graaff E., Wauters E., van Baren J., Hillebrand M.,
RA Joosse M., Kwon J.M., Nowotny P., Che L.K., Norton J., Morris J.C.,
RA Reed L.A., Trojanowski J., Basun H., Lannfelt L., Neystat M., Fahn S.,
RA Dark F., Tannenberg T., Dodd P.R., Hayward N., Kwok J.B.-J.,
RA Schofield P.R., Andreadis A., Snowden J., Craufurd D., Neary D.,
RA Owen F., Oostra B.A., Hardy J., Goate A., van Swieten J., Mann D.,
RA Lynch T., Heutink P.;
RA "Association of missense and 5'-splice-site mutations in tau with the
RT inherited dementia FTDP-17.";
RL Nature 393:702-705(1998).
RN [20]
RP VARIANT PPND LYS-595, AND VARIANT FTDP17 LEU-617.
RX MEDLINE=99007274; PubMed=9789048;
RA Clark L.N., Poorkaj P., Wszolek Z., Geschwind D.H., Nasreddine Z.S.,
RA Miller B., Li D., Payami H., Avert F., Markopoulou K., Andreadis A.,
RA D'Souza I., Lee V.M.-Y., Reed L., Trojanowski J.O., Zhukareva V.,
RA Bird T., Schellenberg G., Wilhelmsen K.C.;
RA "Pathogenic implications of mutations in the tau gene in
RT pallido-ponto-nigral degeneration and related neurodegenerative
RT disorders linked to chromosome 17.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13103-13107(1998).
RN [21]
RP VARIANTS FTDP17 VAL-588; LYS-596 DEL; LEU-617 AND TRP-722.
RX MEDLINE=99138654; PubMed=9973279;
RA Rizzo P., van Swieten J.C., Joosse M., Hasegawa M., Stevens M.,
RA Tibben A., Niermeijer M.F., Hillebrand M., Ravid R., Oostra B.A.,
RA Goedert M., van Duijn C.M., Heutink P.;
RA "High prevalence of mutations in the microtubule-associated protein
RT tau in a population study of frontotemporal dementia in the
RT Netherlands.";
RL Am. J. Hum. Genet. 64:414-421(1999).
RN [22]
RP VARIANTS FTDP17 LEU-617; MET-653 AND TRP-722.
RX MEDLINE=99229757; PubMed=10214944;
RA Nacharaju P., Lewis J., Easson C., Yen S., Hackett J., Hutton M.,
RA Yen S.H.;
RA "Accelerated filament formation from tau protein with specific FTDP-17
RT missense mutations.";
RL FEBS Lett. 447:195-199(1999).
RN [23]
RP VARIANT FTDP17/CBD SER-617.
Query Match 100.0%; Score 50; DB 1; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSPGSPGT 9
Db 513 YSSPGSPGT 521
RESULT 8
ID P2BL_CRYNE STANDARD; PRT; 639 AA.
AC 042773;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Serine/threonine protein phosphatase 2B catalytic subunit A1
DE (EC 3.1.3.16) (Calcineurin A1).
GN CNAL.
OC Cryptococcus neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

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OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=H99;
RX MEDLINE=97327538; PubMed=9184205;
RA Odom A., Muir S., Lim E., Toffaletti D.L., Perfect J., Heitman J.;
RA "Calcineurin is required for virulence of Cryptococcus neoformans.";
RL EMBO J. 16:2576-2589(1997).
CC -1- FUNCTION: CALCIUM-DEPENDENT, CALMODULIN-STIMULATED PROTEIN
CC PHOSPHATASE. THIS SUBUNIT MAY HAVE A ROLE IN THE CALMODULIN
CC ACTIVATION OF CALCINEURIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
CC phosphate.
CC -1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B). THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY.
CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-2B
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF042082; AAB97372.1; -
DR HSP; P08129; 1FJM.
DR InterPro; IPR000934; Ser_thr_phosphatse.
DR Pfam; PF00149; Stphosphatase; 1.
DR PRINTS; PR00114; STPHPTASE.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
DR HydroLase; Calmodulin-binding; Iron; Manganese.
KW SEQUENCE 639 AA; 71499 MW; 4B92EBE361C80579 CRC64;
SQ
Query Match 78.0%; Score 39; DB 1; Length 639;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SPGSPGT 9
Db 556 SPGSPGT 562
RESULT 9
ID PETL_RAT STANDARD; PRT; 710 AA.
AC P51574;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Oligopeptide transporter, small intestine isoform (peptide transporter
DE 1) (Intestinal H+/peptide cotransporter) (Proton-coupled dipeptide
DE cotransporter).
GN SLG15A1 OR PETTL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Small intestine;
RX MEDLINE=96180982; PubMed=8605246;
RA Miyamoto K., Shiraga T., Morita K., Yamamoto H., Haga H.,
RA Taketani Y., Tamai I., Sai Y., Tsuji A., Takeda E.;
RA "Sequence, tissue distribution and developmental changes in rat
RT intestinal oligopeptide transporter.";
RL Biochim. Biophys. Acta 1305:34-38(1996).
RN [2]
RP SEQUENCE FROM N.A.

```

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
 RA MEDLINE=96108664; PubMed=8531138;
 RX Saito H., Okuda M., Terada T., Sasaki S., Inui K.;
 RT "Cloning and characterization of a rat H⁺/peptide cotransporter
 RT mediating absorption of beta-lactam antibiotics in the intestine and
 RL kidney.";
 CC J. Pharmacol. Exp. Ther. 275:1631-1637 (1995).
 CC -1- FUNCTION: PROTON-COUPLED INTAKE OF OLIGOPETIDES OF 2 TO 4
 CC AMINO ACIDS WITH A PREFERENCE FOR DIPEPTIDES. MAY CONSTITUTE
 CC A MAJOR ROUTE FOR THE ABSORPTION OF PROTEIN DIGESTION END-
 CC PRODUCTS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----
 CC EMBL; D50664; BAA09318.1; -;
 CC EMBL; D50306; BAA08844.1; -;
 CC InterPro: IPR000109; PTR2.
 CC Pfam: PF00854; PTR2. 2.
 CC PROSITE: PS01022; PTR2_1; 1.
 CC PROSITE: PS01023; PTR2_2; 1.
 CC Peptide transport; Transmembrane; Symport; Glycoprotein.
 FT TRANSMEM 1 21 POTENTIAL.
 FT DOMAIN 22 53 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 54 74 POTENTIAL.
 FT DOMAIN 75 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 POTENTIAL.
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 139 POTENTIAL.
 FT DOMAIN 140 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 182 POTENTIAL.
 FT DOMAIN 183 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 219 POTENTIAL.
 FT DOMAIN 220 276 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 277 297 POTENTIAL.
 FT DOMAIN 298 327 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 328 348 POTENTIAL.
 FT DOMAIN 349 361 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 362 382 POTENTIAL.
 FT DOMAIN 383 586 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 587 607 POTENTIAL.
 FT DOMAIN 608 621 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 647 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 648 668 POTENTIAL.
 FT DOMAIN 669 710 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 510 510 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 532 532 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 539 539 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 241 241 R -> G (IN REF. 2).
 FT CONFLICT 259 259 N -> E (IN REF. 2).
 FT CONFLICT 279 280 IM -> MV (IN REF. 2).
 CC SEQUENCE 710 AA; 78928 MW; 435727A6C76F2D7B CRC64;

Query Match 76.0%; Score 38; DB 1; Length 710;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPG 8

Db 441 SSPGSPG 447

RESULT 10
 PDDL_HUMAN
 ID PDDL_HUMAN STANDARD; PRT; 756 AA.
 AC P51178;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
 DE (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III).
 GN PLCD1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RX MEDLINE=95197554; PubMed=7890667;
 RA Cheng H.F., Jiang M.J., Chen C.L., Liu S.M., Wong L.P.,
 RA Lomasney J.W., King K.;
 RT "Cloning and identification of amino acid residues of human
 RT phospholipase C delta 1 essential for catalysis.";
 RL J. Biol. Chem. 270:5495-5505(1995).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-Inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 CC EMBL; U09117; AAA73567.1; -;
 CC HSSP; P10688; LMAI.
 DR MIM; 602142; -;
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PL-PLC.
 DR InterPro: IPR000909; PL-PLC_X.
 DR InterPro: IPR001711; PL-PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00036; ehand; 2.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR ProDom; PD001202; PL-PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00148; PLCXc; 1.
 DR SMART; SM00149; PLCYc; 1.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR PROSITE; PS00003; PH_DOMAIN; 1.
 DR PROSITE; PS00004; C2_DOMAIN; 1.
 DR PROSITE; PS00007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS00008; PIPLC_Y_DOMAIN; 1.
 KW Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat.
 FT DOMAIN 21 130 PH.

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DR InterPro: IPR002064; DNA_pol_B.
 DR Pfam: PF00136; DNA_pol_B; 2.
 DR Pfam: PF03104; DNA_pol_B_exo; 1.
 DR PRINTS: PR00106; DRAPOLB.
 DR SMART: SM00486; POLB; 1.
 DR PROSITE: PS00116; DNA_POLYMERASE_B; 1.
 DR TRANSFERASE: DNA-directed DNA polymerase; DNA replication;
 KW DNA-binding; DNA repair; Nuclear protein; Zinc-finger.
 FT FT
 FT ZN_FING 3034 3049
 FT C4-TYPE (POTENTIAL).
 FT C4-TYPE (POTENTIAL).
 FT G -> A (IN REF. 2).
 FT A -> T (IN REF. 2).
 FT E -> Q (IN REF. 2).
 FT R -> Q (IN REF. 2).
 FT L -> P (IN REF. 2).
 FT L -> F (IN REF. 2).
 FT P -> L (IN REF. 2).
 FT A -> T (IN REF. 2).
 FT V -> G (IN REF. 3).
 SQ SEQUENCE 3122 AA; 350654 MW; A39846CAF7363BA8 CRC64;

Query Match 76.0%; Score 38; DB 1; Length 3122;
 Best Local Similarity 87.5%; Pred. No. 2.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
 DB 2108 YSSPDSPG 2115

RESULT 12

ID CDNI_FELCA STANDARD: PRT; 164 AA.
 AC O19002;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1 (p21) (CDK-interacting protein 1).
 GN CDKN1A OR CIP1 OR WAF1.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lymph node;
 RX MEDLINE=98036042; PubMed=9370275;
 RA Okuda M., Minehata K., Setoguchi A., Cho K.-W., Nakamura N.,
 RA Nishigaki K., Watari T., Cevallo S., O'Brien S.J., Tsujimoto H.,
 RA Hasegawa A.;
 RT "Cloning and chromosome mapping of the feline genes p21WAF1 and
 RT p27Kip1";
 RL Gene 198:141-147(1997).
 CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
 CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
 CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
 CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
 CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
 CC
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 CC
 CC EMBL; D84650; BAA23168.1;
 CC HSSP; P46527; 1JUSU.

FT CA_BIND 153 164 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 189 200 EF-HAND 2 (POTENTIAL).
 FT DOMAIN 296 440 DOMAIN X.
 FT DOMAIN 492 609 DOMAIN Y.
 FT DOMAIN 616 720 C2 DOMAIN.
 FT ACT_SITE 311 311 BY SIMILARITY.
 FT ACT_SITE 356 356 BY SIMILARITY.
 SQ SEQUENCE 756 AA; 85763 MW; AD9A4251C5EBADFB CRC64;

Query Match 76.0%; Score 38; DB 1; Length 756;
 Best Local Similarity 75.0%; Pred. No. 56;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
 DB 507 FSSPGTPG 514

RESULT 11

ID DPOZ_MOUSE STANDARD: PRT; 3122 AA.
 AC Q61493; O9QW6; O9JMD6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (Seizure related
 DE protein 4).
 GN REV3L OR POLZ OR SE24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/OLA; TISSUE=Testis;
 RC MEDLINE=99202265; PubMed=10102037;
 RA Van Sloun P.P.H., Romeijn R.J., Eeken J.C.J.;
 RT "Molecular cloning, expression and chromosomal localisation of the
 RT mouse Rev3l gene encoding the catalytic subunit of polymerase zeta";
 RL Mutat. Res. 433:109-116(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kajiwara K.;
 RT "Molecular analyses of Sez4 encoding murine homologue of yeast REV3 in
 RT brain neurons";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP SEQUENCE OF 2368-3122 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryonic brain;
 RX MEDLINE=96216731; PubMed=8645260;
 RA Kajiwara K., Nagawara H., Shimizu-Nishikawa K., Ookura T., Kimura M.,
 RA Sugaya E.;
 RT "Molecular characterization of seizure-related genes isolated by
 RT differential screening";
 RL Biochem. Biophys. Res. Commun. 219:795-799(1996).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
 CC + [DNA](N).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
 CC
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 CC
 CC EMBL; AF083464; AAC98785.1;
 CC EMBL; AB031049; BAA90768.1;
 CC EMBL; D78644; BAA11461.1;
 CC MGD; MG1:1337131; Rev31.

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DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Cell cycle; Nuclear protein; Zinc-finger.
FT ZNFING 13 41 C4-TYPE (POTENTIAL).
FT DOMAIN 141 156 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 164 AA; 18315 MW; 0F7912A76C78BF38_CRC64;

Query Match
Best Local Similarity 74.0%; Score 37; DB 1; Length 164;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPCT 9
Db 129 ASFGAGGT 136

RESULT 13
TI22_MOUSE
ID TI22_MOUSE STANDARD; PRT; 387 AA.
AC Q9EON3:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TSC22-related inducible leucine zipper protein 2.
GN TIL22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ersler M.A.; Belyavsky A.V.; Visser J.W.M.;
RT "Identification and characterization of a family of leucine zipper
RL genes related to TSC22.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR (BY SIMILARITY).
CC -1- SUBUNIT: FORMS HOMODIMER OR HETERODIMER. CAN FORM AN HETERODIMER
CC WITH TSC-22.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.
CC -----
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CC -----
DR EMBL: AF201286; AAC41219.1; -
DR InterPro: IPR000580; TSC-22_Dip_Bun.
DR Pfam: PF01166; TSC22; 1.
DR PRODOM: PD007152; TSC-22_Dip_Bun; 1.
DR PROSITE: PS01289; TSC22; 1.
KW Transcription regulation; Repressor; Nuclear protein.
FT DOMAIN 336 357 LEUCINE-ZIPPER.
SQ SEQUENCE 387 AA; 39987 MW; C78BB96B5B2DFB90_CRC64;

Query Match
Best Local Similarity 74.0%; Score 37; DB 1; Length 387;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
Db 19 YEGPGSPG 26

RESULT 14
TI22_HUMAN
ID TI22_HUMAN STANDARD; PRT; 395 AA.
AC Q9YJQ8:

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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE TSC22-related inducible leucine zipper protein 2 (TSC-22-like protein
DE THG-1).
DE TIL22.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kester H.A.; Blanchetot C.; den Hertog J.; van der Saag P.T.;
RA van der Burg B.;
RT "Transforming growth factor-beta-stimulated clone-22 is a member of a
RT family of leucine zipper proteins that can homo- and heterodimerize
RT and has transcriptional repressor activity.";
RL J. Biol. Chem. 274:27439-27447(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR.
CC -1- SUBUNIT: FORMS HOMODIMER OR HETERODIMER. CAN FORM AN HETERODIMER
CC WITH TSC-22.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.
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CC -----
DR EMBL: AJ133115; CAB43491.1; -
DR EMBL: BC001966; AAH01966.1; -
DR InterPro: IPR000580; TSC-22_Dip_Bun.
DR Pfam: PF01166; TSC22; 1.
DR PRODOM: PD007152; TSC-22_Dip_Bun; 1.
DR PROSITE: PS01289; TSC22; 1.
KW Transcription regulation; Repressor; Nuclear protein.
FT DOMAIN 344 365 LEUCINE-ZIPPER.
FT CONFLICT 355 356 NA -> KR (IN REF. 1).
SQ SEQUENCE 395 AA; 41026 MW; DA08B5617C9BB151_CRC64;

Query Match
Best Local Similarity 74.0%; Score 37; DB 1; Length 395;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
Db 19 YEGPGSPG 26

RESULT 15
VE2_PAPVE
ID VE2_PAPVE STANDARD; PRT; 415 AA.
AC PI1329;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Probable regulatory protein E2.
GN E2.
OS European elk papillomavirus (EEPV).
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10565;
RN [1]

```

Wed May 22 11:04:29 2002

RP SEQUENCE FROM N.A.
RX MEDLINE=87219878; PubMed=3034730;
RA Ahola H., Bergman P., Stroem A.C., Moreno-Lopez J., Petterson U.;
RT "Organization and expression of the transforming region from the
RT European elk papillomavirus (EEPV).";
RL Gene 50:195-205(1986).
CC -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACNNNNNGT-3') PRESENT
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC -1- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC EMBL; M15953; AAA66854.1; -
CC PIR; D29499; W2WLEP.
CC HSP; P03122; 2BOP.
CC InterPro: IPR001866; E2_N.
CC InterPro: IPR000427; Early2_C.
CC Pfam; PF00511; E2_C; 1.
CC Pfam; PF00508; E2_N; 1.
CC ProDom; PD000672; Early2_C; 1.
CC ProDom; PD000678; E2_N; 1.
CC Early protein; Transcription regulation; Activator; DNA-binding;
KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ SEQUENCE 415 AA; 46245 MW; 0B7BF6AEFE0AC80C CRC64;

Query Match 74.0%; Score 37; DB 1; Length 415;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSPGSPGT 9
II:IIIII:
Db 268 YSAPSSPGS 276

RESULT 16
ID NTR1_HUMAN STANDARD; PRT; 418 AA.
AC P30989; Q9H4T5; Q9H4H1;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Neurotensin receptor type 1 (NT-R1) (high-affinity leucocastine-
DE insensitive neurotensin receptor) (NTRH).
GN NTR1 OR NTRR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=93154505; PubMed=8381365;
RA Vita N., Laurent P., Lefort S., Chalou P., Dumont X., Kaghad M.,
RA Gully D., le Fur G., Ferrara P., Caput D.;
RT "Cloning and expression of a complementary DNA encoding a high
RT affinity human neurotensin receptor.";
RL FEBS Lett. 317:139-142(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Bauck O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
Buck D., Burrill W., Butler A.P., Carder C., Carter N.P., Clee C.M.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clegg S.,
Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaslahti M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
Ray V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
Marsh S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
RA "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS
CC ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC EMBL; X70070; CAA49675.1; -
CC EMBL; AL357033; CAC14923.1; -
CC EMBL; AL035669; CAC12747.1; -
CC PIR; S29506; S29506.
CC GCRdb; GCR_0577; -
CC GCRdb; GCR_2067; -
CC MIM; 162651; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC InterPro: IPR003985; NTL_rec.
CC InterPro: IPR003984; NT_rec.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR01479; NEUROTENSINR.
CC PRINTS; PR01480; NEUROTENSINR.
CC PROSITE; PS00437; G_PROTEIN_REC_F1_1; 1.
CC PROSITE; PS00437; G_PROTEIN_REC_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 63 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 64 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 120 2 (POTENTIAL).
FT DOMAIN 121 142 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 143 164 3 (POTENTIAL).
FT DOMAIN 165 187 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 188 209 4 (POTENTIAL).
FT DOMAIN 210 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 259 5 (POTENTIAL).
FT DOMAIN 260 303 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 304 325 6 (POTENTIAL).
FT DOMAIN 326 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 367 7 (POTENTIAL).
FT DOMAIN 368 418 CYTOPLASMIC (POTENTIAL).


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FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 141 224 BY SIMILARITY.
FT LIPID 383 PALMITATE (POTENTIAL).
FT CONFLICT 200 200 T -> A (IN REF. 2).
SQ SEQUENCE 418 AA; 46288 MW; BBBDEEC2BB6E390 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 418;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPCT 9
Db 6 SAPGTPCT 13

RESULT 17
IL5R_HUMAN STANDARD; PRT; 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-5 receptor alpha chain precursor (IL-5R-alpha) (CD125
  antigen).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;
RT "Molecular basis of the membrane-anchored and two soluble isoforms of
  the human interleukin 5 receptor alpha subunit";
RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
RN [3]
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=92005669; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of
  an IL5-specific alpha chain and a beta chain shared with the receptor
  for GM-CSF.";
RL Cell 66:1175-1184(1991).
RN [1]
RP FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
  BINDS TO IL-5.
RN [2]
RP SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
  CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
RN [3]
RP SUBCELLULAR LOCATION: Type I membrane protein.
RN [4]
RP ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
  HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
  ALTERNATIVE SPLICING.
RN [5]
RP TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
RN [6]
RP SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
RN [7]
RP SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
RN [8]
RP DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry;
  WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw125.htm".
RN [9]
RP THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M96652; AAA59152.1; -
DR EMBL; M96651; AAA59151.1; -
DR EMBL; M75914; AAA36110.1; -
DR EMBL; A28249; CAA01793.1; -
DR EMBL; A24587; CAA01731.1; -
DR EMBL; A26251; CAA01794.1; -
DR PIR; A40267; A40267.
DR MIM; 147851; -
DR InterPro; IPR002996; CRLA.
DR InterPro; IPR003532; Hematopo_receptor_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT DOMAIN 21 342 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 343 362 POTENTIAL.
FT DOMAIN 363 420 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 333 335 NDE -> FSR (IN SOLUBLE ISOFORM S1).
FT VARSPLIC 336 420 MISSING (IN SOLUBLE ISOFORM S1).
FT VARSPLIC 333 333 MISSING (IN SOLUBLE ISOFORM S2).
FT VARSPLIC 334 420 MISSING (IN SOLUBLE ISOFORM S2).
SQ SEQUENCE 420 AA; 47700 MW; 420681FBC6B51700 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 420;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 18
DHAL_DEIRA STANDARD; PRT; 515 AA.
AC Q9RYG9; O32502;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Aldehyde dehydrogenase (EC 1.2.1.3).
GN ALDA OR DRA0348.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RN [2]
RP STRAIN=R1.
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vanatavean J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarov K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.N.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
  radiodurans R1.";
RL Science 286:1571-1577(1999).
RN [2]
RP SEQUENCE OF 1-258 FROM N.A.
RX STRAIN=K08301;
RA Narumi I., Du Z., Alatas Z., Kitayama S., Watanabe H.;
RT "Isolation and characterization of pprA, a novel Deinococcus
  radiodurans gene involved in DNA repair.";

```

Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
-1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
-1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

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EMBL; AE001863; AAF12436.1; -
EMBL; AB003475; BAA21372.1; -
HSSP; P05091; 1CW3.
TIGR; DRA0348; -
InterPro: IPR002086; Aldehyde_dehydr.
Pfam; PF00171; aldehyd; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
Oxidoreductase; NAD; Complete proteome.
NP_BIND 228 234 NAD (ADP PART) (BY SIMILARITY).
ACT_SITE 272 272 BY SIMILARITY.
ACT_SITE 311 311 BY SIMILARITY.
SEQUENCE 515 AA; 56409 MW; D8BB5DDF7D2DBBC0 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 515;
Best Local Similarity 55.6%; Pred. NO. 54;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSPGSPGT 9
Db 13 YANPGTPGS 21

RESULT 19
ZYX_CHICK
ID ZYX_CHICK STANDARD; PRT; 542 AA.
AC Q04584;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zyxin.
DE Zyxin.
GN ZYX.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107157; PubMed=1469049;
RA Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
RT "zyxin and cCRP: two interactive LIM domain proteins associated with the cytoskeleton";
RL J. Cell Biol. 119:1573-1587(1992).
CC -1- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION.
CC SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN CYTOSKELETON NEAR THE ADHESION PLAQUES.
CC -1- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC IONS.

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EMBL; X69190; CAA48936.1; -
PIR; A44358; A44358.
InterPro: IPR001781; LIM.
InterPro: IPR001841; Znf_ring.
Pfam; PF00412; LIM; 3.
ProDom; PD000094; LIM; 3.
SMART; SM00132; LIM; 3.
SMART; SM00184; RING; 1.
PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS00023; LIM_DOMAIN_2; 3.
Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.
KW Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.
FT DOMAIN 83 90 PRO-RICH.
FT DOMAIN 103 130 PRO-RICH.
FT DOMAIN 352 411 LIM 1.
FT DOMAIN 412 471 LIM 2.
FT DOMAIN 472 538 LIM 3.
FT VARIANT 463 463 D -> V.
SQ SEQUENCE 542 AA; 58537 MW; 9D898AC180C680FC CRC64;

Query Match 74.0%; Score 37; DB 1; Length 542;
Best Local Similarity 75.0%; Pred. NO. 57;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSPGSPGT 9
Db 2 ASPGTPGT 9

RESULT 20
YQ36_CAEEL
ID YQ36_CAEEL STANDARD; PRT; 963 AA.
AC Q09457;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative cuticle collagen C09G5.6.
GN C09G5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Palmer S.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).
CC -1- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-LINKS (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE COLLAGENS.

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EMBL; Z46791; CAA86755.1; -
WormPep; C09G5.6; CE01486.
InterPro: IPR002486; Col_cuticle_N.
InterPro: IPR000087; Collagen.
Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col_cuticle_N; 1.
KW Hypothetical protein; Cuticle; Connective tissue; Repeat; Multigene family; Collagen.
FT DOMAIN 392 423 TRIPLE-HELICAL REGION.

Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
-1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
-1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

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EMBL; AE001863; AAF12436.1; -
EMBL; AB003475; BAA21372.1; -
HSSP; P05091; 1CW3.
TIGR; DRA0348; -
InterPro: IPR002086; Aldehyde_dehydr.
Pfam; PF00171; aldehyd; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
Oxidoreductase; NAD; Complete proteome.
NP_BIND 228 234 NAD (ADP PART) (BY SIMILARITY).
ACT_SITE 272 272 BY SIMILARITY.
ACT_SITE 311 311 BY SIMILARITY.
SEQUENCE 515 AA; 56409 MW; D8BB5DDF7D2DBBC0 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 515;
Best Local Similarity 55.6%; Pred. NO. 54;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSPGSPGT 9
Db 13 YANPGTPGS 21

RESULT 19
ZYX_CHICK
ID ZYX_CHICK STANDARD; PRT; 542 AA.
AC Q04584;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zyxin.
DE Zyxin.
GN ZYX.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107157; PubMed=1469049;
RA Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
RT "zyxin and cCRP: two interactive LIM domain proteins associated with the cytoskeleton";
RL J. Cell Biol. 119:1573-1587(1992).
CC -1- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION.
CC SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN CYTOSKELETON NEAR THE ADHESION PLAQUES.
CC -1- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC IONS.

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EMBL; X69190; CAA48936.1; -
PIR; A44358; A44358.
InterPro: IPR001781; LIM.
InterPro: IPR001841; Znf_ring.
Pfam; PF00412; LIM; 3.
ProDom; PD000094; LIM; 3.
SMART; SM00132; LIM; 3.
SMART; SM00184; RING; 1.
PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS00023; LIM_DOMAIN_2; 3.
Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.
KW Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.
FT DOMAIN 83 90 PRO-RICH.
FT DOMAIN 103 130 PRO-RICH.
FT DOMAIN 352 411 LIM 1.
FT DOMAIN 412 471 LIM 2.
FT DOMAIN 472 538 LIM 3.
FT VARIANT 463 463 D -> V.
SQ SEQUENCE 542 AA; 58537 MW; 9D898AC180C680FC CRC64;

Query Match 74.0%; Score 37; DB 1; Length 542;
Best Local Similarity 75.0%; Pred. NO. 57;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSPGSPGT 9
Db 2 ASPGTPGT 9

RESULT 20
YQ36_CAEEL
ID YQ36_CAEEL STANDARD; PRT; 963 AA.
AC Q09457;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative cuticle collagen C09G5.6.
GN C09G5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Palmer S.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).
CC -1- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-LINKS (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE COLLAGENS.

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EMBL; Z46791; CAA86755.1; -
WormPep; C09G5.6; CE01486.
InterPro: IPR002486; Col_cuticle_N.
InterPro: IPR000087; Collagen.
Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col_cuticle_N; 1.
KW Hypothetical protein; Cuticle; Connective tissue; Repeat; Multigene family; Collagen.
FT DOMAIN 392 423 TRIPLE-HELICAL REGION.

FT DOMAIN 441 503 TRIPLE-HELICAL REGION.
FT DOMAIN 506 567 TRIPLE-HELICAL REGION.
FT DOMAIN 663 666 POLY-PRO.
FT DOMAIN 685 688 POLY-PRO.
SQ SEQUENCE 963 AA; 107031 MW; AFE895A75909F66E CRC64;

Query Match 74.0%; Score 37; DB 1; Length 963;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
Db 559 SARGAPGT 566

RESULT 21

RGSC-RAT
ID RGSC-RAT STANDARD; PRT; 1387 AA.
AC O08774; O88383;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Regulator of G-protein signaling 12 (RGS12).
GN RGS12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97312490; PubMed=9168931;
RA Snow B.E., Antonio L., Suggs S., Gutstein H.B., Siderovski D.P.;
RT "Molecular cloning and expression analysis of rat Rgs12 and Rgs14.";
RL Biochem. Biophys. Res. Commun. 233:770-777(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98316347; PubMed=96511375;
RA Snow B.E., Hall R.A., Krums A.M., Brothers G.M., Bouchard D.,
RA Brothers C.A., Chung S., Mangion J., Gilman A.G., Lefkowitz R.J.,
RA Siderovski D.P.;
RT "GTPase activating specificity of RGS12 and binding specificity of an
alternatively spliced PDZ (PSD-95/Dlg/20-1) domain.";
RL J. Biol. Chem. 273:17749-17755(1998).
CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
THEIR INACTIVE GDP-BOUND FORM.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO ISOFORMS THAT ARISE
FROM ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN AND LUNG
AND LOWER LEVELS IN TESTIS, HEART, AND SPLEEN.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PID DOMAIN.

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CC EMBL; U92280; AAC53176.1;
CC EMBL; AF035151; AAC40154.1;
CC HSP; P49799; IAGR
DR InterPro; IPR003109; GoLoco.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR000050; PID_domain.
DR InterPro; IPR003116; RBD.

DR InterPro; IPR000342; RGS.
DR Pfam; PF02188; GoLoco; 1.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00640; PID; 1.
DR Pfam; PF02196; RBD; 2.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; RGS; 1.
DR SMART; SM00390; GoLoco; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00462; PTB; 1.
DR SMART; SM00455; RBD; 2.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS01179; PID; 1.
DR PROSITE; PS0132; RGS; 1.
KW Signal transduction inhibitor; Nuclear protein; Alternative splicing.
FT DOMAIN 21 97 PDZ.
FT DOMAIN 227 339 RGS.
FT DOMAIN 715 832 RGS.
FT DOMAIN 1368 1373 POLY-PRO.
FT VARSPLIC 1 648 MISSING (IN ISOFORM PDZ-LESS).
FT VARSPLIC 649 666 SEFRRRRSLTRSLDDLE -> MNLEKGLSDSDVFDQQ
(IN ISOFORM PDZ-LESS).
SQ SEQUENCE 1387 AA; 150468 MW; 958047D106B08310 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 1387;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 1296 HSTPGPGT 1304

RESULT 22

WA_EWEMI
ID WA_EWEMI STANDARD; PRT; 1986 AA.
AC Q03149;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Conidial green pigment synthase (EC 2.3.1.-).
GN WA.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93101122; PubMed=1465094;
RA Mayorga M.E., Timberlake W.E.;
RT "The developmentally regulated Aspergillus nidulans wa gene encodes a
polypeptide homologous to polyketide and fatty acid synthases.";
RL Mol. Gen. Genet. 235:205-212(1992).
CC -1- FUNCTION: THIS PROTEIN CONDENSES CARBON UNITS TO FORM AN
INTERMEDIATE YELLOW POLYKETIDE PIGMENT THAT IS POLYMERIZED
BY CONIDIAL LACCASE TO FORM THE GREEN PIGMENT IN MATURE
ASEXUAL SPORES (CONIDIA).
CC -1- COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTHETHEINES
(POTENTIAL).
CC -1- PATHWAY: BIOSYNTHESIS OF CONIDIAL GREEN PIGMENT.
CC -1- SIMILARITY: CONTAINS 2 ACYL CARRIER DOMAINS.

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EMBL: X65866; CAA46695.1; -
 PIR; S28353; S28353.
 DR InterPro: IPR001227; Acyltransf_domain.
 DR InterPro: IPR000794; Ketoacyl-synt.
 DR InterPro: IPR003880; Phosphopant_attach.
 DR Pfam: PF00698; Acyltransf; 1.
 DR Pfam: PF0109; ketoacyl-synt; 1.
 DR Pfam: PF02801; ketoacyl-synt_C; 1.
 DR Pfam: PF00550; pp-binding; 2.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; 1.
 DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE: PS00075; ACP_DOMAIN; 2.
 KW Transferrase: Phosphopantetheine; Multifunctional enzyme; Repeat.
 FT DOMAIN 529 582 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
 FT DOMAIN 991 1024 ACYL/MALONYL TRANSFERASES (BY SIMILARITY).
 FT DOMAIN 1650 1719 ACYL CARRIER (ACP) 1.
 FT DOMAIN 1772 1841 ACYL CARRIER (ACP) 2.
 FT ACT_SITE 548 548 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
 FT ACT_SITE 1001 1001 ACYL/MALONYL TRANSFERASES (BY SIMILARITY).
 FT BINDING 1682 1682 PHOSPHOPANTETHEINE (BY SIMILARITY).
 FT BINDING 1804 1804 PHOSPHOPANTETHEINE (BY SIMILARITY).
 SQ SEQUENCE 1986 AA; 216634 MW; 74EF0940FF40EE9A CRC64;

Query Match 74.0%; Score 37; DB 1; Length 1986;
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 III IIII
 DB 1749 SSPASPGT 1756

RESULT 23
 SAXI_MOUSE
 ID SAXI_MOUSE STANDARD; PRT; 305 AA.
 AC P42580;
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 15-JUL-1998 (Rel. 36; Last annotation update)
 DE Homeobox protein SAX-1 (NKX-1.1).
 GN SAXI OR NKX1-1 OR NKX-1.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=95399317; PubMed=7669696;
 RA Schubert F.R., Fainsod A., Gruenbaum Y., Gruss P.;
 RT "Expression of the novel murine homeobox gene Sax-1 in the developing nervous system."
 RL Mech. Dev. 51:99-114(1995).
 RN [2]
 RP SEQUENCE OF 289-305 FROM N.A.
 RC STRAIN=BALB/C;
 RA Hong S.B., Kim S.-J., Noh M.-J., Lee Y.M., Kim Y.S., Yoo O.J.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY FUNCTION IN CELL SPECIFICATION, PARTICULARLY IN THE CNS.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING POSTERIOR CENTRAL NERVOUS SYSTEM. FIRST SEEN IN THE ECTODERM LATERAL TO THE PRIMITIVE STREAK, LATER IT ENCOMPASSES THE NEURAL PLATE. STARTING AT DAY 9.5 PC, IT IS EXPRESSED IN DISTINCT AREAS OF SPINAL CORD, HINDBRAIN, MIDBRAIN AND FOREBRAIN.
 CC -!- SIMILARITY: BELONGS TO THE NK-1 FAMILY OF HOMEBOX PROTEINS.
 CC
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 DR EMBL: X75384; CAA53153.1; -
 DR EMBL: U58137; AAB06948.1; -
 DR HSSP: P02836; 3HDD.
 DR MGD; MGI:104806; Saxl.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS: PR00024; HOMEBOX.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 FT DOMAIN 88 96 POLY-GLU.
 FT DOMAIN 143 148 POLY-ARG.
 FT DNA_BIND 156 215 HOMEBOX.
 FT DOMAIN 239 242 POLY-GLY.
 SQ SEQUENCE 305 AA; 32012 MW; E02E09A04053FF1B CRC64;

Query Match 72.0%; Score 36; DB 1; Length 305;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :IIIIII:
 DB 134 ASPGSPGS 141

RESULT 24
 PYCA_METJA
 ID PYCA_METJA STANDARD; PRT; 501 AA.
 AC Q58626;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
 GN PYCA OR MJ1229.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 OC NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=868087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kierlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."
 RL Science 273:1058-1073(1996).
 RN [2]
 RP SEQUENCE OF 1-12, AND FUNCTION.
 RX MEDLINE=21034791; PubMed=11195096;
 RA Mukhopadhyay B., Patel V.J., Wolfe R.S.;
 RT "A stable archaeal pyruvate carboxylase from the hyperthermophile Methanococcus jannaschii."
 RL Arch. Microbiol. 174:406-414(2000).
 CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND.
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +

"Cloning of the human and mouse type X collagen genes and mapping of the mouse type X collagen gene to chromosome 10."; Eur. J. Biochem. 206:217-224(1992).

[4]
 SEQUENCE OF 385-627 FROM N.A.

STRAIN=C57BL;
MEDLINE=92182017; PubMed=1543751;

Elima K., Metsaeranta M., Kallio J., Peraelae M., Eerola I.,
Garofalo S., de Crombrughe B., Vuorio E.

"Specific hybridization probes for mouse alpha 2(IX) and alpha 1(X) collagen mRNAs.";

Biochim. Biophys. Acta 1130:78-80(1992).

CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.

- |- SUBUNIT: HOMOTRIMER.
- |- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING SEQUENCE.
- |- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING SEQUENCE.

-I- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.

-|- SIMILARITY: CONTAINS 1 CIQ DOMAIN.

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EMail: Y67348, CAA47763]:-

EMBL	U07340	C9A44741.1	-
EMBL	X65121	C9A44741.1	-
EMBL	X63013	C9A44741.1	-

EMBL; Z21610; CAA79736.1; -
PTR: S28807; S28807.

PIR; S31216; S31216.
PIR; S22215; S22215.

MGI: 88445; Coll10a1.
InterPro: IPR001073; Clq.

InterPro; IPR000087; Collagen.
Pfam; PF00386; Clq; 1.

pfam: PF01391; Collagen; 6.
PRINTS; PR00007; COMPLEMNTC1Q.

SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.

RESULT 28
 TRI2_STRCO STANDARD: PRT; 1171 AA.
 AC Q9RKB9;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Putative Tricorn protease homolog 2 (EC 3.4.21.-).
 GN TRI2 OR SCE87.19.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D., Thomson N.R., Parkhill J., Barrell B.G.,
 RA Rajandream M.A.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Degrades oligopeptides in a sequential manner
 CC (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S41 (SERINE PROTEASE).
 CC
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 CC
 DR EMBL; AL132674; CAB59664.1;
 DR MEROPS; S41A;
 DR InterPro; IPR003581; TSPc.
 DR SMART; SM00245; TSPc; 1.
 KW Hydrolase; Serine protease.
 FT DOMAIN 842 941
 FT SITE 1022 1022
 FT ACT_SITE 827 827
 FT ACT_SITE 1051 1051
 FT ACT_SITE 1052 1052
 SQ SEQUENCE 1171 AA; 125660 MW; 9C53019CEC0B0A25 CRC64;
 Query Match 72.0%; Score 36; DB 1; Length 1171;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 SPGSPGT 9
 Db 487 TPGSPGT 493
 RESULT 29
 MAP2_HUMAN STANDARD: PRT; 1827 AA.
 AC P11137; Q99976; Q99975;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Microtubule-associated protein 2 (MAP 2) (MAP2B) (Contains: MAP2C).
 GN MAP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Price R.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.

[2]
 RN RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain;
 RX MEDLINE=94124038; PubMed=8294038;
 RA Albala J.S., Kalcheva N., Shafit-zagardo B.;
 RT "Characterization of the transcripts encoding two isoforms of human
 RL microtubule-associated protein-2 (MAP-2).";
 RL Gene 136:377-378(1993).
 RN [3]
 RP SEQUENCE OF 493-1562 FROM N.A.
 RX MEDLINE=88274407; PubMed=2455776;
 RA Kosik K.S., Orecchio L.D., Bakalis S., Duffy L., Neve R.L.;
 RT "Partial sequence of MAP2 in the region of a shared epitope with
 RL Alzheimer neurofibrillary tangles.";
 RL J. Neurochem. 51:587-598(1988).
 CC -1- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
 CC STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
 CC SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
 CC FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
 CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS
 CC
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 CC
 DR EMBL; U01828; AAA03354.1;
 DR EMBL; U89330; AAB48098.1;
 DR EMBL; U89329; AAB48097.1;
 DR EMBL; M25668; AAA59552.1;
 DR PIR; PLO024; QRHUMT.
 DR MIM; L57130;
 DR InterPro; IPR001084; Tubulin-bind.
 DR Pfam; PF00418; tubulin-binding; 3.
 DR PROSITE; PS00329; TAU_MAP; 2.
 KW Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
 FT DOMAIN 147 1467 CALMODULIN-BINDING (POTENTIAL).
 FT REPEAT 1661 1691 TAU/MAP MOTIF.
 FT REPEAT 1692 1722 TAU/MAP MOTIF.
 FT REPEAT 1723 1754 TAU/MAP MOTIF.
 FT VARSPLIC 152 1507 MISSING (IN ISOFORM MAP2C).
 FT CONFLICT 9 9 A -> G (IN REF. 2).
 FT CONFLICT 37 37 R -> A (IN REF. 2).
 FT CONFLICT 108 108 A -> G (IN REF. 2).
 FT CONFLICT 152 155 MISSING (IN REF. 2).
 FT CONFLICT 187 187 S -> K (IN REF. 2).
 FT CONFLICT 1655 1655 A -> GL (IN REF. 2).
 FT CONFLICT 1736 1736 V -> A (IN REF. 2).
 SQ SEQUENCE 1827 AA; 199610 MW; BAC36D0030F5F455 CRC64;
 Query Match 72.0%; Score 36; DB 1; Length 1827;
 Best Local Similarity 72.7%; Pred. No. 3e+02;
 Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 Qy 1 YSS--PGSPGT 9
 Db 1609 YSSRTPGTPGT 1619
 RESULT 30
 MAP2_MOUSE STANDARD: PRT; 1828 AA.
 ID MAP2_MOUSE
 AC P20357;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Microtubule-associated protein 2 (MAP 2).

GN	MAP2 OR MTAP2.	RT	"Complete cDNA sequence encoding rat high and low molecular weight MAP2c.";
OS	Mus musculus (Mouse).	RL	Nucleic Acids Res. 18:2822-2822(1990).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	RN	[2]
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	RP	SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
CC	NCBI_TaxID=10090;	RC	STRAIN=Wistar; Tissue=Brain;
RN	[1]	RX	MEDLINE=91060576; PubMed=2174050;
RP	SEQUENCE FROM N.A.	RA	Kindler S., Schulz B., Goedert M., Garner C.C.;
RX	MEDLINE=89083571; PubMed=3205744;	RT	"Molecular structure of microtubule-associated protein 2b and 2c from rat brain.";
RA	Wang D., Lewis S.A., Cowan N.J.;	RL	J. Biol. Chem. 265:19679-19684(1990).
RT	"Complete sequence of a cDNA encoding mouse MAP2c.";	RN	[3]
RL	Nucleic Acids Res. 16:11369-11370(1988).	RP	SEQUENCE OF 1-151; 1515-1694 AND 1726-1861 FROM N.A.
RP	[2]	RX	MEDLINE=90221819; PubMed=2326166;
RX	Wang D., Wang D., Cowan N.J.;	RA	Doll T., Papadrikopoulou A., Matus A.;
RT	"Microtubule-associated protein MAP2 shares a microtubule binding motif with tau protein.";	RT	"Nucleotide and amino acid sequences of embryonic rat MAP2c.";
RL	Science 242:936-939(1988).	RL	Nucleic Acids Res. 18:361-361(1990).
CC	-!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.	RN	[4]
CC	-!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.	RP	DISCUSSION OF SEQUENCE.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RX	MEDLINE=89365159; PubMed=2770869;
DR	EMBL; M21041; AAA39490.1; -	RA	Papadrikopoulou A., Doll T., Tucker R.P., Garner C.C., Matus A.;
DR	PIR; S06467; S06467.	RT	"Embryonic MAP2 lacks the cross-linking sidearm sequences and dendritic targeting signal of adult MAP2c.";
DR	PIR; A0115; A40115.	RL	Nature 340:650-652(1989).
DR	MGI; MGI:97175; Mtap2.	RN	[5]
DR	InterPro; IPR001084; Tubulin-bind.	RP	SEQUENCE OF 1695-1725 FROM N.A.
DR	Pfam; PF00418; tubulin-binding; 3.	RX	MEDLINE=94110302; PubMed=8482767;
DR	PROSITE; PS00229; TAU_MAP; 2.	RA	Doll T., Meichsner M., Riederer B.M., Honegger P., Matus A.;
DR	Microtubules; Repeat; Calmodulin-binding. (POTENTIAL).	RT	"An isoform of microtubule-associated protein 2 (MAP2) containing four repeats of the tubulin-binding motif.";
FT	DOMAIN 1452 1472	RL	J. Cell Sci. 106:633-640(1993).
FT	REPEAT 1662 1692	CC	-!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
FT	REPEAT 1693 1723	CC	-!- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
FT	REPEAT 1724 1755	CC	-!- DEVELOPMENTAL STAGE: MAP2C IS EXPRESSED DURING EMBRYONIC BRAIN DEVELOPMENT AND UNTIL POSTNATAL DAY 10. MAP2B IS EXPRESSED THROUGHOUT BRAIN DEVELOPMENT.
FT	SEQUENCE 1828 AA; 198980 MW; 200BC59E360538CA CRC64;	CC	-!- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
Query Match	72.0%; Score 36; DB 1; Length 1828;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Best Local Similarity	72.7%; Pred. No. 3e+02;	CC	EMBL; X51842; CAA36135.1; -
Matches	8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;	DR	EMBL; X17682; CAA35667.1; -
Oy	1 YSS--PGSPGT 9	DR	EMBL; X71487; CAA50588.1; -
Db	1613 YSSRTPTGTPGT 1623	DR	PIR; S07887; S07887.
		DR	PIR; S10003; S10003.
		DR	PIR; A37981; A37981.
RESULT 31		DR	InterPro; IPR001084; Tubulin-bind.
ID	MAP2_RAT	DR	Pfam; PF00418; tubulin-binding; 4.
AC	P15146;	DR	PROSITE; PS00229; TAU_MAP; 3.
DT	01-APR-1990 (Rel. 14, Created)	KW	Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
DT	01-JUN-1994 (Rel. 29, Last sequence update)	FT	DOMAIN 1454 1474
DT	16-OCT-2001 (Rel. 40, Last annotation update)	FT	REPEAT 1664 1694
DE	Microtubule-associated protein 2 (MAP2) [Contains: MAP2C].	FT	REPEAT 1695 1725
GN	MAP2.	FT	REPEAT 1726 1756
OS	Rattus norvegicus (Rat).	FT	REPEAT 1757 1788
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT	VARSPPLIC 152 1514
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	FT	MISSING (IN ISOFORM MAP2C).
CC	NCBI_TaxID=10116;	FT	MISSING (IN ISOFORM WITH 3 TAU/MAP REPEATS).
RN	[1]	FT	SEQUENCE 1861 AA; 202409 MW; 42DCF116D21EF54E CRC64;
RP	SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.		
RC	STRAIN=Wistar; Tissue=Brain;	Query Match	72.0%; Score 36; DB 1; Length 1861;
RX	MEDLINE=90251471; PubMed=2339070;	Best Local Similarity	72.7%; Pred. NO. 3.1e+02;
RA	Kindler S., Schwanke B., Schulz B., Garner C.C.;	Query Match	72.0%; Score 36; DB 1; Length 1861;
		Best Local Similarity	72.7%; Pred. NO. 3.1e+02;

Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 QY 1 YSS--PCSPGT 9
 ||| ||:||||
 Db 1615 YSSRTCTCTCT 1625

RESULT 32
 CDNL_MOUSE
 ID CDNL_MOUSE STANDARD; PRT; 159 AA.
 AC P39689;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1 (Melanoma differentiation
 associated protein) (P21) (CDK-interacting protein 1).
 GN CDKN1A OR CIP1 OR WAF1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BXSB; TISSUE=Spleen;
 RX MEDLINE=94366751; PubMed=8084607;
 RA Huppi K., Sliwarski D., Dosik J., Michieli P., Chedid M., Reed S.,
 RA Mock B., Givol D., Mushinski J.F.;
 RT "Molecular cloning, sequencing, chromosomal localization and
 expression of mouse p21 (Waf1).";
 RL Oncogene 9:3017-3020(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95316868; PubMed=7796420;
 RA El-Deiry W.S., Tokino T., Waldman T., Velculescu V., Oliner J.D.,
 RA Burrell M., Hill D.E., Rees J.L., Hamilton S.R., Kinzler K.W.,
 RA Vogelstein B.;
 RT "Topological control of p21WAF1/CIP1 expression in normal and
 neoplastic tissues";
 RL Cancer Res. 55:2910-2919(1995).
 RN [3]
 RP SEQUENCE OF 1-143 FROM N.A.
 RX MEDLINE=94061997; PubMed=8242752;
 RA El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons R.,
 RA Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;
 RA "WAF1, a potential mediator of p53 tumor suppression.";
 RL Cell 75:817-825(1993).
 CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
 ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
 DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
 ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
 KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- INDUCTION: BY P53, MEZEREIN (ANTILEUKEMIC COMPOUND) AND INTERFERON
 BETA.
 CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
 CC
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 CC
 CC EMBL; U09507; AAB60456.1; -
 CC EMBL; U24173; AAC52220.1; -
 CC PIR; A49438; A49438.
 CC HSSP; P46527; 1JSU.
 CC MGD; MGI:104556; Cdkn1a.
 CC InterPro; IPR003175; CDI.
 CC Pfam; PF02234; CDI; 1.
 CC Cell cycle; Nuclear protein; 2inc-finger.
 CC ZN_FING 12 40
 CC C4-TYPE (POTENTIAL).

FT CONFLICT 30 30 R -> S (IN REF. 3).
 FT CONFLICT 56 57 TP -> RQ (IN REF. 3).
 SQ SEQUENCE 159 AA; 17785 MW; 37B7C22B9A2FD089 CRC64;
 Query Match 70.0%; Score 35; DB 1; Length 159;
 Best Local Similarity 85.7%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SPGSPGT 9
 ||| |||
 Db 125 SPGSPGT 131
 RESULT 33
 UR2R_RAT
 ID UR2R_RAT STANDARD; PRT; 386 AA.
 AC P49684; P48041;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urotensin II receptor (UR-II-R) (G protein-coupled sensory epithelial
 neuro peptide-like receptor) (SENR).
 GN GPR14.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96115583; PubMed=8666380;
 RA Marchese A., Heiber M., Nguyen T., Heng H.H.O., Saldivia V.R.,
 RA Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
 RA O'Dowd B.F., Docherty J.M.;
 RT "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
 and GPR14, encoding receptors related to interleukin 8, neuropeptide
 Y, and somatostatin receptors.";
 RL Genomics 29:335-344(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Circumvallate papillae;
 RX MEDLINE=95251679; PubMed=7733947;
 RA Tal M., Ammar D.A., Karpuf M., Krizhanovsky V., Naim M.,
 RA Thompson D.A.;
 RT "A novel putative neuropeptide receptor expressed in neural tissue,
 including sensory epithelia.";
 RL Biochem. Biophys. Res. Commun. 209:752-759(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=WISTAR; TISSUE=Urinary bladder;
 RX Sugra H., Takao K.;
 RT "Expression of the rat SENR in the urinary bladder tissues.";
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR UROTENSIN II. THE ACTIVITY OF
 THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A
 PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (BY
 SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN NEURAL AND SENSORY
 TISSUES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; U32673; AAC52593.1; -
 CC EMBL; U23483; AAA80111.1; -
 CC EMBL; AB012210; BAA25251.1; -

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CC -----
CC EMBL; D90205; BAA14231.1; -
CC PIR; S12357; S12357.
CC MGI; 96558; IL5ra.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR003532; Hematopoietic_receptor_S_F2.
CC PROSITE; PS01356; HEMATOPOI_REC_S_F2; 1_-F2.
CC Receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 17
CC CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
CC DOMAIN 18 339 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 340 361 POTENTIAL.
CC CYTOPLASMIC (POTENTIAL).
CC BY SIMILARITY.
CC DISULFID 131 152 BY SIMILARITY.
CC CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 415 AA; 46989 MW; A4326D2922571C08 CRC64;
SQ
Query Match 70.0%; Score 35; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 SPSPGPT 9
Db 119 SPSPGPT 124
RESULT 35
HXKG-ASPNG STANDARD; PRT; 495 AA.
AC Q92407;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Glucokinase (EC 2.7.1.2) (Glucose kinase) (GLK).
GN GLKA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 120.49 / N400;
RX MEDLINE=97008939; PubMed=8856049;
RA Panneman H., Ruijter G.J.G., van den Broeck H.C., Driever E.T.M.,
RA Visser J.;
RT "Cloning and biochemical characterisation of an Aspergillus niger
RT glucokinase. Evidence for the presence of separate glucokinase and
RT hexokinase enzymes."
RL J. Biochem. 240:518-525(1996).
CC -!- FUNCTION: THE ENZYME HAS GREAT AFFINITY FOR GLUCOSE. MANNOSE, 2-
CC DEOXYGLUCOSE AND GLUCOSAMINE CAN SERVE AS SUBSTRATES. ACTIVITY IS
CC RELATIVELY CONSTANT BETWEEN PH 7.5 AND PH 9.0. BELOW PH 7.5, THE
CC ACTIVITY DECREASES WITH PH.
CC -!- CATALYTIC ACTIVITY: ATP + D-glucose = ADP + D-glucose 6-phosphate.
CC -!- SUBUNIT: MONOMER (PROBABLE).
CC -----
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CC -----

DR HSP; P34996; IIDD.
DR GCRDb; GCR_1427; -
DR GCRDb; GCR_1443; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1.1;
DR PRINTS; P00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_REC_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 55 77 1 (POTENTIAL).
FT DOMAIN 78 87 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 88 113 2 (POTENTIAL).
FT DOMAIN 114 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 146 3 (POTENTIAL).
FT DOMAIN 147 167 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 168 186 4 (POTENTIAL).
FT DOMAIN 187 209 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 210 232 5 (POTENTIAL).
FT DOMAIN 233 258 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 259 284 6 (POTENTIAL).
FT DOMAIN 285 299 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 300 321 7 (POTENTIAL).
FT DOMAIN 322 386 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 33 33 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 123 199 BY SIMILARITY.
FT CONFLICT 315 315 F -> L (IN REF. 1).
FT SEQUENCE 386 AA; 42707 MW; FAME95CC6A4CA27C CRC64;
SQ
Query Match 70.0%; Score 35; DB 1; Length 386;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 SPSPGPT 9
Db 341 SPSPGPT 347
RESULT 34
IL5R_MOUSE STANDARD; PRT; 415 AA.
AC P21183;
AT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interleukin-5 receptor alpha chain precursor (IL-5R-alpha).
GN IL5RA OR IL5R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9109260; PubMed=2265612;
RA Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RA Takatsu K.;
RT "Molecular cloning and expression of the murine interleukin-5
RT receptor."
RL EMBO J. 9:4367-4374(1990).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
CC ON B-CELLS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -----
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CC  EMBL; X99626; CAA67949.1;
DR  HSP; Q26609; 1BDG.
DR  InterPro; IPR001312; Hexokinase.
DR  Pfam; PF00349; hexokinase.1.
DR  PRINTS; PR00475; HEXOKINASE.
DR  PRODOM; P001109; Hexokinase; 1.
DR  PROSITE; PS00378; HEXOKINASES; 1.
KW  transferase; Kinase; Glycolysis; ATP-binding.
FT  BINDING 93 175 ATP (POTENTIAL).
FT  NP_BIND 149 175 GLUCOSE-BINDING (POTENTIAL).
FT  NP_BIND 472 477 ATP (POTENTIAL).
SQ  SEQUENCE 495 AA; 54536 MW; 02C94EF07D1809F8 CRC64;

Query Match 70.0%; Score 35; DB 1; Length 495;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 218 YTSFGTGT 226

RESULT 36
AMH2_HUMAN
ID AMH2_HUMAN STANDARD; PRT; 573 AA.
AC Q16671; Q13762;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Anti-mullerian hormone type II receptor precursor (EC 2.7.1.37) (AMH
DE type II receptor) (MIS type II receptor) (MISRII) (MRII).
GN AMH2 OR AMHR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96083584; PubMed=7493017;
RA Imbeaud S., Faure E., Lamarre I., Mattei M.-G., di Clemente N.,
RA Tizard R., Carre-Eusebe D., Belville C., Tragethon L., Tonkin C.,
RA Nelson J., McAuliffe M., Bidart J.-M., Lababidi A., Josso N.,
RA Cate R.L., Picard Y.-Y.;
RT "Insensitivity to anti-mullerian hormone due to a mutation in the
RT human anti-mullerian hormone receptor.";
RL Nat. Genet. 11:382-388(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=96028015; PubMed=7488027;
RA Visser J.A., McLuskey A., van Beers T., Weghuis D.O., van Kessel A.G.,
RA Grootegeest J.A., Themmen A.P.N.;
RT "Structure and chromosomal localization of the human anti-mullerian
RT hormone type II receptor gene.";
RL Biochem. Biophys. Res. Commun. 215:1029-1036(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Testis;
RX MEDLINE=200555680; PubMed=10589763;
RA Mastakos P.T., MacLaughlin D.T., Maheswaran S., Teixeira J.,
RA Fuller A.F. Jr., Shah P.C., Kehas D.J., Kenneally M.K.,
RA Domokowski D.M., Ha T.U., Preffer F.I., Donahoe P.K.;
RT "Human ovarian cancer, cell lines, and primary ascites cells express
RT the human Mullerian inhibiting substance (MIS) type II receptor,
RT bind, and are responsive to MIS.";
RL Clin. Cancer Res. 5:3488-3499(1999).
CC -1- FUNCTION: RECEPTOR FOR ANTI-MULLERIAN HORMONE.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DISEASE: DEFECTS IN AMH2 ARE THE CAUSE OF PERSISTENT MULLERIAN
CC DUCT SYNDROME TYPE II (PMS-2); A FORM OF MALE
CC PSEUDOHERPHERODITISM CHARACTERIZED BY A FAILURE OF MUELLERIAN

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CC  DUCT REGRESSION IN OTHERWISE NORMAL MALES.
CC  -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC  TGFβ RECEPTOR SUBFAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X89013; CAA61418.1;
DR  EMBL; U29700; AAC50328.1;
DR  EMBL; X91156; CAA62593.1;
DR  EMBL; X91157; CAA62593.1; JOINED.
DR  EMBL; X91158; CAA62593.1; JOINED.
DR  EMBL; X91159; CAA62593.1; JOINED.
DR  EMBL; X91160; CAA62593.1; JOINED.
DR  EMBL; X91161; CAA62593.1; JOINED.
DR  EMBL; X91162; CAA62593.1; JOINED.
DR  EMBL; X91163; CAA62593.1; JOINED.
DR  EMBL; X91164; CAA62593.1; JOINED.
DR  EMBL; X91165; CAA62593.1; JOINED.
DR  EMBL; X91166; CAA62593.1; JOINED.
DR  EMBL; AF172932; AAD48497.1;
DR  MIM; 600956;
DR  InterPro; IPR000472; Activin_rec.
DR  InterPro; IPR000719; Euk_pkinase.
DR  Pfam; PF002290; Ser_thr_pkinase.
DR  Pfam; PF00069; pkinase; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR  PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW  Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW  Transmembrane; Glycoprotein; Signal; Pseudohermaphroditism.
FT  SIGNAL 1 17
FT  CHAIN 18 573 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR.
FT  DOMAIN 18 149 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 150 170 POTENTIAL.
FT  DOMAIN 171 573 CYTOPLASMIC (POTENTIAL).
FT  DOMAIN 203 518 PROTEIN KINASE.
FT  NP_BIND 209 217 ATP (BY SIMILARITY).
FT  BINDING 230 230 ATP (BY SIMILARITY).
FT  ACT_SITE 333 333 BY SIMILARITY.
FT  CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
FT  CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
FT  CONFLICT 161 161 L -> V (IN REF. 2; CAA62593).
SQ  SEQUENCE 573 AA; 62749 MW; 1347C10C2942FDBA CRC64;

Query Match 70.0%; Score 35; DB 1; Length 573;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGSPGT 9
DB 126 PGSPGT 131

RESULT 37
MRKC_KLEPN
ID MRKC_KLEPN STANDARD; PRT; 828 AA.
AC P21647;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane usher protein mrkc precursor.
GN MRKC.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;

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RN SEQUENCE FROM N.A.
RP STRAIN=IA565;
RX MEDLINE=91100386; PubMed=1670938;
RA Allen B.L., Gerlach G.-F., Clegg S.;
RT "Nucleotide sequence and functions of mrk determinants necessary for
RL expression of type 3 fimbriae in Klebsiella pneumoniae.";
RL J. Bacteriol. 173:916-920(1991).
CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF THE TYPE 3
CC FIMBRIAL SUBUNIT (MRKA).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (by similarity).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC
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CC -----
CC EMBL; M55912; AAA25095.1; -.
CC PIR; D39142; D39142.
CC InterPro; IPR000015; Fimb_usher.
CC Pfam; PF00577; Usher; 1.
CC PROSITE; PS01151; FIMBRIAL_USHER; 1.
CC Outer membrane; Transmembrane; Fimbria; Transport; Signal.
CC SIGNAL 1 18 POTENTIAL.
CC FT CHAIN 19 828 OUTER MEMBRANE USHER PROTEIN MRKC.
CC FT DISULFID 813 827 POTENTIAL.
CC FT SEQUENCE 828 AA; 91049 MW; B30EDF5798249FC9 CRC64;
CC
CC Query Match 70.0%; Score 35; DB 1; Length 828;
CC Best Local Similarity 100.0%; Pred. No. 1.9e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 4 PGSPGT 9
CC |||||
CC Db 693 PGSPGT 698
CC
CC RESULT 38
CC VGLB_HSV1F STANDARD; PRT; 903 AA.
CC AC P06436;
CC DT 01-JAN-1988 (Rel. 06, Created)
CC DT 01-JAN-1988 (Rel. 06, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Glycoprotein B precursor.
CC GN GB OR UL27.
CC OS Herpes simplex virus (type 1 / strain F).
CC OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC OC Alphaherpesvirinae; Simplexvirus.
CC OX NCBI_TaxID=10304;
CC [1]
CC RN SEQUENCE FROM N.A.
CC RX MEDLINE=85083254; PubMed=2981343;
CC RA pellett P.E., Kousoulas K.G., Pereira L., Roizman B.;
CC RT "Anatomy of the herpes simplex virus 1 strain F glycoprotein B gene:
CC primary sequence and predicted protein structure of the wild type and
CC of monoclonal antibody-resistant mutants.";
CC RL J. Virol. 53:243-253(1985).
CC [2]
CC RN SEQUENCE OF 1-176 FROM N.A.
CC RX MEDLINE=88306232; PubMed=2457278;
CC RA Hammerschmidt W., Contraths F., Mankertz J., Buhk H.-J., Pauli G.,
CC Ludwig H.;
CC RT "Common epitopes of glycoprotein B map within the major DNA-binding
CC proteins of bovine herpesvirus type 2 (BHV-2) and herpes simplex
CC virus type 1 (HSV-1).";
CC RT Virology 165:406-418(1988).
CC
CC -1- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC GB, GC, GG, GD, GI, AND GE.
CC -1- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC REQUIRED FOR VIRAL GROWTH.
CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC
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CC -----
CC EMBL; M14164; AAA45776.1; -.
CC EMBL; M21633; AAA45788.1; -.
CC PIR; A03750; VGBEB1.
CC InterPro; IPR000234; Glycoprot_B.
CC Pfam; PF00606; Glycoprotein_B; 1.
CC ProDom; PD000693; Glycoprot_B; 1.
CC Glycoprotein; Transmembrane; Signal.
CC SIGNAL 1 29
CC FT CHAIN 30 903 GLYCOPROTEIN B.
CC FT DOMAIN 31 729 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 730 745 POTENTIAL.
CC FT TRANSMEM 751 770 POTENTIAL.
CC FT TRANSMEM 774 794 POTENTIAL.
CC FT DOMAIN 795 903 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 673 673 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT SEQUENCE 903 AA; 100104 MW; 73BDCA7813DB35E8 CRC64;
CC
CC Query Match 70.0%; Score 35; DB 1; Length 903;
CC Best Local Similarity 85.7%; Pred. No. 2.1e+02;
CC Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 2 SSPGSPG 8
CC |||||
CC Db 32 SSPGTPG 38
CC
CC RESULT 39
CC VGLB_HSV11 STANDARD; PRT; 904 AA.
CC AC P10211;
CC DT 01-MAR-1989 (Rel. 10, Created)
CC DT 01-MAR-1989 (Rel. 10, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Glycoprotein B precursor.
CC GN GB OR UL27.
CC OS Herpes simplex virus (type 1 / strain 17).
CC OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC OC Alphaherpesvirinae; Simplexvirus.
CC OX NCBI_TaxID=10299;
CC [1]
CC RN SEQUENCE FROM N.A.
CC RX MEDLINE=88274327; PubMed=2839594;
CC RA McGeoch D.J., Dairymple M.A., Davison A.J., Taylor P.;
CC RA McNab D., Perry L.J., Scott J.E., Taylor P.;
CC RT "The complete DNA sequence of the long unique region in the genome of
CC herpes simplex virus type 1.";
CC RL J. Gen. Virol. 69:1531-1574(1988).
CC -1- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC GB, GC, GG, GD, GI, AND GE.
CC -1- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC REQUIRED FOR VIRAL GROWTH.

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us-09-734-281-1.rsp

Wed May 22 11:04:29 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2002, 11:18:10 ; Search time 41.2 Seconds
(without alignments)
37.790 Million cell updates/sec

Title: US-09-734-281-1

Perfect score: 50

Sequence: 1 YSSPCSPCT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database :

SPTREMBL19.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	372	11 Q91WK4	Q91WK4 mus musculus
2	42	84.0	641	3 Q91R79	Q91R79 cryptococcus
3	41	82.0	15	6 Q91R79	Q91R79 bos taurus
4	41	82.0	626	10 Q92RY1	Q92RY1 glycine max
5	40	80.0	376	4 Q96CK9	Q96CK9 homo sapien
6	40	80.0	435	2 Q68641	Q68641 oerskovia x
7	39	78.0	150	2 Q9XAE0	Q9XAE0 streptomyces
8	39	78.0	272	2 Q9S283	Q9S283 streptomyces
9	39	78.0	389	6 Q9BEG5	Q9BEG5 bos taurus
10	39	78.0	391	6 Q9BEG6	Q9BEG6 bos taurus
11	39	78.0	405	4 Q9NWW9	Q9NWW9 homo sapien
12	39	78.0	424	4 Q9UKS6	Q9UKS6 homo sapien
13	39	78.0	424	4 Q9H331	Q9H331 homo sapien
14	39	78.0	513	4 Q9BRM0	Q9BRM0 homo sapien
15	39	78.0	651	4 Q9P2L4	Q9P2L4 homo sapien
16	39	78.0	2232	5 P91365	P91365 caenorhabditis

17	38	76.0	280	5	Q95TC5	Q95TC5 drosophila
18	38	76.0	453	11	Q63422	Q63422 rattus norv
19	38	76.0	517	17	Q974W1	Q974W1 sulfolobus
20	38	76.0	711	5	Q9USM3	Q9USM3 podocoryne
21	38	76.0	1019	5	Q961G7	Q961G7 drosophila
22	38	76.0	1345	1	Q54437	Q54437 staphylothe
23	37	74.0	168	5	Q17289	Q17289 caenorhabdi
24	37	74.0	238	4	Q9H4T5	Q9H4T5 homo sapien
25	37	74.0	302	3	Q43060	Q43060 schizosacch
26	37	74.0	333	4	Q15469	Q15469 homo sapien
27	37	74.0	387	11	Q9B2V9	Q9B2V9 mus musculu
28	37	74.0	387	11	Q99PD5	Q99PD5 mus musculu
29	37	74.0	393	6	Q99147	Q99147 oryctolagus
30	37	74.0	396	4	Q14631	Q14631 homo sapien
31	37	74.0	406	3	Q74658	Q74658 candida alb
32	37	74.0	406	3	Q9URP9	Q9URP9 candida alb
33	37	74.0	407	3	Q74661	Q74661 candida alb
34	37	74.0	420	4	Q14633	Q14633 homo sapien
35	37	74.0	539	4	Q95196	Q95196 homo sapien
36	37	74.0	539	11	Q9QY32	Q9QY32 mus musculu
37	37	74.0	541	6	Q01106	Q01106 oryctolagus
38	37	74.0	723	11	Q9D677	Q9D677 mus musculu
39	37	74.0	734	4	Q75112	Q75112 homo sapien
40	37	74.0	742	11	Q9CW54	Q9CW54 mus musculu
41	37	74.0	847	4	Q16584	Q16584 homo sapien
42	37	74.0	850	11	Q9JJ15	Q9JJ15 mus musculu
43	37	74.0	1523	3	Q9HFX4	Q9HFX4 candida alb
44	37	74.0	3494	4	Q9GRU9	Q9GRU9 homo sapien
45	37	74.0	3620	6	Q9TU53	Q9TU53 canis famil
46	37	74.0	3623	4	Q60494	Q60494 homo sapien
47	37	74.0	6875	6	Q28733	Q28733 oryctolagus
48	37	74.0	26926	4	Q10466	Q10466 homo sapien
49	36	72.0	114	10	Q9ATC9	Q9ATC9 malus domes
50	36	72.0	119	10	Q43548	Q43548 malus domes
51	36	72.0	149	11	Q9JKX0	Q9JKX0 mus musculu
52	36	72.0	179	11	Q9JKW9	Q9JKW9 mus musculu
53	36	72.0	209	16	Q98K79	Q98K79 thizobium l
54	36	72.0	216	11	Q9JFX1	Q9JFX1 mus musculu
55	36	72.0	221	2	Q9RJC5	Q9RJC5 streptomyce

ALIGNMENTS

RESULT 1
Q91WK4
ID Q91WK4 PRELIMINARY; PRT; 372 AA.
AC Q91WK4;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=EYE, AND RETINA;
RC Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC014748; AAH14748.1; .
SQ SEQUENCE 372 AA; 38861 MW; B07745D23BC62A2 CRC64;

Query Match 100.0%; Score 50; DB 11; Length 372;
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
Qy 1 YSSPCSPCT 9
Db 128 YSSPCSPCT 136

us-09-734-281-1.rspt

Wed May 22 11:04:32 2002

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RESULT 2
QY879 PRELIMINARY; PRT; 641 AA.
ID QY879
AC QY879; 1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE CALCINEURIN A CATALYTIC SUBUNIT.
GN CNL1.
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JEC21;
RX MEDLINE=20107115; PubMed=10639477;
RA CRUZ M.C., Sia R.A.L., Olson M., Cox G.M., Heitman J.;
RT "Comparison of the Roles of Calcineurin in Physiology and Virulence in
RL Serotype D and Serotype A Strains of Cryptococcus neoformans.";
RL Infect. Immun. 68:982-985(2000).
CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
DR EMBL: AF159511; AAD44336.1; -.
DR HSP: P48452; 1TCO.
DR InterPro: IPR000934; Ser_thr_phosphatse.
DR Param: PF00149; STPHPTASE.
DR PRINTS: PR00114; STPHPTASE.
DR SMART: SM00156; PPZAC; 1.
DR PROSITE: PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
DR Hydrolase: Iron; Manganese.
KW SEQUENCE 641 AA; 71813 MW; DD68607843D8E6DB CRC64;
SQ

Query Match 84.0%; Score 42; DB 3; Length 641;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPG 9
Db 554 FGSPGSPG 562

RESULT 3
QY879 PRELIMINARY; PRT; 15 AA.
ID QY879
AC QY879; 1999 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-JUN-2000 (TREMREL. 14, Last annotation update)
DE TAU PROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=94043150; PubMed=8226879;
RA Paudel H.K., Lew J., Ali Z., Wang J.H.;
RT "Brain proline-directed protein kinase phosphorylates tau on sites
RT that are abnormally phosphorylated in tau associated with Alzheimer's
RT paired helical filaments.";
RL J. Biol. Chem. 268:23512-23518(1993).
KW SEQUENCE 15 AA; 1449 MW; FBCBEEFEBC2B342 CRC64;
SQ

Query Match 82.0%; Score 41; DB 6; Length 15;
Best Local Similarity 87.5%; Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 YSPGSPG 8
Db 554 FGSPGSPG 562

RESULT 4
QY879 PRELIMINARY; PRT; 626 AA.
ID QY879
AC QY879; 1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE NDX1 HOMEBOX PROTEIN (FRAGMENT).
GN NDX1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC Jorgensen J.E., Gronlund M., Pallisgaard N., Larsen K., Marcker K.A.,
RA Jensen E.;
RT "A new class of plant homeobox genes is expressed in specific regions
RT of determinate symbiotic root nodules.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ011831; CA09794.1; -.
DR InterPro: IPR001356; Homeobox.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR Homeobox; DNA-binding; Nuclear protein.
KW NON_TER 1
FT SEQUENCE 626 AA; 69101 MW; 0DCF8C371CD61B11 CRC64;
SQ

Query Match 82.0%; Score 41; DB 10; Length 626;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPG 8
Db 498 YSPGSPG 505

RESULT 5
QY879 PRELIMINARY; PRT; 376 AA.
ID QY879
AC QY879; 2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE SIMILAR TO ZINC FINGER PROTEIN 16 (K0X 9).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG CARCINOMA;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC014165; AAH14165.1; -.
KW SEQUENCE 376 AA; 41145 MW; 68B1A638CC0758BC CRC64;
SQ

Query Match 80.0%; Score 40; DB 4; Length 376;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSPGSPG 9
Db 20 YSPGSPG 27

```


Wed May 22 11:04:32 2002

us-09-734-281-1.rspt

RC STRAIN-HOLSTEIN;
 RA DroegemueLLer C., Distl O., Leeb T.;
 RT "Identification of a highly polymorphic microsatellite within the
 RL bovine ectodysplasin A (Edl) gene on BTA Xq22-24.";
 DR Anim. Genet. 31:416-416(2000).
 DR EMBL: AJ300468; CAC29151.1;
 DR EMBL: AJ300469; CAC29151.1; JOINED.
 DR EMBL: AJ278907; CAC29151.1; JOINED.
 DR InterPro: IPR000087; Collagen.
 DR InterPro: IPR000478; TNF_family.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS50049; TNF2; 1.
 SQ SEQUENCE 391 AA; 41567 MW; 1F87AD67A04EB7AA CRC64;

Query Match 78.0%; Score 39; DB 6; Length 391;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSPGSPGT 9
 Db 78 FSGPGTGT 86

RESULT 11
 Q9NWV9 PRELIMINARY; PRT; 405 AA.
 ID Q9NWV9 PRELIMINARY; PRT; 405 AA.
 AC Q9NWV9;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE CDNA FLJ20570 FIS, CLONE REC00956 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
 RA Hiraoka M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T.,
 RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK000577; BAA91267.1;
 DR InterPro: IPR001060; FCH.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00611; FCH; 1.
 DR SMART: SM00055; FCH; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR NON_TER 405
 FT SEQUENCE 405 AA; 46494 MW; 6EA81D7782B53D92 CRC64;

Query Match 78.0%; Score 39; DB 4; Length 405;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
 Db 341 SPGSPGT 347

RESULT 12
 Q9UKS6 PRELIMINARY; PRT; 424 AA.
 ID Q9UKS6
 AC Q9UKS6;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE SH3 DOMAIN-CONTAINING PROTEIN 6511.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DR InterPro: IPR001450; 4Fe4S_ferredoxin.
 DR InterPro: IPR000561; EGF-like
 DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 272 AA; 27508 MW; 6E8523635D929BB5 CRC64;

Query Match 78.0%; Score 39; DB 2; Length 272;
 Best Local Similarity 66.7%; Pred. No. 25;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSPGSPGT 9
 Db 170 YAPPGAPGT 178

RESULT 9
 Q9BEG5 PRELIMINARY; PRT; 389 AA.
 ID Q9BEG5
 AC Q9BEG5;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE ECTODYSPLASIN 1, ISOFORM A2.
 GN EDL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HOLSTEIN;
 RA DroegemueLLer C., Distl O., Leeb T.;
 RT "Identification of a highly polymorphic microsatellite within the
 RL bovine ectodysplasin A (Edl) gene on BTA Xq22-24.";
 RL Anim. Genet. 31:416-416(2000).
 DR EMBL: AJ300468; CAC29152.1;
 DR EMBL: AJ300469; CAC29152.1; JOINED.
 DR EMBL: AJ278907; CAC29152.1; JOINED.
 DR InterPro: IPR000087; Collagen.
 DR InterPro: IPR000478; TNF_family.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS50049; TNF2; 1.
 SQ SEQUENCE 389 AA; 41339 MW; 60BE0077C7C83986 CRC64;

Query Match 78.0%; Score 39; DB 6; Length 389;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSPGSPGT 9
 Db 78 FSGPGTGT 86

RESULT 10
 Q9BEG6 PRELIMINARY; PRT; 391 AA.
 ID Q9BEG6
 AC Q9BEG6;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE ECTODYSPLASIN 1, ISOFORM A1.
 GN EDL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2002705; PubMed=10531379;
 RA Howard L., Nelson K.K., MacLewicz R.A., Blobel C.P.;
 RT "Interaction of the metalloprotease disintegrins MDC9 and MDC15 with
 RT two SH3 domain-containing proteins, endophilin I and SH3PXL";
 RL J. Biol. Chem. 274:31693-31699(1999).
 DR EMBL; AF130979; AAF04472.1; -;
 DR HSSP; P29355; 1SEM.
 DR InterPro; IPR001060; FCH.
 DR Pfam; PF00611; FCH; 1.
 DR PRINTS; PR00452; SH3; 1.
 DR SMART; SM00055; FCH; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR KINASE.
 SQ SEQUENCE 424 AA; 48515 MW; 924A7BF79C8DC395 CRC64;

Query Match 78.0%; Score 39; DB 4; Length 424;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPT 9
 Db 341 SPGSPT 347

RESULT 13
 Q9H331
 ID Q9H331 PRELIMINARY; PRT; 424 AA.
 AC Q9H331
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE PACSIN3 (PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE 3) (UNKNOWN)
 DE (PROTEIN FOR MGC:19935) (PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE
 IN NEURONS 3).
 GN PACSIN3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11082044;
 RA Modregger J., Ritter B., Witter B., Paulsson M., Plomann M.;
 RT "All three PACSIN isoforms bind to endocytic proteins and inhibit
 RT endocytosis";
 RL J. Cell Sci. 113:4511-4521(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21100457; PubMed=11179684;
 RA Sumoy L., Pluvinet R., Andreu N., Estivill X., Escarceller M.;
 RT "PACSIN 3 is a novel SH3 domain cytoplasmic adapter protein of the
 RT pacsln-syndapin-fap52 gene family";
 RL Gene 262:199-205(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=UTERUS;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UTERUS, LEIOMYOSARCOMA;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF149825; AAG31023.1; -;
 DR EMBL; AF242530; AAK29207.1; -;
 DR EMBL; BC011889; AAH11889.1; -;

DR EMBL; BC007914; AAH07914.1; -;
 DR HSSP; P29355; 1SEM.
 DR InterPro; IPR001060; FCH.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR SMART; SM00055; FCH; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR KINASE.
 SQ SEQUENCE 424 AA; 48486 MW; 6DBD940AE6D1F352 CRC64;

Query Match 78.0%; Score 39; DB 4; Length 424;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPT 9
 Db 341 SPGSPT 347

RESULT 14
 Q9BRM0
 ID Q9BRM0 PRELIMINARY; PRT; 513 AA.
 AC Q9BRM0
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
 DE HYPOTHETICAL PROTEIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UTERUS, AND LEIOMYOSARCOMA;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006174; AAH06174.1; -;
 DR InterPro; IPR001798; Kelch.
 DR Pfam; PF01344; Kelch; 1.
 FT NON_TER
 SQ SEQUENCE 513 AA; 54599 MW; 21FD050215015520 CRC64;

Query Match 78.0%; Score 39; DB 4; Length 513;
 Best Local Similarity 87.5%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPGSPT 9
 Db 379 SPGSPTS 386

RESULT 15
 Q9P2L4
 ID Q9P2L4 PRELIMINARY; PRT; 651 AA.
 AC Q9P2L4
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE KIAA1332 PROTEIN (FRAGMENT).
 GN KIAA1332.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;

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us-09-734-281-1.l.rspt

"Prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code
for large proteins in vitro."

RT DNA Res. 7:65-73(2000).
RL EMBL; AB037753; BAA92570.1; -.
DR InterPro; IPR001798; Kech. 2.
DR Pfam; PF01344; Kech; 2.
FT NON_TER 1
SQ SEQUENCE 651 AA; 70304 MW; 1CF1DEB5F03DCB3C CRC64;

Query Match 78.0%; Score 39; DB 4; Length 651;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPSPGPGT 9
| | | | |
Db 517 SSPGSPGS 524

RESULT 16

ID P91365 PRELIMINARY; PRT; 2232 AA.
AC P91365;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE K06A9.1. PROTEIN.
GN K06A9.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Geisel C., Gattung S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -/- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED BY
CC OF THE A FORM.
CC ENBL; U80846; AAC70889.1; -.
DR EMBL; U80846; AAC70890.1; -.
KW Alternative splicing.
FT VARSPLIC 842 866
VASSPAPSTSONPNPSTSSGSMI -> LATTSAKPSPVT
CLEMYD (IN ISOFORM B).
PYPSQSTSPVESSTPSPGSPGTLTSPSPSOSTTIGST
QGSTSPGLSTSEMTSPGSPGTLTSPSTVSDST
SSGSTVTVSGTSPSPSTSPGSPGTLTSPSTVSDST
SSGSTVTVSGTSPSPSTSPGSPGTLTSPSTVSDST
SSGSTVTVSGTSPSPSTSPGSPGTLTSPSTVSDST
LVASKLNNEILTGYIDNFGYSAGLNDHQYPTDYNGIKS
VPFIDGTDDIDLDKVDKSLATADWTPPVADOTCMIFI
SAAPDEYGGTTIKSTYFETVGVGLVGGAKSIPGLSIDK
NIVITNNMNDRDASAVVSKLELLPTA (IN ISOFORM
B).

SQ SEQUENCE 2232 AA; 213840 MW; 08D69FA63BE14CC8 CRC64;

Query Match 78.0%; Score 39; DB 5; Length 2232;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPSPGPGT 9
| | | | |
Db 886 SPSPGPGT 892

RESULT 17

ID Q95TC5 PRELIMINARY; PRT; 280 AA.
AC Q95TC5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GH02414P.
GN CG3960.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060231; AAL25270.1; -.
SQ SEQUENCE 280 AA; 29901 MW; 571CBAAE823B3BE2 CRC64;

Query Match 76.0%; Score 38; DB 5; Length 280;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
| | | | |
Db 125 YNPGSPG 132

RESULT 18

ID Q63422 PRELIMINARY; PRT; 453 AA.
AC Q63422;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PROTON-DEPENDENT PEPTIDE TRANSPORTER (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE=SMALL INTESTINE;
RX MEDLINE=96067558; PubMed=7488096;
RA Erickson R.H., Gum J.R. Jr., Lindstrom M.M., McKean D., Kim Y.S.;
RT "Regional expression and dietary regulation of rat small intestinal
RT peptide and amino acid transporter mRNAs";
RL Biochem. Biophys. Res. Commun. 216:249-257(1995).
DR EMBL; L46873; AAC42076.1; -.
DR InterPro; IPR002637; Hmlp-like.
DR InterPro; IPR000109; PTR2.
DR Pfam; PF00854; PTR2; 1.
DR PROSITE; PS01023; PTR2_1; 1.
DR PROSITE; PS01023; PTR2_2; 1.
FT NON_TER 1 1
FT NON_TER 453 453
SQ SEQUENCE 453 AA; 49905 MW; 0706EE059904B082 CRC64;

Query Match 76.0%; Score 38; DB 11; Length 453;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPG 8
| | | | |
Db 420 SSPGSPG 426

RESULT 19

Q974W1

ID Q974W1 PRELIMINARY; PRT; 517 AA.
 AC 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN SF0549.
 GN SF0549.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Akai R., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kishida M., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain 7.";
 RL DNA Res. 8:123-140(2001).
 RM EMBL: AP000982; BAB65546.1; --
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 517 AA; 57965 MW; E129448C73A27A24 CRC64;

 Query Match 76.0%; Score 38; DB 17; Length 517;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 YSPGSPGT 9
 Db 204 YASPTPGT 212

 RESULT 20
 Q9U5M3 PRELIMINARY; PRT; 711 AA.
 ID Q9U5M3
 AC Q9U5M3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PAIRED BOX PROTEIN.
 GN PAX-B.
 OS Podocoryne carnea.
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
 OC Hydractiniidae; Podocoryne.
 OX NCBI_TaxID=6096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20302558; PubMed=10842067;
 RA Groeger H., Callaerts P., Gehring W.J., Schmid V.;
 RT "Characterization and expression analysis of an ancestor-type PAX gene
 RT in the hydrozoan jellyfish Podocoryne carnea.";
 RL Mech. Dev. 94:157-169(2000).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
 CC -1- SIMILARITY: WITH OTHER HOMEBOX PROTEINS.
 DR EMBL: AJ249563; CAB61522.1; --
 DR HSSP: P26367; 6PAX.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR001523; Paired_box.
 DR Pfam: PF00046; homeobox; 1.
 DR Pfam: PF00292; PAX; 1.
 DR PRINTS; PR00027; PAIREDBOX.
 DR SMART: SM00389; HOX; 1.
 DR SMART: SM00351; PAX; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 DR PROSITE: PS00034; PAIRED_BOX; 1.
 KW DNA-binding; Developmental protein; Homeobox; Nuclear protein;

KW Paired box; Transcription regulation.
 SQ SEQUENCE 711 AA; 79326 MW; ACID9099E25249B1 CRC64;

 Query Match 76.0%; Score 38; DB 5; Length 711;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 SSPGSPG 8
 Db 211 SSPGSPG 217

 RESULT 21
 Q961G7 PRELIMINARY; PRT; 1019 AA.
 ID Q961G7
 AC Q961G7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE GH23906P
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Y, CN BW SP;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY051598; AAK93022.1; --
 SQ SEQUENCE 1019 AA; 112156 MW; 207885C035945EAF CRC64;

 Query Match 76.0%; Score 38; DB 5; Length 1019;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 1 YSPGSPG 8
 Db 864 YNQGSPG 871

 RESULT 22
 Q54437 PRELIMINARY; PRT; 1345 AA.
 ID Q54437
 AC Q54437;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE STABLE PROTEASE PRECURSOR.
 OS Staphylothermus marinus.
 OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
 OC Staphylothermus.
 OX NCBI_TaxID=2280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F1;
 RX MEDLINE=95139068; PubMed=7837271;
 RA Peters J., Nitsch M., Kuhlmoen B., Golbik R., Lupas A.,
 RA Kellermann J., Engelhardt H., Pfander J.-P., Muller S., Goldie K.,
 RA Engel A., Stetter K.-O., Baumeister W.;
 RT "Tetrabrachion: a filamentous archaeobacterial surface protein assembly
 RT of unusual structure and extreme stability.";
 RL J. Mol. Biol. 245:385-401(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F1;

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us-09-734-281-1.rspt

RA Mayr J., Lupas A., Kellermann J., Eckerskorn C., Baumeister W.,
 RA Peters J.,
 RT "A hyperthermostable protease of the subtilisin family bound to the
 RL surface layer of the archaeon *Staphylothermus marinus*."
 RL Curr. Biol. 0:0-0(1996).
 DR EMBL: U57968; AAB02323.1; -.
 DR MEROPS: S08.096; -.
 DR InterPro: IPR000209; Peptidase_S8.
 DR Pfam: PF00082; Peptidase_S8; 3.
 DR PRINTS: PR00723; SUBTILISIN.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
 DR PROSITE: PS00136; SUBTILASE_ASP; UNKNOWN_1.
 DR PROSITE: PS00138; SUBTILASE_SER; UNKNOWN_1.
 KW Signal; Protease.
 FT SIGNAL 1 24 POTENTIAL.
 SQ SEQUENCE 1345 AA; 148446 MW; DA0878E437A52EC3 CRC64;

Query Match 76.0%; Score 38; DB 1; Length 1345;
 Best Local Similarity 77.8%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
 ||| |
 DB 596 YSSNGAPGT 604

RESULT 23
 ID 017289 PRELIMINARY; PRT; 168 AA.
 AC 017289;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 18.6 KDA PROTEIN.
 GN R52.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RL investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Du Z., Goela D., Ozersky P.;
 RT "The sequence of *C. elegans* cosmid R52.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF025471; AAB71062.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 168 AA; 18604 MW; 4D72C56A94F38F88 CRC64;

Query Match 74.0%; Score 37; DB 5; Length 168;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||
 DB 40 TTPGSPGT 47

RESULT 24
 ID 09H4T5 PRELIMINARY; PRT; 238 AA.
 AC 09H4T5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE BA93B14.3 (NEUROTENSIN RECEPTOR 1 (HIGH AFFINITY)(NTR))
 DE (FRAGMENT).
 GN NTSR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Heath P.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL357033; CAC14923.1; -.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00037; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_2; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 238
 SQ SEQUENCE 238 AA; 25503 MW; 258BE57EACCF6EF0 CRC64;

Query Match 74.0%; Score 37; DB 4; Length 238;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||
 DB 6 SAPGTPGT 13

RESULT 25
 ID 043060 PRELIMINARY; PRT; 302 AA.
 AC 043060;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE HYPOTHETICAL 33.3 KDA PROTEIN C4C3.07 IN CHROMOSOME II.
 GN SPBC4C3.07.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA Wood V., Rajandream M.A., Barrell B.G., Lauber J., Hilbert H.,
 RA Duesterhoeft A.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO PROTEASOME REGULATORY SUBUNIT S12/MOV-34.
 DR EMBL: AL021730; CAAL6829.1; -.
 DR InterPro: IPR000555; Mov34.
 DR InterPro: IPR003640; Mov34_2.
 DR Pfam: PF01398; Mov34; 1.
 DR ProDom: PD005425; Mov34_2; 1.
 DR SMART: SM00232; JAB_MPN; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 302 AA; 33251 MW; A046E087CF08D84 CRC64;

Query Match 74.0%; Score 37; DB 3; Length 302;
 Best Local Similarity 66.7%; Pred. No. 63;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSSPGSPCT 9
Db 123 YASPAEPGT 131

RESULT 26
Q15469
ID Q15469 PRELIMINARY; PRT; 333 AA.
AC Q15469;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSILSR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MEDLINE=92121815; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5
receptor."
RL J. Exp. Med. 175:341-351(1992).
DR EMBL: X62156; CA44081.1; -.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003532; Hematopo_receptor_S_F2.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;

Query Match 74.0%; Score 37; DB 4; Length 333;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPCT 9
Db 119 HAPGSPGT 127

RESULT 27
Q9D2V9
ID Q9D2V9 PRELIMINARY; PRT; 387 AA.
AC Q9D2V9;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 0610009M14RIK PROTEIN.
GN 0610009M14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzei J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RE EMBL: AK018735; BAB31377.1; -.
DR HSPP: P80220; IDIP.
DR MGD: MGI:1926079; 0610009M14RIK.
DR InterPro: IPR000580; TSC-22_Dip_Bun.
DR Pfam: PF01166; TSC22; 1.
DR PRODOM: PD007152; TSC-22_Dip_Bun; 1.
DR PROSITE: PS01289; TSC22; 1.
SQ SEQUENCE 387 AA; 39978 MW; D4160FA3AB2DFB90 CRC64;

Query Match 74.0%; Score 37; DB 11; Length 387;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSSPGSPG 8
Db 19 YEGPGSPG 26

RESULT 28
Q99PD5
ID Q99PD5 PRELIMINARY; PRT; 387 AA.
AC Q99PD5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LEUCINE ZIPPER PROTEIN THG-1PIT.
GN 0610009M14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Fiorenza M.T., Mukhopadhyay M., Westphal H.;
RT "Thg-1pit, a putative Lhx3 target gene."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF315352; AAK02018.1; -.
DR HSPP: P80220; IDIP.
DR MGD: MGI:1926079; 0610009M14RIK.
DR InterPro: IPR000580; TSC-22_Dip_Bun.
DR Pfam: PF01166; TSC22; 1.
DR PRODOM: PD007152; TSC22; 1.
DR PROSITE: PS01289; TSC22; 1.
SQ SEQUENCE 387 AA; 39908 MW; D047B988643CE237 CRC64;

Query Match 74.0%; Score 37; DB 11; Length 387;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSSPGSPG 8
Db 19 YEGPGSPG 26

RESULT 29
Q99147
ID Q99147 PRELIMINARY; PRT; 393 AA.
AC Q99147;
DT 01-NOV-1996 (Tremblrel. 01, Created)

01-NOV-1996	(TReMBLrel. 01, Last sequence update)
01-DEC-2001	(TReMBLrel. 19, Last annotation update)
TIIN (FRAGMENT)	
Oryctolagus cuniculus (Rabbit).	
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
NCBI_taxID=9986;	
[11]	
SEQUENCE FROM N.A.	
STRAIN=NEW ZEALAND WHITE; TISSUE=HEART;	
MEDLINE=91305130; PubMed=1712941;	
Fritz J.D., Greaser M.L., Wolff J.;	
"A novel 3' Extension Technique using Random Primers in RNA-PCR."	
Nucleic Acids Res. 19:3747-3747(1991).	
EMBL; X59596; CAA42165.1; ...	
InterPro; IPR003962; FNIII_repeat.	
InterPro; IPR003961; FN_III.	
InterPro; IPR003600; Ig_like.	
Pfam; PF00041; fn3; 2.	
PRINTS; PR00014; FNTYPEIII.	
SMART; SM00060; FN3; 2	
SMART; SM00410; IG_like; 1.	
Repeat.	
NON_TER	1
NON_TER	393
SEQUENCE	393 AA; 43475 MW; 0672492F4091CBE7 CRC64;

Query Match 74.0%; Score 37; DB 6; Length 393;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	YSSPGSPGT	9
Dp	55	YKEPGPPGT	63

RESULT	30
ID	QI14631
PRT:	PRELIMINARY; PRT: 396 AA.
AC	Q14631;
NOV-1996	(TREMBRel. 01, Created)
NOV-1996	(TREMBRel. 01, Last sequence update)
DEC-2001	(TREMBRel. 19, Last annotation update)
TREMBREL	-5 RECEPTOR TYPE 2 PRECURSOR.
HSIL5R2.	
Homo sapiens (Human).	
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TaxID=9606;	
[1]	
SEQUENCE FROM N.A.	
TISSUE=PERIPHERAL BLOOD;	
MEDLINE=92121815; PubMed=1732409;	
Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;	
"Molecular cloning and expression of the human interleukin 5	
receptor.";	J. Exp. Med. 175:341-351(1992).
EMBL; X61177; CAA43484.1; -	
InterPro; IPR002996; CRIA.	
InterPro; IPR003532; Hematopo_receptor_S_F2.	
PROSITE; PS01356; HEMATOP_REC_SF2; UNKNOWN_1.	
Signal; Receptor.	
SIGNAL	1 20 POTENTIAL.
CHAIN	21 396 INTERLEUKIN-5 RECEPTOR TYPE 2.
SEQUENCE	396 AA; 44998 MW; LAB6061984ZCDA5 CRC64;
SO	

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Query Match      74.0%; Score 37; DB 4; Length 396;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Cov      1 YSPGSPGT 9

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119 HAPPGSPGT 127

Db

RESULT 31
074658
IID 074658 PRELIMINARY; PRT; 406 AA.
AC 074658;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AGGLUTININ-LIKE PROTEIN (FRAGMENT).
OS ALS2.
OC Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_Taxid=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1161;
RX MEDLINE=98440424; PubMed=9765564;
RA Hoyer L.L., Payne T.L., Hecht J.E.;
RT "Identification of Candida albicans ALS2 and localization of
RT als proteins to the fungal cell surface.";
RL J. Bacteriol. 180:5334-5343(1998).
RD EMBL; AF024581; AAC64236.1; -.
FT NON_TER 1
FT SPOUNCE 406 AA; 40585 MW; 9A6C92C1B2A93A81 CRC64;
SO

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Query Match          74.0%; Score 37; DB 3; Length 406;
Best Local Similarity 75.0%; Pred. NO. 86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy	2	SSPGSPGT	9
		: :	
D _b	189	SNPGAPGT	196

RESULT	32
Q9URP9	PRELIMINARY; PRRT; 406 AA.
ID	Q9URP9
AC	Q9URP9;
DT	01-WAY-2000 (TEMBLrel. 13, Created)
DT	01-WAY-2000 (TEMBLrel. 13, Last sequence update)
DT	01-WAY-2000 (TEMBLrel. 13, Last annotation update)
DT	01-WAY-2000 (TEMBLrel. 13, Last annotation update)
DE	AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN	ALS4.
OS	Candida albicans (Yeast).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX	NCBI_TaxID=5476;
[1]	SEQUENCE FROM N.A.
RN	STRAIN=1161;
RC	MEDLINE=98440424; PubMed=9765564;
RX	Hoyer L.L., Payne T.L., Hecht J.E.;
RA	"Identification of Candida albicans ALS2 and ALS4 and localization of
RT	als proteins to the fungal cell surface.";
RT	J. Bacteriol. 180:5334-5343(1998).
RL	EMBL; AF024585; AAC64240.1; -.
RR	NON TER
FT	SEQUENCE 406 AA: 40592 MW: E0117B4CB4ECB4C3 CRC64;

	Query Match	74.0%;	Score 37;	DB 3;	Length 406;
	Best Local Similarity	75.0%;	Pred. No. 86;		
	Matches 6;	Conservative	2;	Mismatches	0;
				Indels	0;
					Gaps
QY	2 SSPGSPGT	9			
		1:11:111			
DB	189 SNPGAPGT	196			

RESULT 33
O74661 ID 074661 PRELIMINARY; PRT; 407 AA.
AC 074661;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN ALS4.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11161;
RX MEDLINE=98440424; PubMed=9765564;
RA Hoyer L.L., Payne T.L., Hecht J.E.;
RT "Identification of Candida albicans ALS2 and ALS4 and localization of
RT als proteins to the fungal cell surface.";
RL J. Bacteriol. 180:5334-5343(1998).
DR EMBL: AF024587; AAC64242.1; -;
FT NON_TER 1
SQ SEQUENCE 407 AA; 40649 MW; FC846B7A1640CF44 CRC64;

Query Match 74.0%; Score 37; DB 3; Length 407;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSPGSPGT 9
I:::||||
DB 189 SNPGAPGT 196

RESULT 34
Q14633 ID Q14633 PRELIMINARY; PRT; 420 AA.
AC Q14633;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSIL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RX MEDLINE=92121815; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5
RT receptor.";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL: X61176; CAA43483.1; -;
DR InterPro: IPR002996; CRIA.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2.
KW Signal; Receptor.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 420 AA; 47670 MW; 8DC56DFC8BEFF524 CRC64;

Query Match 74.0%; Score 37; DB 4; Length 420;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSPGSPGT 9
I:::|||||

Db 119 HAPPGSPGT 127

RESULT 35
O95196 ID 095196 PRELIMINARY; PRT; 539 AA.
AC 095196;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NEUROGLYCAN C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=99133557; PubMed=9950058;
RA Yasuda Y., Tokita Y., Aono S., Matsui F., Ono T., Sonta S.,
RT Watanabe E., Nakanishi Y., Oohira A.;
RT "Cloning and chromosomal mapping of the human gene of neuroglycan C
RT (NGC), a neural transmembrane chondroitin sulfate proteoglycan with an
RT EGF module.";
RL Neurosci. Res. 32:313-322(1998).
DR EMBL: AF059274; AAC69612.1; -;
DR InterPro: IPR000561; EGF-like.
DR SMART: SM00181; EGF; 1.
SQ SEQUENCE 539 AA; 57024 MW; 5B22E9E8DE34290E CRC64;

Query Match 74.0%; Score 37; DB 4; Length 539;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 SSPGSPGT 9
I:::|||||
DB 227 SFGSPGT 234

RESULT 36
O9QY32 ID 09QY32 PRELIMINARY; PRT; 539 AA.
AC 09QY32;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE NEUROGLYCAN C.
GN CSPG5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=BRIN;
RX MEDLINE=20085050; PubMed=10617623;
RA Aono S., Keino H., Ono T., Yasuda Y., Tokita Y., Matsui F.,
RT Taniguchi M., Sonta S.-I., Oohira A.;
RT "Genomic Organization and Expression Pattern of Mouse Neuroglycan C in
RT the Cerebellar Development.";
RL J. Biol. Chem. 275:337-342(2000).
DR EMBL: AF133700; AAF23362.1; -;
DR MGI: MGI:1352747; Cspg5.
DR InterPro: IPR000561; EGF-like.
DR SMART: SM00181; EGF; 1.
SQ SEQUENCE 539 AA; 57352 MW; 7D566881555460ED CRC64;

Query Match 74.0%; Score 37; DB 11; Length 539;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 SSPGSPGT 9
Db      228 SPFGSPGT 235

RESULT 37
Q01106 PRELIMINARY: PRT; 541 AA.
ID AC Q01106;
AC Q01106;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TITIN (FRAGMENT)
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX MEDLINE=92258380; PubMed=1592406;
RA Label S., Gautel M., Lakey A., Trinick J.;
RT "Towards a molecular understanding of titin.";
RL EMBO J. 11:1711-1716(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RA Fritz J.D., Greaser M.L., Wolff J.;
RT "A novel 3' extension method using random primers.";
RL Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: M98338; AAA31480.1; -.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003599; Ig.
DR Pfam: PF00041; fn3; 4.
DR PRINTS: PR00014; FNTYPEIII.
DR SMART: SM00060; FN3; 4.
DR SMART: SM00409; IG; 1.
KW Repeat.
FT NON_TER
SQ SEQUENCE 541 AA; 60088 MW; 0DAA2541E1318B99 CRC64;

Query Match 74.0%; Score 37; DB 6; Length 541;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 YSSPGSPGT 9
Db      55 YKEPGPGT 63

RESULT 38
Q9D677 PRELIMINARY: PRT; 723 AA.
ID AC Q9D677;
AC Q9D677;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 4632412M04RIK PROTEIN.
GN 4632412M04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SKIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schrml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
DR EMBL: AK014569; BAB29434.1; -.
DR HSSP: P49799; IAGR.
DR MGD: MGI:1924302; 4632412M04RIK.
DR InterPro: IPR003109; GOLoco.
DR InterPro: IPR003116; RBD.
DR InterPro: IPR000342; RGS.
DR Pfam: PF02188; GOLoco; 1.
DR Pfam: PF02196; RBD; 2.
DR Pfam: PF06615; RGS; 1.
DR PRINTS: PR01301; RGS-PROTEIN.
DR ProDom: PD001580; RGS; 1.
DR SMART: SM00390; GOLoco; 1.
DR SMART: SM00455; RBD; 2.
DR SMART: SM00315; RGS; 1.
DR PROSITE: PS50132; RGS; 1.
SQ SEQUENCE 723 AA; 78539 MW; EBCBFD7D5A56BF51 CRC64;

Query Match 74.0%; Score 37; DB 11; Length 723;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSSPGSPGT 9
Db      632 HSTPGPGT 640

RESULT 39
Q75112 PRELIMINARY: PRT; 734 AA.
ID AC Q75112;
AC Q75112;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE KIAA0613 PROTEIN (FRAGMENT).
GN KIAA0613.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
CC -1- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
IONS.
DR EMBL: AB014513; BAA31589.1; -.
DR HSSP: Q05158; 1Q1I.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001781; LIM.

```


DR InterPro: IPR001478; PDZ.
DR InterPro: IPR002965; P-rich_extensn.
DR Pfam: PF00412; LIM; 3.
DR Pfam: PF00595; PDZ; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR ProDom: PD000094; LIM; 3.
DR SMART: SM00132; LIM; 3.
DR SMART: SM00228; PDZ; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
DR PROSITE: PS0023; LIM_DOMAIN_2; 3.
DR PROSITE: PS0106; PDZ; 1.
KW LIM domain; Metal-binding; Zinc.
FT NON_TER 1
SQ SEQUENCE 734 AA; 77738 MW; 5CB9AC39CC690FB8 CRC64;

Query Match 74.0%; Score 37; DB 4; Length 734;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
DB 135 ASPGTPGT 142

RESULT 40
Q9CW54
ID Q9CW54 PRELIMINARY; PRT: 742 AA.
AC Q9CW54;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1200016K18RIK PROTEIN (FRAGMENT).
GN 1200016K18RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
DR EMBL: AK004813; BAB23584.1; ..
DR HSSP: P49799; IAGR.
DR MGD: MGI:1918979; 1200016K18RIK.
DR InterPro: IPR000634; dehydrtse_ser_thr.
DR InterPro: IPR003109; GoLoco.
DR InterPro: IPR003116; RBD.
DR InterPro: IPR000342; RGS.
DR Pfam: PF02188; GoLoco; 1.
DR Pfam: PF02196; RBD; 2.

DR Pfam: PF00615; RGS; 1.
DR PRINTS: PR01301; RGS; 1.
DR ProDom: PD001580; RGS; 1.
DR SMART: SM00390; GoLoco; 1.
DR SMART: SM00455; RBD; 2.
DR SMART: SM00315; RGS; 1.
DR PROSITE: PS00165; DEHYDRATASE_SER_THR; UNKNOWN_1.
DR PROSITE: PS0132; RGS; 1.
FT NON_TER 1
SQ SEQUENCE 742 AA; 80828 MW; ACAFE5225ECBE74D CRC64;
Query Match 74.0%; Score 37; DB 11; Length 742;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YSSPGSPGT 9
DB 651 HSTPGPPT 659

Search completed: May 21, 2002, 11:23:51
Job time: 341 sec

us-09-734-281-1.rspt

Wed May 22 11:04:32 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2002, 11:18:07 ; Search time 51.55 Seconds
(without alignments)
19.392 Million cell updates/sec

Title: US-09-734-281-2

Perfect score: 50

Sequence: 1 YSSPGSPCT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database :

A_Geneseq_032802.*

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2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
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8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	50	100.0	9	14	AA1980.DAT.*
2	50	100.0	12	14	AA1981.DAT.*
3	50	100.0	12	14	AA1982.DAT.*
4	50	100.0	12	18	AA1983.DAT.*
5	50	100.0	12	21	AA1984.DAT.*
6	50	100.0	14	21	AA1985.DAT.*
7	50	100.0	34	15	AA1986.DAT.*
8	50	100.0	34	15	AA1987.DAT.*
9	50	100.0	67	15	AA1988.DAT.*
10	50	100.0	78	22	AA1989.DAT.*
11	50	100.0	106	17	AA1990.DAT.*

12	50	100.0	112	16	AA1991.DAT.*
13	50	100.0	351	21	AA1992.DAT.*
14	50	100.0	352	10	AA1993.DAT.*
15	50	100.0	352	14	AA1994.DAT.*
16	50	100.0	352	19	AA1995.DAT.*
17	50	100.0	390	17	AA1996.DAT.*
18	50	100.0	441	15	AA1997.DAT.*
19	50	100.0	441	17	AA1998.DAT.*
20	50	100.0	441	18	AA1999.DAT.*
21	50	100.0	441	21	AA2000.DAT.*
22	43	86.0	13	13	AA2001.DAT.*
23	43	86.0	13	18	AA2002.DAT.*
24	43	86.0	13	18	AA2003.DAT.*
25	40	80.0	263	18	AA2004.DAT.*
26	40	80.0	435	18	AA2005.DAT.*
27	39	78.0	7	14	AA2006.DAT.*
28	39	78.0	7	14	AA2007.DAT.*
29	39	78.0	263	22	AA2008.DAT.*
30	39	78.0	376	22	AA2009.DAT.*
31	39	78.0	424	21	AA2010.DAT.*
32	39	78.0	424	22	AA2011.DAT.*
33	39	78.0	424	22	AA2012.DAT.*
34	38	76.0	98	22	AA2013.DAT.*
35	37	74.0	284	22	AA2014.DAT.*
36	37	74.0	335	13	AA2015.DAT.*
37	37	74.0	335	14	AA2016.DAT.*
38	37	74.0	350	22	AA2017.DAT.*
39	37	74.0	351	22	AA2018.DAT.*
40	37	74.0	353	13	AA2019.DAT.*
41	37	74.0	395	22	AA2020.DAT.*
42	37	74.0	396	13	AA2021.DAT.*
43	37	74.0	396	13	AA2022.DAT.*
44	37	74.0	418	17	AA2023.DAT.*
45	37	74.0	418	22	AA2024.DAT.*
46	37	74.0	420	13	AA2025.DAT.*
47	37	74.0	420	13	AA2026.DAT.*
48	37	74.0	420	19	AA2027.DAT.*
49	37	74.0	421	13	AA2028.DAT.*
50	37	74.0	464	22	AA2029.DAT.*
51	37	74.0	494	22	AA2030.DAT.*
52	37	74.0	539	21	AA2031.DAT.*
53	37	74.0	542	22	AA2032.DAT.*
54	37	74.0	542	22	AA2033.DAT.*
55	37	74.0	545	18	AA2034.DAT.*

ALIGNMENTS

RESULT 1

AA1980.DAT.* AAR36557 standard; peptide; 9 AA.

XX AAR36557;

XX AC

XX DT

XX 10-AUG-1993 (first entry)

XX Peptide sequence for abnormally phosphorylated tau protein.

XX Alzheimer's disease; Down's syndrome; Pick's disease; monoclonal antibody; detection; SSPE; antigen.

XX Synthetic.

XX OS

XX FH

XX Key

XX Modified-site 3

XX Location/Qualifiers

XX FT

XX /note= "may be phosphorylated"

XX Misc-difference 6

XX /note= "may be phosphorylated"

XX W09308302-A.

XX 29-APR-1993.

PHF-tau (143-254)
Human Tau protein.
Paired helical fil.
Human tau-protein.
Human microtubule.
Truncated human ta
Human tau protein.
Human tau protein.
Human tau protein.
Human paired heli
Phosphopeptide as
Human tau protein
Human tau protein
Oerskovia xanthine
Oerskovia xanthine
Alzheimer paired h
Phosphorylated tau
Novel signal trans
Human protein SEQ
Human ORFX ORF1602
Human protein SEQ
Human EXMAD-5 SEQ
Human polypeptide
Novel human diagno
Soluble human IL-5
shIL-5R-alpha. Sy
Human polypeptide,
Chicken zyxine fra
AHSV protein. Afr
Human polypeptide
Sequence of human
Sequence of secret
Human neurotensin
Non-endogenous hum
Sequence of human
Human interleukin-
Human IL-5 recepto
Human polypeptide,
Human polypeptide
Human brain proteo
Novel human diagno
Chicken zyxine. G
Human brain Neuro

RESULT	2
AAR38235	
ID	AAR38235 standard; peptide; 12 AA.
XX	
AC	AAR38235;
XX	
DT	08-OCT-1993 (first entry)
XX	
DE	Alzheimer paired helical filament tau protein epitope 197-208.
XX	
KW	Alzheimer tau protein; phosphorylation-dependent; PHF;
KW	neuronal microtubule; mitogen activated protein kinase; MAP kinase.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Modified-site 3..4
FT	/label= Phosphorylation_motif
FT	Modified-site 6..7
FT	/label= Phosphorylation_motif
FT	Modified-site 9..10
FT	/label= Phosphorylation_motif
XX	
PN	WO9311231-A.
XX	
ED	10-JUN-1993.
XX	
PX	07-DEC-1992; 92WO-EF02829.
PF	
XX	
PR	06-DEC-1991; 91EP-0120974.
PR	16-NOV-1992; 92EP-0119551.
XX	

XX The sequence is that of an epitope of tau protein which specifically
CC

CC occurs in a phosphorylated state in tau protein from Alzheimer's
 CC paired helical fragments. It may be used as part of a method for the
 CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
 CC also be used in an in vitro model for the study of the generation of
 CC the Alzheimer state of proteins and the testing of substances which
 CC prevent the conversion of normal to Alzheimer tau protein. The
 CC epitope occurs at residues 197-208 of human tau protein.
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 50; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 YSSPGSPGT 9
 DB 1 YSSPGSPGT 9
 |||||

RESULT 4
 AAW34857
 ID AAW34857 standard; peptide; 12 AA.
 XX AC AAW34857;
 XX DT 27-MAR-1998 (first entry)
 XX DE Human tau protein fragment.
 XX KW Antibody; phosphorylated tau protein; paired helical filament;
 XX KW detection; Alzheimer's disease; human.
 XX OS Homo sapiens.

Key Location/Qualifiers
 Modified-site 6 /note= "phosphoserine"
 WO9734145-A1.
 18-SEP-1997.

13-MAR-1997; 97WO-JP00804.
 13-MAR-1996; 96JP-0056090.
 (MITU) MITSUBISHI CHEM CORP.
 Inahori K, Ishiguro K, Park J, Sato K, Uchida T;
 WPI: 1997-470978/43.

Antibody prepared using a partial peptide containing part of
 phosphorylated tau protein - used for detecting Alzheimer's disease
 Example; Page 28; 48pp; Japanese.

An antibody, prepared using a partial peptide containing the
 phosphorylated residue of the phosphorylated tau protein, e.g. the
 present sequence, in a paired helical filament, can be used to
 detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 protein in brain extracts or tissue fragments.

Query Match 100.0%; Score 50; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 YSSPGSPGT 9
 |||||

Db 4 ysspgspgt 12

RESULT 5

AAW81390
 ID AAW81390 standard; protein; 12 AA.

XX AC AAW81390;

XX DT 19-JUN-2000 (first entry)

XX DE Human phosphorylated tau protein derived peptide fragment, PS199.

XX KW Phosphorylated tau protein; human; paired helical filament; fragment;
 XX KW polyclonal antibody; Alzheimer's disease; cerebrospinal fluid; CSF;
 XX KW diagnosis; detection.

XX OS Homo sapiens.
 XX OS Synthetic.

Key Location/Qualifiers
 Modified-site 6 /note= "Phosphorylated"

JP2000034300-A.

02-FEB-2000.

17-JUL-1998; 98JP-0204040.

17-JUL-1998; 98JP-0204040.

(MITU) MITSUBISHI CHEM CORP.

WPI: 2000-285529/25.

Anti-phosphated tau protein antibody - for the detection of Alzheimer
 disease

Claim 4; Page 4; 12pp; Japanese.

The invention relates to an antibody against a phosphorylated tau
 protein (AAW81386), which is a component of the paired helical filament
 found in the plaques associated with Alzheimer's disease. A
 phosphorylated tau protein fragment selected from peptides
 AAW81387-Y81390 is conjugated to keyhole limpet haemocyanin (KLH), and
 used to raise polyclonal antibodies in a rabbit. The antibodies of the
 invention are specific for phosphorylated tau protein and may be used to
 detect phosphorylated tau protein in the cerebrospinal fluid (CSF) of a
 patient suspected of having Alzheimer's disease. Use of the antibodies of
 the invention provides specific diagnosis of Alzheimer's disease.
 Sequences AAW81387-Y81390 represent phosphorylated peptides derived from
 tau protein used to raise anti-phosphorylated tau antibodies. The
 N-terminal residue is not part of the full-length tau protein, but
 facilitates KLH conjugation.

Sequence 12 AA;

Query Match 100.0%; Score 50; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 4 ysspgspgt 12
 |||||

RESULT 6

AAW21959
 ID AAW21959 standard; Peptide; 14 AA.

XX AC AAW21959;

Wed May 22 11:04:33 2002

us-09-734-281-2.rag

XX DT 02-JAN-2001 (first entry)

XX DE Phosphorylated tau peptide #3.

XX WW-domain; protein-protein interaction; cell growth regulation;
XX protein degradation regulation; Alzheimer's; Dementia pugilistica;
XX Down's syndrome; Parkinson's disease; Pick's; neurodegenerative;
XX microtubule assembly; hyperplasia; neoplasia; malignancy;
XX psoriasis; retinosis; atherosclerosis; leukaemia; lymphoma; papilloma;
XX pulmonary fibrosis; rheumatoid arthritis; multiple sclerosis;
XX muscular dystrophy; tau.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 7 /note= "Phosphorylated residue"

FT XX

PN WO200048621-A2.

XX PD 24-AUG-2000.

XX PF 18-FEB-2000; 2000WO-US04278.

XX PR 18-FEB-1999; 99US-0252404.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX PI Lu KP, Zhou XZ;

XX PI WPI; 2000-594014/56.

XX DR Mediating protein-protein interactions, useful for regulating cell
XX growth and for treating neurodegenerative disorders, comprises
XX modulating binding of WW domain containing polypeptide with
XX phosphorylated ligand -

XX XX Example 10; Page 45; 82pp; English.

XX PS The present invention relates to a method for mediating protein-protein
XX interaction, which comprises modulating the binding of a WW-domain
XX containing peptide with a phosphorylated ligand. WW-domains are highly
XX conserved regions of approximately 40 amino acid residues with two
XX invariant tryptophans (W) in a triple stranded beta-sheet. When a
XX WW-domain containing peptide is phosphorylated at serine or threonine
XX residues, dephosphorylation of ligands bound to the peptide is inhibited.
XX WW-domain peptides may be useful for mediating protein-protein
XX interaction, regulating cell growth, regulating protein degradation,
XX restoring the function of tau to bind microtubules and promote or restore
XX microtubule assembly in neurodegenerative diseases e.g. Alzheimer's,
XX Dementia pugilistica, Down's syndrome, Parkinson's disease, Pick's
XX disease, multiple sclerosis, muscular dystrophy, Corticobasal
XX degeneration, Frontotemporal dementias, Myotonic dystrophy, Niemann-Pick
XX disease, prion disease with tangles, progressive supranuclear palsy and
XX subacute sclerosing panencephalitis. In addition, inhibitors or
XX stimulators of interactions between WW-domains and ligands of the present
XX invention can be used to treat hyperplastic and neoplastic disorders e.g.
XX all forms of malignancies, psoriasis, retinosis, benign tumour growth,
XX resulting from plaque formation, leukaemias, atherosclerosis
XX lymphomas, papillomas, pulmonary fibrosis and rheumatoid arthritis. The
XX present sequence is a phosphorylated tau peptide. Tau is a WW-domain
XX containing peptide ligand. This peptide was used to investigate the
XX interactions between Tau and the WW-domain of Pin1 peptide. It was found
XX that the Pin1 WW-domain mediates specific interactions between Pin1 and
XX tau.

XX OS Sequence 14 AA;

Query Match 100.0%; Score 50; DB 21; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

Db 2 YSSPGSPGT 10

RESULT 7

AAR61330

ID AAR61330 standard; Protein: 34 AA.

XX AAR61330;

AC AAR61330;

XX 24-APR-1995 (first entry)

DT

XX Peptide phosphorylated by human tau-protein kinase.

DE Tau-protein kinase I enzyme; TPK-I; Phosphorylated peptide.

XX Synthetic.

XX EP616032-A.

XX 21-SEP-1994.

XX 01-MAR-1994; 94EP-0103057.

XX 02-MAR-1993; 93JP-0041160.

PR 22-MAR-1993; 93JP-0085143.

PR 02-AUG-1993; 93JP-0191246.

XX (TAKA/) TAKASHIMA A.

PA (MITU) MITSUBISHI KASEI CORP.

XX Hoshino T, Imahori K, Saito K, Sato S, Shiratsuchi A;

PI Takashima A;

XX WPI; 1994-287181/36.

XX Newly isolated tau-protein kinase I enzyme - with specificity for
XX tau-protein providing means for prevention and treatment of
XX Alzheimer's disease

XX Example 4; Page 25; 30pp; English.

XX AAR61330 is a peptide which has been phosphorylated by human
XX tau-protein kinase (AAR61326).

XX Sequence 34 AA;

Query Match 100.0%; Score 50; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

Db 7 YSSPGSPGT 15

RESULT 8

AAW34875

ID AAW34875 standard; peptide: 34 AA.

XX AAW34875;

AC AAW34875;

XX 27-MAR-1998 (first entry)

DT

XX Human tau protein fragment.

DE Antibody; phosphorylated tau protein; paired helical filament;
XX detection; Alzheimer's disease; human.

XX Homo sapiens.

OS

XX PN WO9734145-AL.
 XX PD 18-SEP-1997.
 XX PF 13-MAR-1997; 97WO-JP00804.
 XX PR 13-MAR-1996; 96JP-0056090.
 XX PA (MITU) MITSUBISHI CHEM CORP.
 XX PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
 XX DR WPI; 1997-470978/43.
 XX PT Antibody prepared using a partial peptide containing part of
 XX PT phosphorylated tau protein - used for detecting Alzheimer's disease
 XX PS Example; Pages 36-37; 48pp; Japanese.
 XX CC An antibody, prepared using a partial peptide containing the
 XX CC phosphorylated residue of the phosphorylated tau protein, e.g. the
 XX CC present sequence, in a paired helical filament, can be used to
 XX CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 XX CC protein in brain extracts or tissue fragments.
 XX SQ Sequence 34 AA;

Query Match 100.0%; Score 50; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels. 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 7 ysspgspgt 15
 |||||

RESULT 9
 AAR59837
 ID AAR59837 standard; peptide; 67 AA.
 AC AAR59837;
 DT 04-MAR-1995 (first entry)
 DE Sequence of human microtubule-associated protein tau.
 KW Tau protein; brain; cerebral cortex; hybridoma ECACC 92100853;
 KW Alzheimer's disease; monoclonal antibody; paired helical filament.
 OS Homo sapiens.
 XX WO9413795-A.
 XX PD 23-JUN-1994.
 XX PF 10-DEC-1993; 93WO-EP03499.
 XX PR 14-DEC-1992; 92EP-0403403.
 XX PA (INNO-) INNOGENETICS NV SA.
 XX PI Mercken M, Van De Voorde A, Vandermeeren M, Vanmechelen E;
 XX DR WPI; 1994-234211/28.
 XX CC Monoclonal antibody reactive with tau protein - used to develop
 XX CC prods. for detection of brain diseases involving tau or paired
 XX CC helical filaments esp. Alzheimer's disease
 XX PS Claim 6; Page 38; 52pp; English.

CC Paired helical filament (PHF) tau was partially purified from
 CC postmortem tissue, consisting mostly of grey matter from the frontal
 CC and temporal cortex obtd. from Alzheimer patients. The tissue (5-10g)
 CC was homogenised with 10 vols of cold buffer (10mM Tris, 1mM EGTA,
 CC 0.8M NaCl, 10% sucrose, pH 7.4). After centrifugation for 20 mins at
 CC 4 degrees C, the supernatant was adjusted to 1% (wt/vol) N-
 CC lauroylsarcosine and 1% (vol/vol) 2-mercaptoethanol and incubated
 CC while rotating on a mixer for 2.5 hrs at 37 degrees C. The mixt. was
 CC centrifuged at 108,000 g for 35 mins at 20 degrees C. The PHF-tau
 CC contg. pellet was washed with PBS and resuspended in 1ml of the same
 CC buffer. Hybridomas which produced MAb's reactive with tau protein
 CC were obtd. from the spleen cells of Balb/C mice primed s.c. with
 CC partially purified PHF. A MAb which forms an immunological complex
 CC with a human tau protein of sequence in AAR59837 is secreted by the
 CC hybridoma deposited at ECACC on Oct. 8 1992 under No. 92100853.
 XX SQ Sequence 67 AA;

Query Match 100.0%; Score 50; DB 15; Length 67;
 Best Local Similarity 100.0%; Pred. No. 0.74; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 43 ysspgspgt 51
 |||||

RESULT 10
 AAB85640
 ID AAB85640 standard; peptide; 78 AA.
 AC AAB85640;
 DT 29-OCT-2001 (first entry)
 DE Tau peptide region (residues 155-232).
 XX KW Taupath; phospho-tau (181); neurological marker; monoclonal antibody;
 KW HT7; AT270; neurotropic; neuroprotective; cerebroprotective; epitope.
 XX OS Homo sapiens.
 XX PN WO20015725-A2.
 XX PD 02-AUG-2001.
 XX PF 18-JAN-2001; 2001WO-EP00560.
 XX PR 24-JAN-2000; 2000EP-0870008.
 XX PR 27-JAN-2000; 2000US-0178391.
 XX PR 22-NOV-2000; 2000EP-0870280.
 XX PA (INNO-) INNOGENETICS NV.
 XX PI Vanmechelen E, Vanderstichele H;
 XX DR WPI; 2001-476242/51.
 XX PT Determining the ratio of phospho-tau / total tau is useful for
 XX PT diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease,
 XX PT versus a non tauopathy -
 XX PS Example 1; Fig 1; 71pp; English.
 XX CC The invention provides a method of diagnosis of tauopathies in an
 XX CC individual that comprises determining the ratio of phospho-tau (181)/
 XX CC total tau. Tau and phospho tau are useful as neurological markers for the
 XX CC manufacture of a diagnostic kit for the diagnosis of a tauopathy and/or
 XX CC the differential diagnosis of a tauopathy versus a non tauopathy. A
 XX CC phospho-peptide liable to form an immunological complex with monoclonal
 XX CC antibody HT7 and MAb AT270 comprising at least the minimal epitope of HT7
 XX CC or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy

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CC and/or for the differential diagnosis of a tauopathy versus a non
CC tauopathy. The kit is useful for the diagnosis of Alzheimer's disease,
CC Pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal
CC dementia with Parkinsonism linked to chromosome 17, Creutzfeldt Jacob
CC disease, stroke and/or neurotoxicity in patients with leukemia. The
CC phosphopeptide kits and methods are useful for therapeutic monitoring and
CC for determining the effectiveness of a treatment. The present sequence
CC represents a tau peptide fragment.

XX Sequence 78 AA;

Query Match 100.0%; Score 50; DB 22; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 43 YSSPGSPGT 51

RESULT 11
AAR92516
ID AAR92516 standard; peptide; 106 AA.

XX AC AAR92516;
XX 20-SEP-1996 (first entry)

XX Microtubule-associated tau protein epitope corresp. to pos. 146-251.
XX Epitope; microtubule-associated protein; tau; phosphorylation; subclass;
KW paired helical fibre; neurofibrillary tangle; dementia; neurological;
KW Alzheimer's disease; monoclonal antibody; brain; pathology.

XX Synthetic.
XX WO9604309-A1.

XX 15-FEB-1996.
XX 31-JUL-1995; 95WO-EP03032.
XX 29-JUL-1994; 94EP-0870131.
XX (INNO-) INNOGENETICS NV.

XX Van DE VOORDE A, Vanmechelen E;
XX WPI; 1996-129338/13.

XX Monoclonal antibodies specific for phosphorylated tau - for improved
XX detection and diagnosis of e.g. Alzheimer's Disease

XX Claim 2; Page 32; 42pp; English.

XX This is the amino acid of an epitope derived from the microtubule-
XX associated tau protein. The phosphorylated subclass of tau protein
XX from which this epitope originates, forms a major part of the paired
XX helical fibres which make up neurofibrillary tangles seen in patients
XX suffering from dementia e.g. Alzheimer's disease. The epitope is esp.
XX isolated from patients who have recently died from Alzheimer's disease.
XX It is used to generate monoclonal antibodies for the in vitro detection
XX or diagnosis of brain/neurological diseases such as Alzheimer's disease
XX or other diseases where neurofibrillary tangles are a pathological
XX symptom.

XX Sequence 106 AA;

Query Match 100.0%; Score 50; DB 17; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 52 YSSPGSPGT 60

RESULT 12
AAR76937
ID AAR76937 standard; Peptide; 112 AA.

XX AC AAR76937;
XX 04-DEC-1995 (first entry)
XX PHF-tau (143-254) peptide.

XX PHF-tau; paired helical filament tau protein; monoclonal antibody;
KW MAB; phosphorylation; neurological disease; Alzheimer disease;
KW cerebrospinal fluid.

XX Homo sapiens.
XX WO9517429-A.

XX 29-JUN-1995.
XX 14-DEC-1994; 94WO-EP04146.
XX 21-DEC-1993; 93EP-0403133.

XX (INNO-) INNOGENETICS NV.

XX Van De Voorde A, Vandermeeren M, Vanmechelen E;
XX WPI; 1995-240616/31.

XX Novel monoclonal antibodies specific for abnormally phosphorylated
XX paired helical filament tau protein (PHF-Tau) - useful for post
XX mortem or in vitro detection of neurological diseases eg. Alzheimer's
XX disease

XX Claim 1; Page 44; 57pp; English.

XX Novel MABs AT180 and AT270 (ECACC 92122204, 93070774) form
XX immunological complexes with a phosphorylated epitope, given in
XX AAR76937, of abnormally phosphorylated tau protein (PHF-tau). The
XX MABs are used to specifically detect PHF-tau in cerebrospinal fluid.

XX Sequence 112 AA;

Query Match 100.0%; Score 50; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 55 YSSPGSPGT 63

RESULT 13
AAY15200
ID AAY15200 standard; Protein; 351 AA.

XX AC AAY15200;

XX 28-FEB-2000 (first entry)

XX Human Tau protein.

XX Human Tau gene; neurofibrillary tangle formation; abnormal tau filament;
KW brain; mutation; phosphorylation; isoform ratio; diagnosis; tauopathy;
KW treatment; neurodegenerative disorder; Frontotemporal Dementia;

KW Familial Multiple System Tauopathy with presenile Dementia; MSTD;
 KW Pick's Disease; Progressive Supranuclear Palsy; PSP; Alzheimer's Disease;
 KW Corticobasal Degeneration; CD; Prion Protein Cerebral Amyloid Angiopathy;
 XX cognitive disorder.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Protein 1.351
 FT /label= Tau_protein
 FT /note= "Microtubule related protein"

XX W09962548-A1.

XX 09-DEC-1999.

XX 28-MAY-1999; 99WO-US12036.

XX 01-JUN-1998; 98US-0087557.

XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX Ghatti B, Spillantini MG, Murrell JR, Goedert M, Farlow MR;
 XX Klug A;

XX WPI; 2000-086858/07.

XX N-PSDB; AAZ29262.

XX Diagnosing a tauopathy, especially a Fronto-Temporal Dementia -
 XX Disclosure; Page 85; 90pp; English.

XX The present amino acid sequence is a form of human Tau protein.
 XX There are six tau isoforms, expressed in the normal adult brain with a
 XX slight preponderance of those with 3 repeats over those with 4 repeats.
 XX Mutations in the tau gene affects phosphorylation and leads to formation
 XX of neurofibrillary tangles and alters the tau isoform ratio. The
 XX increased ratio of 4:3 repeat and abnormal tau filaments is closely
 XX related to neurodegenerative disorders. This sequence can be used for
 XX diagnosis and treatment of tauopathies, like Fronto-Temporal Dementia,
 XX Familial Multiple System Tauopathy with presenile Dementia (MSTD),
 XX Pick's Disease, Progressive Supranuclear Palsy (PSP), Corticobasal
 XX Degeneration (CD) or Alzheimer's Disease. A composition that decreases
 XX the ratio of 4:3 repeat tau isoforms, along with an agent for treatment
 XX of a cognitive disorder, is useful for treating a tauopathy. It may also
 XX be useful in diagnosis of Prion Protein Cerebral Amyloid Angiopathy and
 XX other prion protein associated disease characterized by abnormal tau
 XX filament formation.

XX Sequence 351 AA;

Query Match 100.0%; Score 50; DB 21; Length 351;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 139 ysspgspgt 147
 |||||

RESULT 14

AAP91294

ID AAP91294 standard; protein; 352 AA.

XX AAP91294;

XX 18-DEC-1989 (first entry)

XX Paired helical filament (PHF) core protein.

XX Paired helical filament (PHF) core protein; Alzheimer's disease;
 KW neurofibrillary tangles.

XX Homo sapiens.
 XX OS
 XX XX
 XX PN W08903993-A.
 XX XX
 XX PD 05-MAY-1989.
 XX XX
 XX PF 19-OCT-1988; 88WO-GB00867.
 XX XX
 XX PR 19-OCT-1987; 87GB-0024412.
 XX XX
 XX PA (MEDI) MEDICAL RESEARCH COUNCIL.
 XX XX
 XX PI Wischik CM, Milstein C, Klug A;
 XX DR WPI; 1989-150854/20.
 XX XX
 XX PT Paired helical filament core protein - used for providing reagents
 XX PT sensitive to neurofibrillary tangles used for diagnosing Alzheimer's
 XX PT disease.
 XX XX
 XX PS Disclosure; fig 1; 29pp; English.
 XX XX
 XX CC Paired helical filament core protein was sequenced from DNA obtained
 XX CC from brain tissue contg. Alzheimer neurofibrillary tangles. The protein
 XX CC can be used to make MAB's to the PHF core or nucleotide probes, used to
 XX CC diagnose Alzheimer's disease. The protein sequence QIVVKP (AAs 218-223)
 XX CC was used to design the probes.
 XX CC See also AAN91707.
 XX XX
 XX SQ Sequence 352 AA;

Query Match 100.0%; Score 50; DB 10; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 DB 139 ysspgspgt 147
 |||||

RESULT 15

AAR32708

ID AAR32708 standard; protein; 352 AA.

XX AAR32708;

XX 15-JUN-1993 (first entry)

XX Human tau-protein.

XX Alzheimer's disease; diagnosis; subtyping; monitoring; assay.

XX Homo sapiens.

XX W09303369-A.

XX 18-FEB-1993.

XX 03-AUG-1992; 92WO-US06382.

XX 01-AUG-1991; 91US-0738778.

XX (VOOR/) VOORHEIS P H.

XX Voorheis PH;

XX WPI; 1993-076670/09.

XX N-PSDB; AAZ37305.

XX Method for diagnosing, subtyping and monitoring Alzheimer's
 PT disease - by assaying a sample of body fluid for the presence of a

XX This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin 1, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 50; DB 19; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSPGSPGPT 9
 Db 139 yspgspgpt 147
 |||||

RESULT 17
 AAW05283
 ID AAW05283 standard; Protein: 390 AA.
 AC AAW05283;
 XX 20-DEC-1996 (first entry)
 DT Truncated human tau protein.
 DE
 XX Tau protein; inhibition; modulation; prophylaxis; treatment;
 KW Alzheimer's disease; motor neurone disease; Lewy body disease;
 KW progressive supranuclear palsy; Pick's disease.
 KW Homo sapiens.
 OS
 XX WO9630766-A1.
 PN 03-OCT-1996.
 PD 25-MAR-1996; 96WO-EP01307.
 PF 27-MAR-1995; 95GB-0006197.
 PR (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PA Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
 PI WPI: 1996-455570/45.
 XX Assay for inhibitors of tau-tau interaction - used for identifying
 CC cpds., partic. phenothiazine cpds., for treating pathological
 CC tau-tau or neuro:filament aggregation
 CC Claim 11; : 97pp; English.
 CC Detecting an agent which modulates or inhibits tau-tau protein
 CC association comprises contacting two tau proteins, distinct from
 CC each other yet capable of binding to the other and where one of the
 CC tau proteins is labelled, in the presence of the agent suspected of
 CC being capable of modulating or inhibiting tau-tau interaction.

PT tau-peptide using an anti-tau antibody
 PS Disclosure; Fig 1; 43pp; English.
 XX The sequence is that one form of human tau protein (from Goedert
 CC et al., PNAS USA 85: 4051-4055) which was used for the prodn.
 CC of anti-tau peptide antibodies. These are used as part of a method
 CC for diagnosing, subtyping or monitoring Alzheimer's disease by
 CC assaying a sample of body fluid for the presence of a tau-peptide
 CC using an anti-tau antibody or the presence of an anti-tau-peptide
 CC autoantibody. The methods can be used for confirming a clinical
 CC diagnosis of Alzheimer's disease and in following the course of the
 CC disease and treatment.
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 50; DB 14; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSPGSPGPT 9
 Db 139 yspgspgpt 147
 |||||

RESULT 16
 AAY20248
 ID AAY20248 standard; Protein: 352 AA.
 AC AAY20248;
 XX 22-JUL-1999 (first entry)
 DT Human microtubule associated protein Tau wild type fragment.
 DE
 XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 KW Homo sapiens.
 OS
 XX WO9845322-A2.
 PN 15-OCT-1998.
 PD 02-APR-1998; 98WO-IB00705.
 PF 10-APR-1997; 97US-0043163.
 PR (UYUT-) RIJKSUNIV UTRECHT.
 XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
 XX WPI: 1998-609901/51.
 DR N-PSDB; AAX75754.
 XX Diagnosing disease by detecting frameshift mutations in RNA or
 CC corresponding protein mutations - used to diagnose cancer and
 CC neurological diseases, particularly Alzheimer's disease, and also
 CC for treatment and prevention with specific ribozymes or wild-type
 CC RNA
 XX Disclosure; Figure 3; 258pp; English.

CC Agents identified as being modulators or inhibitors of tau-tau
 CC interaction may be used for the prophylaxis and treatment of
 CC Alzheimer's disease, motor neurone disease, Lewy body disease,
 CC Pick's disease or progressive supranuclear palsy. This sequence of
 CC the human tau protein is truncated at amino acid residue 390. The
 CC full length protein is given in AAW05282.
 XX
 SQ Sequence 390 AA;

Query Match 100.0%; Score 50; DB 17; Length 390;
 Best Local Similarity 100.0%; Pred. No. 4.2; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

Qy 1 YSSPGSPGT 9
 Db 197 YSSPGSPGT 205
 |||||

RESULT 18
 AAR58810
 ID AAR58810 standard; protein; 441 AA.
 XX
 AC AAR58810;
 XX
 DT 27-MAR-1995 (first entry)
 XX
 DE Human tau protein.
 XX
 KW Tau; cerebrospinal fluid; immunoassay; antibody; detection;
 KW diagnosis; central nervous system; CNS; cytopathies; cytopathy;
 KW Alzheimer's disease.
 XX

OS Homo sapiens.

XX W09418560-A.

XX 18-AUG-1994.

XX 10-FEB-1994; 94WO-JP00196.

XX 12-FEB-1993; 93JP-0046133.

XX (TEIJ) TEIJIN LTD.

XX Eguchi H, Hosoda K, Kobayashi S, Kubota T, Mori H;
 XX Nakamoto T;
 XX WPI; 1994-279910/34.

XX Sandwich immunoassay of tau protein in cerebrospinal fluid - for
 XX diagnosis of Alzheimer's disease and other CNS cytopathies
 XX
 PS Claim 1; Page 16-18; 36pp; Japanese.

XX Detection of the human tau protein (or fragments of it) in samples
 CC of cerebrospinal fluid enables the diagnosis of central nervous
 CC system cytopathies such as Alzheimer's disease. Detection is
 CC performed using labelled antibodies which recognise sites within the
 CC region defined by the amino acid residues 251-441. The antibodies
 CC are preferably polyclonal.
 XX
 SQ Sequence 441 AA;

Query Match 100.0%; Score 50; DB 15; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.7; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

Qy 1 YSSPGSPGT 9
 Db 197 YSSPGSPGT 205
 |||||

RESULT 19
 AAW05282
 ID AAW05282 standard; protein; 441 AA.
 XX
 AC AAW05282;
 XX
 DT 20-DEC-1996 (first entry)
 XX
 DE Human tau protein.
 XX

XX Tau protein; inhibition; modulation; prophylaxis; treatment;
 KW Alzheimer's disease; motor neurone disease; Lewy body disease;
 KW progressive supranuclear palsy; Pick's disease.
 XX
 OS Homo sapiens.
 XX
 PN W09630766-A1.
 XX
 PD 03-OCT-1996.
 XX
 PF 25-MAR-1996; 96WO-EP01307.
 XX
 PR 27-MAR-1995; 95GB-0006197.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
 XX WPI; 1996-455570/45.
 DR N-PSDB; AAT39591.
 XX

XX Assay for inhibitors of tau-tau interaction - used for identifying
 PT cpds., partic. phenothiazine cpds., for treating pathological
 PT tau-tau or neuro:fibrilament aggregation
 XX
 PS Example 2; Page 53-54; 97pp; English.
 XX
 CC Detecting an agent which modulates or inhibits tau-tau protein
 CC association comprises contacting two tau proteins, distinct from
 CC each other yet capable of binding to the other and where one of the
 CC tau proteins is labelled, in the presence of the agent suspected of
 CC being capable of modulating or inhibiting tau-tau interaction.
 CC Agents identified as being modulators or inhibitors of tau-tau
 CC interaction may be used for the prophylaxis and treatment of
 CC Alzheimer's disease, motor neurone disease, Lewy body disease,
 CC Pick's disease or progressive supranuclear palsy.
 XX
 SQ Sequence 441 AA;

Query Match 100.0%; Score 50; DB 17; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.7; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

Qy 1 YSSPGSPGT 9
 Db 197 YSSPGSPGT 205
 |||||

RESULT 20
 AAW34856
 ID AAW34856 standard; protein; 441 AA.
 XX
 AC AAW34856;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Human tau protein.
 XX

XX Antibody; phosphorylated tau protein; paired helical filament;
 KW detection; Alzheimer's disease; human.
 XX

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OS Homo sapiens.
 XX W09734145-A1.
 PN
 XX 18-SEP-1997.
 PD
 XX 13-MAR-1997; 97WO-JP00804.
 PF
 XX 13-MAR-1996; 96JP-0056090.
 PR
 XX (MITU) MITSUBISHI CHEM CORP.
 PA
 XX Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
 PI WPI; 1997-470978/43.
 DR
 XX Antibody prepared using a partial peptide containing part of
 PT phosphorylated tau protein - used for detecting Alzheimer's disease
 PT
 XX Claim 2; Pages 25-27; 48pp; Japanese.
 PS
 XX An antibody, prepared using a partial peptide containing the
 CC phosphorylated residue of the phosphorylated tau protein, e.g. the
 CC present sequence, in a paired helical filament, can be used to
 CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 CC protein in brain extracts or tissue fragments.
 CC
 XX Sequence 441 AA;
 SQ

Query Match 100.0%; Score 50; DB 18; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.7; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 QY 1 YSSPGSPGT 9
 DB 197 ysspgspgt 205
 |||||

RESULT 21
 AAY81386
 ID AAY81386 standard; protein; 441 AA.
 XX
 AC AAY81386;
 XX
 XX 19-JUN-2000 (first entry)
 DT
 XX Human paired helical filament phosphorylated tau protein.
 DE
 XX phosphorylated tau protein; human; paired helical filament;
 KW polyclonal antibody; Alzheimer's disease; cerebrospinal fluid; CSF;
 KW diagnosis; detection.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 XX Modified-site 199 /note= "Phosphorylated"
 FT
 XX Modified-site 231 /note= "Phosphorylated"
 FT
 XX Modified-site 235 /note= "Phosphorylated"
 FT
 XX JP2000034300-A.
 PN
 XX 02-FEB-2000.
 PD
 XX 17-JUL-1998; 98JP-0204040.
 PF
 XX 17-JUL-1998; 98JP-0204040.
 PR
 XX (MITU) MITSUBISHI CHEM CORP.
 PA
 XX

DR WPI; 2000-285529/25.
 XX Anti-phosphated tau protein antibody - for the detection of Alzheimer
 PT disease
 PT
 XX Claim 1; Page 8-9; 12pp; Japanese.
 PS
 XX The invention relates to an antibody against a phosphorylated tau
 CC protein (AAY81386), which is a component of the paired helical filament
 CC found in the plaques associated with Alzheimer's disease. A
 CC phosphorylated tau protein fragment selected from peptides
 CC AAY81387-Y81390 is conjugated to keyhole limpet haemocyanin (KLH), and
 CC used to raise polyclonal antibodies in a rabbit. The antibodies of the
 CC invention are specific for phosphorylated tau protein and may be used to
 CC detect phosphorylated tau protein in the cerebrospinal fluid (CSF) of a
 CC patient suspected of having Alzheimer's disease. Use of the antibodies of
 CC the invention provides specific diagnosis of Alzheimer's disease. The
 CC present sequence represents phosphorylated tau protein.
 XX
 XX Sequence 441 AA;
 SQ

Query Match 100.0%; Score 50; DB 21; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.7; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 QY 1 YSSPGSPGT 9
 DB 197 ysspgspgt 205
 |||||

RESULT 22
 AAR28237
 ID AAR28237 standard; peptide; 13 AA.
 XX
 AC AAR28237;
 XX
 XX 18-MAR-1993 (first entry)
 DT
 XX Phosphopeptide as Alzheimers's disease detection antigen.
 DE
 XX AD; antigen; antibody; paired helical filament; PHF; brain.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 XX Modified-site 6 /note= "at least one of Ser6 and Thr9 is modified
 FT by PO(OH)"
 FT
 XX Modified-site 9 /note= "at least one of Ser6 and Thr9 is modified
 FT by PO(OH)"
 FT
 XX Modified-site 13 /note= "the C-terminal is amidated"
 FT
 XX JP04270299-A.
 PN
 XX 25-SEP-1992.
 PD
 XX 25-FEB-1991; 91JP-0146476.
 PF
 XX 25-FEB-1991; 91JP-0146476.
 PR
 XX (MITU) MITSUBISHI KASEI CORP.
 PA
 XX WPI; 1992-369427/45.
 DR
 XX New phospho:peptide(s) - useful as antigen for detection of
 PT Alzheimer's disease
 PT
 XX Claim 1; Page 2; 4pp; Japanese.
 PS
 XX The C-terminal of the peptide is amidated.
 CC

Key	Location/Qualification
1	...
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Key	Location/Qualifiers
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Key	Location/Qualifiers
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Wed May 22 11:04:33 2002

```

XX FT      CDS      23..955
XX FT      sig_peptide /*tag= a
XX FT      23..120
XX FT      mat_peptide /*tag= b
XX FT      164..952
XX FT      /*tag= c
XX PN      WO9739114-A1.
XX PD      23-OCT-1997.
XX PF      14-APR-1997; 97WO-DK00160.
XX PR      23-AUG-1996; 96DK-0000885.
XX PR      12-APR-1996; 96DK-0000427.
XX PA      (NOVO ) NOVO-NORDISK AS.
XX PI      Diers I, Ferrer P, Halkier T, Hedegaard L;
XX PX      WPI: 1997-526451/48.
XX DR      N-PSDB; AAT89155.
XX      New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia
XX      xanthineolytica, used particularly for the lysis of microbial cells
XX      for obtaining desirable products
XX      Example 2; Page 35-36; 64pp; English.
XX      This polypeptide comprises a novel Oerskovia xanthineolytica (OX)
XX      enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino
XX      acid sequence was deduced from an isolated genomic DNA sequence
XX      (see AAT89155). Claimed DNA constructs that encode the novel BG (see
XX      also AAW29456 for a full-length enzyme), a mannose binding domain (see
XX      AAW29458) or a full-length enzyme, i.e. BG with mannose binding
XX      domain (see AAW29456), can be used to produce recombinant BG
XX      polypeptides, with or without a mannose binding domain, in fungal
XX      or bacterial host cells. BG polypeptides are used for the
XX      degradation or modification of beta-glucan containing material,
XX      especially for the gentle lysis of microbial cell walls, thereby
XX      enabling recovery of desirable intracellular products with a
XX      reduced amount of contaminants. They can also be used for the
XX      production of e.g. pigments, colourants, flavourants, yeast
XX      extracts, pharmaceuticals, food or feed compositions, and to
XX      prepare protoplasts for use in fusion, transformation and cloning
XX      studies.
XX      Sequence 263 AA;
XX
XX      Query Match      80.0%; Score 40; DB 18; Length 263;
XX      Best Local Similarity 87.5%; Pred. No. 1e+02;
XX      Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      2 SSPGSPGT 9
XX      Db      244 sspgpnpt 251
XX
XX      RESULT 26
XX      AAW29456
XX      ID      AAW29456 standard; Protein: 435 AA.
XX      AC      AAW29456;
XX      DT      14-APR-1998 (first entry)
XX      DE      Oerskovia xanthineolytica beta-1,3-glucanase.
XX      KW      Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
XX      KW      fungal cell wall; intracellular product; purification; protoplast.
XX      OS      Oerskovia xanthineolytica LIG109 (DSM 10297).
XX
XX      Query Match      80.0%; Score 40; DB 18; Length 435;
XX      Best Local Similarity 87.5%; Pred. No. 1.6e+02;
XX      Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      2 SSPGSPGT 9
XX      Db      297 sspgpnpt 304
XX
XX      RESULT 27
XX      AAR38233
XX      ID      AAR38233 standard; peptide; 7 AA.
XX      AC      AAR38233;
XX      DT      08-OCT-1993 (first entry)
XX      DE      Alzheimer paired helical filament tau protein epitope 197-203.
XX      KW      Alzheimer tau protein; phosphorylation-dependent; PHF;
XX      KW      neuronal microtubule; mitogen activated protein kinase; MAP kinase.
XX
XX      Location/Qualifiers
XX      1..52
XX      /label= Sig_peptide
XX      53..435
XX      /label= Mat_protein
XX      304..435
XX      /label= Mannose-binding_domain
XX
XX      WO9739114-A1.
XX      23-OCT-1997.
XX      14-APR-1997; 97WO-DK00160.
XX      23-AUG-1996; 96DK-0000885.
XX      12-APR-1996; 96DK-0000427.
XX      (NOVO ) NOVO-NORDISK AS.
XX      Diers I, Ferrer P, Halkier T, Hedegaard L;
XX      WPI: 1997-526451/48.
XX      N-PSDB; AAT89155.
XX      New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia
XX      xanthineolytica, used particularly for the lysis of microbial cells
XX      for obtaining desirable products
XX      Example 2; Page 39-40; 64pp; English.
XX      This sequence comprises the polypeptide precursor of a novel
XX      Oerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase
XX      (BG) activity and which includes a mannose binding domain (MBD).
XX      Its amino acid sequence was deduced from an isolated genomic DNA
XX      sequence (see AAT89156). Claimed DNA constructs that encode the
XX      novel BG lacking a MBD (see AAW29455 and AAW29457), a MBD (see
XX      AAW29458), or the full-length enzyme can be used to produce recombinant
XX      BG polypeptides, with or without a mannose binding domain, in fungal
XX      or bacterial host cells. BG polypeptides are used for the
XX      degradation or modification of beta-glucan containing material,
XX      especially for the gentle lysis of microbial cell walls, thereby
XX      enabling recovery of desirable intracellular products with a
XX      reduced amount of contaminants. They can also be used for the
XX      production of e.g. pigments, colourants, flavourants, yeast
XX      extracts, pharmaceuticals, food or feed compositions, and to
XX      prepare protoplasts for use in fusion, transformation and cloning
XX      studies.
XX      Sequence 435 AA;
XX
XX      Query Match      80.0%; Score 40; DB 18; Length 435;
XX      Best Local Similarity 87.5%; Pred. No. 1.6e+02;
XX      Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      2 SSPGSPGT 9
XX      Db      297 sspgpnpt 304
XX
XX      RESULT 27
XX      AAR38233
XX      ID      AAR38233 standard; peptide; 7 AA.
XX      AC      AAR38233;
XX      DT      08-OCT-1993 (first entry)
XX      DE      Alzheimer paired helical filament tau protein epitope 197-203.
XX      KW      Alzheimer tau protein; phosphorylation-dependent; PHF;
XX      KW      neuronal microtubule; mitogen activated protein kinase; MAP kinase.

```

XX OS Homo sapiens.
 XX FH Key
 FT Modified-site Location/Qualifiers
 FT 3..4
 FT /label= Phosphorylation_motif
 FT 6..7
 FT /label= Phosphorylation_motif
 XX W09311231-A.
 PN 10-JUN-1993.
 PD
 XX 07-DEC-1992; 92WO-EP02829.
 PF
 XX 06-DEC-1991; 91EP-0120974.
 PR 16-NOV-1992; 92EP-0119551.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;
 PI Steiner B;
 XX WPI; 1993-197050/24.
 DR
 XX Tau protein epitope(s). specific antibodies and protein kinase(s)
 PT - used in the prevention, diagnosis and treatment of Alzheimer's
 PT disease
 XX
 PS Claim 5; Page 89; 148pp; English.
 XX
 CC This is one of 26 preferred epitopes which occur in a phosphorylated
 CC state in tau protein from Alzheimer paired helical filaments. The
 CC epitopes all include phosphorylatable serine residues in Ser-Pro
 CC motifs, ile-gly-ser motifs or cys-gly-ser motifs and/or
 CC phosphorylatable threonine residues in Thr-Pro motifs. The pattern
 CC of tau protein phosphorylation differs between Alzheimer's and
 CC non-Alzheimer's individuals. Knowledge of the phosphorylated
 CC epitopes and antibodies which recognise them may be useful in
 CC diagnosis, treatment and prevention of Alzheimer's Disease. The
 CC protein kinases present in mammalian brain which phosphorylate the
 CC different epitopes are also claimed but no sequences are given.
 XX
 SQ Sequence 7 AA;

Query Match 78.0%; Score 39; DB 14; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSP 7
 Db | | | | | | |
 1 ysspgsp 7

RESULT 28
 AAR37552
 ID AAR37552 standard; peptide; 7 AA.
 XX AAR37552;
 AC
 XX 07-OCT-1993 (first entry)
 DT
 XX Phosphorylated tau protein epitope.
 DE
 XX Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
 KW treatment; formation; inhibition; inhibitor.
 KW
 XX Homo sapiens.
 OS
 XX EP544942-A.
 PN
 XX 09-JUN-1993.
 PD

XX 06-DEC-1991; 91EP-0120974.
 PF
 XX 06-DEC-1991; 91EP-0120974.
 PR
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA
 XX Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow EM, Steiner B;
 PI WPI; 1993-183841/23.
 XX
 DR Phosphorylated tau protein epitope associated with Alzheimer's
 XX disease - is used as protein kinase inhibitor for treatment and
 PT diagnosis
 PT
 XX Claim 4; Page 16; 34pp; English.
 PS
 XX
 CC The sequence is that of an epitope of tau protein which specifically
 CC occurs in a phosphorylated state in tau protein from Alzheimer's
 CC paired helical fragments. It may be used as part of a method for the
 CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
 CC also be used in an in vitro model for the study of the generation of
 CC the Alzheimer state of proteins and the testing of substances which
 CC prevent the conversion of normal to Alzheimer tau protein. The
 CC epitope occurs at residues 197-203 of human tau protein.
 XX
 SQ Sequence 7 AA;

Query Match 78.0%; Score 39; DB 14; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSP 7
 Db | | | | | | |
 1 ysspgsp 7

RESULT 29
 AAU17141
 ID AAU17141 standard; Protein; 263 AA.
 XX AAU17141;
 AC
 XX 07-NOV-2001 (first entry)
 DT
 XX Novel signal transduction pathway protein, Seq ID 706.
 DE
 XX
 KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
 KW antiinflammatory; anti-HIV; antibacterial; antinflammatory; cancer;
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;
 KW organ transplant rejection; infection; hepatitis C; blood disorder;
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 KW reproductive system; gastrointestinal; liver disorder; AIDS;
 KW acquired immune deficiency syndrome.
 XX
 OS Homo sapiens.
 OS
 XX WO200154733-A1.
 PN
 XX 02-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01312.
 PF
 XX 31-JAN-2000; 2000US-0179065.
 PR
 XX 04-FEB-2000; 2000US-0180628.
 PR
 XX 24-FEB-2000; 2000US-0184664.
 PR
 XX 02-MAR-2000; 2000US-0186350.
 PR
 XX 16-MAR-2000; 2000US-0189874.
 PR
 XX 17-MAR-2000; 2000US-0190076.
 PR

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18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 14-AUG-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226686.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 29-SEP-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249284.
 PR 17-NOV-2000; 2000US-0249285.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-465460/50.
 N-PSDB; AAS27058.
 Novel polypeptides useful for diagnosing, treating, preventing and/or
 prognosing disorders related to the proteins, including cancers, immune
 disorders and neuronal disorders
 Claim 1; SEQ ID No 706; 880pp; English.
 The invention relates to novel isolated polypeptides (I), and
 polynucleotides (II). (I), (II) and the antibody to (I) are useful for

CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders (e.g. primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B-cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). AAU17059-AAU1763 represent novel signal transduction
 CC pathway protein, amino acid sequences of the invention.
 XX

Query Match 78.0%; Score 39; DB 22; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1.4e-02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 Db 180 spgspgt 186
 |||||

RESULT 30
 AAM80057
 ID AAM80057 standard; Protein; 376 AA.

AC AAM80057;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3703.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

PN WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;

PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R,

XX WPI; 2001-476283/51.

DR N-PSDB; AAK53190.

XX Nucleic acids encoding polypeptides with cytokine-like activities,

PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 415; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX Sequence 376 AA;

Query Match 78.0%; Score 39; DB 22; Length 376;
 Best Local Similarity 100.0%; Pred. No. 2e-02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 Db 358 spgspgt 364
 |||||

RESULT 31
 AAB41838

ID AAB41838 standard; Protein; 424 AA.

XX AAB41838;

DT 08-FEB-2001 (first entry)

DE Human ORF1602 polypeptide sequence SEQ ID NO:3204.

KW Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
 KW vulnery; antiproliferative; antiparkinsonian; nontropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antineoplastic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08621.

PR 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

PA (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX

XX WPI: 2001-007395/01.
 DR N-PSDB; AAC66894.
 XX
 PT Isolated polynucleotide encoding extracellular matrix or
 PT adhesion-associated protein (EXMAD) useful for diagnosing, treating, or
 PT preventing disorders associated with expression of EXMAD such as
 PT proliferative, immune and genetic disorders -
 XX
 PS Claim 1; Page 92-93; 129pp; English.
 XX
 CC The present invention provides the protein and coding sequences for 25
 CC novel extracellular matrix and adhesion-associated proteins (EXMADS).
 CC These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-5,
 CC EXMAD-6, EXMAD-7, EXMAD-8, EXMAD-9, EXMAD-10, EXMAD-11, EXMAD-12,
 CC EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-18, EXMAD-19,
 CC EXMAD-20, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24 and EXMAD-25. They are
 CC useful in the prevention and treatment of cancers, cell proliferation,
 CC cardiovascular, reproductive, immune, musculoskeletal, developmental and
 CC gastrointestinal disorders and inflammation.
 XX
 SQ Sequence 424 AA;

Query Match 78.0%; Score 39; DB 22; Length 424;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 |||||
 Db 341 spgspgt 347

RESULT 34
 AAO05662
 ID AAO05662 standard; Protein; 98 AA.
 AC AAO05662;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 19554.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-514838/56.
 DR N-PSDB; AAI85593.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 19554; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and

CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 98 AA;

Query Match 76.0%; Score 38; DB 22; Length 98;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPG 8
 |||||
 Db 79 sspgspg 85

RESULT 35
 ABG27348
 ID ABG27348 standard; Protein; 284 AA.
 XX
 AC ABG27348;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #27339.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS91535.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 57707; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as

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CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 284 AA;

Query Match 74.0%; Score 37; DB 22; Length 284;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
 Db 56 fgspgspg 63

RESULT 36
 AAR25063
 ID AAR25063 standard; Protein; 335 AA.

AC AAR25063;
 DT 10-DEC-1992 (first entry)
 DE Soluble human IL-5 receptor alpha chain.
 KW Soluble interleukin-5; chronic asthma; eosinophilia;
 KW screening antagonists; ss.

OS Homo sapiens.
 XX EP492214-A.
 XX 01-JUL-1992.
 XX 06-DEC-1991; 91EP-0120951.
 XX 27-DEC-1990; 90EP-0811030.
 XX 30-APR-1991; 91EP-0810327.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Devos R, Fiers W, Plaetinck G, Tavernier J, Van Der Hayden J;
 PI WPI; 1992-218502/27.
 DR N-PSDB; AAQ25789.

XX Recombinant alpha chain of human interleukin-5 receptor - and DNA
 PT encoding it, for treatment of interleukin-5 mediated disorders
 PT such as chronic asthma

XX Claim 7; Fig 1; 15pp; English.

XX This amino acid sequence was deduced from the nucleotide sequence,
 CC isolated as detailed in AAQ25789. Recombinant IL-5 alpha chain can be
 CC used as an IL-5 antagonist in chronic asthma or other disease
 CC states with demonstrated eosinophilia. It may also be used either
 CC alone or with the beta chain of the whole IL-5 receptor as a tool
 CC for screening for IL-5 antagonists. See also AAQ25790-2, AAQ30767, 8
 CC AAR25064.

XX Sequence 335 AA;

Query Match 74.0%; Score 37; DB 13; Length 335;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 Db 119 happgspgt 127

RESULT 37
 AAR33699
 ID AAR33699 standard; Protein; 335 AA.

AC AAR33699;
 DT 09-JUL-1993 (first entry)
 DE shIL-5R-alpha.

KW probe; murine; interleukin-5; IL-5; receptor; IL-5R; IL-5R-alpha; IgG;
 KW chain; human; hIL-5R; constant domain; heavy; light; immunoglobulin;
 KW IgA; IgM; IgE; chimeric protein; antagonist; asthma; half-life.

XX Synthetic.

XX EP533006-A.

XX 24-MAR-1993.

XX 05-SEP-1992; 92EP-0115246.

XX 18-SEP-1991; 91EP-0810738.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Devos R, Fiers W, Tavernier J;

XX WPI; 1993-095341/12.
 XX N-PSDB; AAQ38440.

XX Deoxyribonucleic acid sequence for chimeric polypeptide prodn. -
 PT comprises parts coding fragment of alpha and/or beta chain of
 PT human interleukin-5 receptor and heavy or light chain of
 PT immunoglobulin, for chronic asthma treatment
 XX Disclosure; Fig 1; 17pp; English.

XX The sequence given represents soluble human interleukin-5 (IL-5)
 CC receptor (IL-5R)-alpha chain. This sequence was used in the
 CC construction of a chimeric human IL-5R-alpha-IgG1 molecule. Chimeric
 CC proteins such as this can be used as IL-5 antagonists in the treatment
 CC of diseases, esp. chronic asthma. The chimeric proteins have an
 CC increased half-life in vivo compared to hIL-5R. See also AAQ38433-40.

XX Sequence 335 AA;

Query Match 74.0%; Score 37; DB 14; Length 335;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 Db 119 happgspgt 127

RESULT 38
 AAM93217
 ID AAM93217 standard; Protein; 350 AA.

XX AAM93217;
 XX AC

XX 06-NOV-2001 (first entry)
 DT

XX

DE Human polypeptide, SEQ ID NO: 2622.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-0114089.

XX

PR 08-JUL-1999; 99JP-0194486.

XX

PR 11-JAN-2000; 2000JP-0118774.

XX

PR 02-MAY-2000; 2000JP-0183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

DR WPI: 2001-524255/58.

XX

DR N-PSDB; AAK94126.

XX

PT 830 Primers useful for synthesizing full length cDNA clones and their

XX

PT use in genetic manipulation.

XX

PS Claim 8; SEQ ID NO 2622; 1380pp + sequence listing; English.

XX

CC The invention relates to primers for synthesizing full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesizing the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

XX

CC Note: The sequence data for this patent did not form part of the printed

XX

CC specification, but was obtained in CD-ROM format directly from EPO.

SQ

Sequence 350 AA;

Query Match

Best Local Similarity 74.0%; Score 37; DB 22; Length 350;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY

1 YSSPGSPGT 9

DB

249 ftspgypgt 257

RESULT 39

AAM52310

ID

AAM52310 standard; Protein; 351 AA.

XX

AC AAM52310;

XX

DT 18-JAN-2002 (first entry)

XX

DE Chicken zyxine fragment.

XX

KW Actin polymerisation; Ena/VASP; vasodilator-stimulated phosphoprotein;

XX

OS metastatic cancer; parasitic infection; cytotoxic; Chicken; zyxine.

XX

WO200171356-A2.

XX

PD 27-SEP-2001.

XX

PA (NAIN-) INST NACIONAL INVESTIGACIONES AGRARIAS.

XX

PI (NATU-) NATURAL ENVIRONMENT RES COUNCIL.

XX

PI Roy P, Sanchez-Vizcaino Rodrique, JM;

XX

PF 21-MAR-2001; 2001WO-FR00843.

XX

PR 22-MAR-2000; 2000FR-0003637.

XX

PA (CNRS) CENT NAT RECH SCI.

XX

PA (CURIE-) INST CURIE.

XX

PI Fradelizi J, Friederich E, Golsteyn RM, Louvard D, Noireaux V;

XX

PI Sykes C;

XX

WPI: 2001-639148/73.

XX

N-PSDB; AAI71780.

XX

PT Identifying modulators of actin polymerization, potentially useful for treating tumor metastasis and parasitic infection, using proteins that contain Ena/VASP binding sites.

XX

PS Claim 16; Pages 77-78; 109pp; French.

XX

CC The present invention relates to a method for identifying modulators of actin polymerisation. The method involves using proteins that contain at least one binding motif for proteins of the Ena/VASP (vasodilator-stimulated phosphoprotein) family in the preparation of reagents for identification/screening of molecules that modulate formation of the actin cytoskeleton. The proteins used in the method (i.e. the proteins with binding motif(s) for Ena/VASP proteins) do not bind to the Arp2/3 protein complex. The modulators identified by the method are potentially useful for treating disorders of actin polymerisation, e.g. metastatic cancer or parasitic infection; and as cytotoxic agents. The present sequence one such protein with binding motif(s) for Ena/VASP proteins, which was used in the method of the present invention.

SQ

Sequence 351 AA;

Query Match

Best Local Similarity 74.0%; Score 37; DB 22; Length 351;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY

2 SSPGSPGT 9

DB

2 aspgtpgt 9

RESULT 40

AAR28314

ID

AAR28314 standard; Protein; 353 AA.

XX

AC AAR28314;

XX

DT 24-MAR-1993 (first entry)

XX

DE AHSV protein.

XX

KW African horse sickness virus; diagnosis; S7.

XX

OS African horse sickness virus serotype 7.

XX

PN EP515235-A.

XX

PD 25-NOV-1992.

XX

PF 26-MAY-1992; 92EP-0304734.

XX

PR 23-MAY-1991; 91GB-0011111.

XX

PR 14-JUN-1991; 91GB-0012875.

XX

PA (NAIN-) INST NACIONAL INVESTIGACIONES AGRARIAS.

XX

PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.

XX

PI Roy P, Sanchez-Vizcaino Rodrique, JM;

us-09-734-281-2.rag

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```

XX WPI; 1992-391791/48.
DR N-PSDB; AAQ30130.
XX
XX DNA coding for African horse sickness virus protein - used for
PT diagnosis, and producing polypeptide(s) for use in diagnosis and
PT vaccines
XX
XX Claim 9; Fig 1; 29pp; English.
XX
XX African horse sickness virus serotype 7 clones were identified by
CC colony hybridisation and Northern blot analysis. A full length clone
CC contained fragments at the 5' and 3' ends of the sequence which are
CC characteristic of orbivirus RNA segments. The DNA fragment may be
CC inserted into an expression system and used in assays for detecting
CC AHSV RNA and as primers in amplification processes.
XX
XX Sequence 353 AA;
SQ
Query Match 74.0%; Score 37; DB 13; Length 353;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSPGSPGT 9
Db 204 sapgapgt 211
1:11:111

```

Search completed: May 21, 2002, 11:18:08
Job time: 478 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2002, 11:19:10 ; Search time 26.77 seconds
(without alignments)
32.305 Million cell updates/sec

Title: US-09-734-281-2

Perfect score: 50

Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database :

PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	316	1 QRHUT2	microtubule-associ
2	50	100.0	341	2 B28820	microtubule-associ
3	50	100.0	364	2 A28820	microtubule-associ
4	50	100.0	374	2 S45264	microtubule-associ
5	50	100.0	402	1 QRBOT2	microtubule-associ
6	50	100.0	432	2 JS0306	microtubule-associ
7	50	100.0	441	1 QRHUT1	microtubule-associ
8	50	100.0	448	1 QRBOT1	microtubule-associ
9	50	100.0	686	2 A38235	microtubule-associ
10	50	100.0	733	2 A45301	microtubule-associ
11	39	78.0	150	2 T35638	microtubule-associ
12	39	78.0	272	2 T36770	hypothetical prote
13	39	78.0	2232	2 T34434	probable expressio
14	38	76.0	710	2 S72497	hypothetical prote
15	38	76.0	756	1 A55943	oligopeptide trans
16	38	76.0	1345	2 T29090	1-phosphatidylinos
17	38	76.0	3122	2 T17202	surface layer-asso
18	37	74.0	168	2 B88066	DNA-directed DNA p
19	37	74.0	302	2 T40490	protein R52.4 [imp
20	37	74.0	335	2 A40267	probable 26s prote
21	37	74.0	353	1 JQ1946	interleukin-5 rece
22	37	74.0	372	2 AE3191	core protein VP7 -
23	37	74.0	393	2 S16844	conserved hypothet
24	37	74.0	415	1 W2MLEP	titin - rabbit (fr
25	37	74.0	418	2 S29506	E2 protein - Europ
26	37	74.0	420	2 S21052	neurotensin recept
27	37	74.0	515	2 S75589	interleukin-5 rece
28	37	74.0	542	2 A44358	aldehyde dehydroge
29	37	74.0	847	1 A53800	zyxin - chicken mixed-lineage prot

30	37	74.0	963	2 T19140	hypothetical prote
31	37	74.0	1387	2 JC5502	G-protein signalin
32	37	74.0	1986	2 S28353	probable polyketid
33	37	74.0	3623	2 T09456	intrinsic factor-B
34	37	74.0	6805	2 S20901	titin - rabbit (fr
35	37	74.0	28926	1 I38344	titin, cardiac mus
36	36	72.0	119	2 T17003	dormancy-associate
37	36	72.0	305	2 S41860	gene Nkx-1.1 prote
38	36	72.0	323	2 A55983	microtubule-associ
39	36	72.0	329	2 T32783	hypothetical prote
40	36	72.0	351	2 A75621	ToxS-related prote
41	36	72.0	381	2 S51375	microtubule-associ
42	36	72.0	425	2 F97437	phosphoribosylamin
43	36	72.0	425	2 A12655	F21F23.21 protein
44	36	72.0	438	2 C86271	microtubule-associ
45	36	72.0	472	2 I67793	microtubule-associ
46	36	72.0	501	2 D64453	microtubule-associ
47	36	72.0	506	2 H83396	biotin carboxylase
48	36	72.0	511	2 S10527	probable aldehyde
49	36	72.0	511	2 S51461	endoglucanase B pr
50	36	72.0	603	2 S31216	BUD8 protein - yea
51	36	72.0	680	2 E70803	collagen alpha 1(X
52	36	72.0	729	2 S18942	hypothetical prote
53	36	72.0	914	2 T00382	hypothetical prote
54	36	72.0	1321	2 Q08382	hypothetical prote
55	36	72.0	1824	1 QRHUMT	microtubule-associ
			1825	2 S13507	microtubule-associ

ALIGNMENTS

RESULT 1

QRHUT2

microtubule-associated protein tau, fetal (clone pl8) - human
C:Species: Homo sapiens (man)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 02-Sep-1997

C:Accession: PN0001

R:Lee, G.; Neve, R.L.; Kosik, K.S.

Neuron 2, 1615-1624, 1989

A:Title: The microtubule binding domain of tau protein.

A:Reference number: JN0009; MUID:90180482

A:Accession: PN0001

A:Molecule type: mRNA

A:Residues: 1-316 <LEE>

A:Note: this sequence differs from a previously reported fetal tau protein sequence

C:Genetics:

A:Gene: GDB:MAPT; MTBT1

A:Cross-references: GDB:119434; OMIM:157140

A:Map position: 17q21-17q21

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bindi

F:158-188/Domain: MAP2/tau repeat homology <MT1>

F:189-219/Domain: MAP2/tau repeat homology <MT2>

F:220-251/Domain: MAP2/tau repeat homology <MT3>

Query Match

Best Local Similarity 100.0%; Score 50; DB 1; Length 316;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

Db 103 YSSPGSPGT 111

RESULT 2

B28820

microtubule-associated protein tau type 2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C:Accession: B28820

R:Lee, G.; Cowan, N.; Kirschner, M.

Science 239, 285-288, 1988

A:Title: The primary structure and heterogeneity of tau protein from mouse brain.

A:Reference number: A94298; MUID:88099510

A:Accession: B28820

A:Molecule type: mRNA

A:Residues: 1-341 <LEE>

A:Cross-references: GB:M18775; NID:g201114; PIDN:AAA40165.1; PID:g201115

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; tandem repeat

F:183-213/Domain: MAP2/tau repeat homology <MT1>

F:214-244/Domain: MAP2/tau repeat homology <MT2>

F:245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 100.0%; Score 50; DB 2; Length 341;

Best Local Similarity 100.0%; Pred. No. 0.64;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

|||||

Db 128 YSSPGSPGT 136

RESULT 3

A28820

microtubule-associated protein tau type 1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C:Accession: A28820

R:Lee, G.; Cowan, N.; Kirschner, M.

Science 239, 285-288, 1988

A:Title: The primary structure and heterogeneity of tau protein from mouse brain.

A:Reference number: A94298; MUID:88099510

A:Accession: A28820

A:Molecule type: mRNA

A:Residues: 1-364 <LEE>

A:Cross-references: GB:M18776; NID:g201116; PIDN:AAA40166.1; PID:g201117

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; tandem repeat

F:183-213/Domain: MAP2/tau repeat homology <MT1>

F:214-244/Domain: MAP2/tau repeat homology <MT2>

F:245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 100.0%; Score 50; DB 2; Length 364;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

|||||

Db 128 YSSPGSPGT 136

RESULT 4

S46264

microtubule-associated protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 13-Aug-1999

C:Accession: S46264

R:Sadot, E.; Marx, R.; Barq, J.; Behar, L.; Ginzburg, I.

J. Mol. Biol. 241, 325-331, 1994

A:Title: Complete sequence of 3'-untranslated region of tau from rat central nervous sys

A:Reference number: S46264; MUID:94334997

A:Accession: S46264

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <SAD>

A:Cross-references: EMBL:X79321; NID:g517393; PIDN:CAA55889.1; PID:g517394

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

F:185-215/Domain: MAP2/tau repeat homology <MT1>

F:216-246/Domain: MAP2/tau repeat homology <MT2>

F:247-277/Domain: MAP2/tau repeat homology <MT3>

F:278-309/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 0.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

|||||

Db 130 YSSPGSPGT 138

RESULT 5

QRB072

microtubule-associated protein tau, form 3 - bovine

N:Contains: microtubule-associated protein tau, form 4; microtubule-associated protei

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 31-Mar-1996

C:Accession: B31939; A48885; A28173

R:Himmier, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.

Mol. Cell. Biol. 9, 1381-1388, 1989

A:Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bind

A:Reference number: A31939; MUID:89261765

A:Accession: B31939

A:Molecule type: mRNA

A:Residues: 1-402 <HIM>

A:Cross-references: GB:M26157; GB:M26158

R:Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.

J. Biol. Chem. 268, 23512-23518, 1993

A:Title: Brain proline-directed protein kinase phosphorylates tau on sites that are

A:Reference number: A48885; MUID:94043150

A:Accession: A48885

A:Molecule type: protein

A:Residues: 'X',157-162,'X',164-165,'X',167-170:192-195,'X',197-201,'X',358-364,'X'

A:Experimental source: brain

A:Note: sequence modified after extraction from NCBI backbone

R:Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.

J. Biol. Chem. 263, 7703-7707, 1988

A:Title: Microtubule-binding domain of Tau proteins.

A:Reference number: A28173; MUID:88227970

A:Accession: A28173

A:Molecule type: protein

A:Residues: 159-172,'X',174-177 <AIZ>

A:Experimental source: brain.

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repea

F:1-402/Product: microtubule-associated protein tau, form 3 #status predicted <BT4>

F:1-234,297-402/Product: microtubule-associated protein tau, form 4 #status predicted <BT

F:101-402/Product: microtubule-associated protein tau, form 4 #status predicted <BT

F:159-177/Region: microtubule binding #status experimental

F:213-243/Domain: MAP2/tau repeat homology <MT1>

F:244-274/Domain: MAP2/tau repeat homology <MT2>

F:275-305/Domain: MAP2/tau repeat homology <MT3>

F:306-337/Domain: MAP2/tau repeat homology <MT4>

F:156,163,196,202,365/Binding site: phosphate (Ser) (covalent) (by proline-directed

F:166/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status

Query Match 100.0%; Score 50; DB 1; Length 402;

Best Local Similarity 100.0%; Pred. No. 0.75;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

|||||

Db 158 YSSPGSPGT 166

RESULT 6

JS0306

microtubule-associated protein tau - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993

C:Accession: JS0306; A33574

R:Kosik, K.S.; Orecchio, L.D.; Bakalis, S.; Neve, R.L.

Neuron 2, 1389-1397, 1989

A:Title: Developmentally regulated expression of specific tau sequences.
A:Reference number: JS0306; MUID:90180457

A:Accession: JS0306
A:Molecule type: mRNA
A:Residues: 1-432 <KOS>
A>Note: the sequence shown is from adult rat brain
A:Note: the partial sequence from fetal rat brain is lacking residues 266-296; the fetal
A:Note: both fetal and adult forms were found in the paired helical filaments character-
R:Kanai, Y.; Takemura, R.; Oshima, T.; Mori, H.; Ihara, Y.; Yanagisawa, M.; Masaki, T.;
J. Cell Biol. 109, 1173-1184, 1989
A:Title: Expression of multiple tau isoforms and microtubule bundle formation in fibrobl
A:Reference number: A33574; MUID:89359509
A:Accession: A33574
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-432 <KAN>
A:Note: a variant lacking residues 63-91 was also found
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; Alzheimer's disease; calmodulin binding; microtubule b
F:243-273/Domain: MAP2/tau repeat homology <WT1>
F:274-304/Domain: MAP2/tau repeat homology <WT2>
F:305-335/Domain: MAP2/tau repeat homology <WT3>
F:336-367/Domain: MAP2/tau repeat homology <WT4>
F:282-313/Disulfide bonds: #status experimental
F:347/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 50; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9

Db 188 YSSPGSPGT 196

RESULT 7

QRHUT1

A:Alternate names: microtubule-binding protein tau, long splice form - human
N:Contexts: microtubule-associated protein tau; neurofibrillary tangle protein pair
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence revision 03-May-1996 #text change 22-Jun-1999
A:Accession: JS0370; A30217; JN0009; S03796; S26665; S26666; S17302; A43444; A27
R:Goedert, M.; Spillantini, M.G.; Jakes, R.; Rutherford, D.; Crowther, R.A.
Neuron 3, 519-526, 1989
A:Title: Multiple isoforms of human microtubule-associated protein tau: sequences and lo
A:Reference number: JS0370; MUID:90380393
A:Accession: JS0370
A:Molecule type: mRNA
A:Residues: 1-441 <GOE>
A:Note: six isoforms are found; the clone ht40 sequence is shown. Residues 45-73, 74-1
the clone ht424 sequence lacks inserts 1 and 2; the clone ht437 sequence lacks insert
R:Goedert, M.; Wischik, C.M.; Crowther, R.A.; Walker, J.E.; Klug, A.
Proc. Natl. Acad. Sci. U.S.A. 85, 4051-4055, 1988
A:Title: Cloning and sequencing of the cDNA encoding a core protein of the paired helica
A:Reference number: A30217; MUID:88234557
A:Accession: A30217
A:Molecule type: mRNA
A:Residues: 1-44,103-274,306-441 <GO2>
A:Cross-references: GB:J03778; NID:9338684; PIDN:AAA60615.1; PID:9338685
R:Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A:Title: The microtubule binding domain of tau protein.
A:Reference number: JN0009; MUID:90180482
A:Accession: JN0009
A:Molecule type: mRNA
A:Residues: 1-44,103-274,306-441 <LEE>
R:Goedert, M.; Spillantini, M.G.; Potier, M.C.; Ulrich, J.; Crowther, R.A.
EMBO J. 8, 393-399, 1989
A:Title: Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated
A:Reference number: S03796; MUID:89251564
A:Accession: S03796

A:Molecule type: mRNA
A:Residues: 1-44,103-441 <GO3>
A:Cross-references: EMBL:X14474; NID:g36724; PIDN:CAA32636.1; PID:g36725
R:Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A:Title: Structure and novel exons of the human tau gene.
A:Reference number: S26662; MUID:93041757
A:Accession: S26662
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 144-185 <AND>
A:Cross-references: EMBL:X61372; NID:g36718; PID:g36719
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A:Accession: S26666
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 187-274 <AN2>
A:Cross-references: EMBL:X61374; NID:g36722; PID:g36723
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A:Accession: S26662
A:Molecule type: DNA
A:Residues: 371-441 <ANW>
A:Cross-references: EMBL:X61373
R:Jakes, R.; Novak, M.; Davison, M.; Wischik, C.M.
EMBO J. 10, 2725-2729, 1991
A:Title: Identification of 3- and 4-repeat tau isoforms within the PHF in Alzheimer'
A:Reference number: S17302; MUID:92007714
A:Accession: S17302
A:Status: preliminary
A:Molecule type: protein
A:Residues: 268-274,306-395 <JAK>
R:Hasegawa, M.; Morishima-Kawashima, M.; Takio, K.; Suzuki, K.; Ihara, Y.
J. Biol. Chem. 267, 17047-17054, 1992
A:Title: Protein sequence and mass spectrometric analyses of tau in the Alzheimer's
A:Reference number: A43444; MUID:92381012
A:Accession: A43444
A:Molecule type: protein
A:Residues: 2-73,103-130;151-180;191-254;260-269;275-290;299-317;322-340;344-347;354;
A:Experimental source: Alzheimer's disease brain
A:Note: sequence extracted from NCBI backbone (NCBIP:112039)
C:Comment: This heterogeneous protein, which is found predominantly in cells of the t
o the core protein of the paired helical filament of Alzheimer's disease.
C:Genetics:
A:Gene: GDB:MAPT
A:Cross-references: GDB:119434; OMIM:157140
A:Map position: 17q21-17q21
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bindi
F:1-274,306-441/Product: microtubule-associated protein tau (clone ht439) #status predi
F:1-73,103-274,306-441/Product: microtubule-associated protein tau (clone ht439) #status pre
F:1-73,103-274,306-441/Product: microtubule-associated protein tau (clone ht439) #status pre
F:1-44,103-274,306-441/Product: microtubule-associated protein tau (clone ht437) #st
F:1-44,103-441/Product: microtubule-associated protein tau, fetal #status pre
F:252-282/Domain: MAP2/tau repeat homology <MT1>
F:283-313/Domain: MAP2/tau repeat homology <MT2>
F:314-344/Domain: MAP2/tau repeat homology <MT3>
F:345-376/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9

Db 197 YSSPGSPGT 205

RESULT 8

ORBOT1

microtubule-associated protein tau, form 1 - bovine
N:Contexts: microtubule-associated protein tau, form 2

us-09-734-281-2.rpr

Wed May 22 11:04:42 2002

C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
 C:Accession: A31939; A33914; S04005; A48885; A28173; B33734
 R:Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
 Mol. Cell. Biol. 9, 1381-1388, 1989
 A:Title: Tau consists of a set of proteins with repeated C-terminal microtubule-binding
 A:Reference number: A31939; MUID:89261765
 A:Accession: A31939
 A:Molecule type: mRNA
 A:Residues: 1-448 <HTM>
 A:Cross-references: GB:M26157; NID:g514913; PIDN:AAA30770.1; PID:g514914
 R:Iqbal, K.; Grundke-Iqbal, I.; Smith, A.J.; George, L.; Tung, Y.C.; Zaidi, T.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5646-5650, 1989
 A:Title: Identification and localization of a tau-peptide to paired helical filaments of
 A:Reference number: A33914; MUID:89315854
 A:Accession: A33914
 A:Molecule type: protein
 A:Residues: 28, 'A', 30-38, 'IG', 41, 'AP', 44, 'LK' <IQB>
 A:Experimental source: brain
 A:Note: 40-Pro was also found
 R:Iqbal, K.; Smith, A.J.; Zaidi, T.; Grundke-Iqbal, I.
 FEBS Lett. 248, 87-91, 1989
 A:Title: Microtubule-associated protein tau. Identification of a novel peptide from bovi
 A:Reference number: S04005; MUID:89252057
 A:Accession: S04005
 A:Molecule type: protein
 A:Residues: 28, 'A', 30-38, 'IG', 41, 'AP', 44, 'LK' <IQ2>
 A:Experimental source: brain
 A:Note: 40-pro was also found
 R:Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
 J. Biol. Chem. 268, 23512-23518, 1993
 A:Title: Brain proline-directed protein kinase phosphorylates tau on sites that are abn
 A:Reference number: A48885; MUID:94043150
 A:Accession: A48885
 A:Molecule type: protein
 A:Residues: 'X', 203-208, 'X', 210-211, 'X', 213-216; 238-241, 'X', 243-247, 'X', 404-410, 'X', 412-
 A:Experimental source: brain
 A:Note: sequence modified after extraction from NCBI backbone
 R:Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
 J. Biol. Chem. 263, 7703-7707, 1988
 A:Title: Microtubule-binding domain of Tau proteins.
 A:Reference number: A28173; MUID:88227970
 A:Accession: A28173
 A:Molecule type: protein
 A:Residues: 205-218, 'X', 220-223 <AIZ>
 A:Experimental source: brain
 C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C:Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
 F:1-448/Product: microtubule-associated protein tau, form 1 #status predicted <BT43>
 F:1-174, 193-448/Product: microtubule-associated protein tau, form 2 #status predicted <B
 F:205-223/Region: microtubule binding #status experimental
 F:239-389/Domain: MAP2/tau repeat homology <MT1>
 F:321-351/Domain: MAP2/tau repeat homology <MT2>
 F:352-383/Domain: MAP2/tau repeat homology <MT3>
 F:202, 209, 242, 248, 411/Binding site: phosphate (Ser) (covalent) (by proline-directed kin
 F:212/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status expe

Query Match 100.0%; Score 50; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 0.84;
 Matches 9; Conservative 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

DB 204 YSSPGSPGT 212

RESULT 9

A38235 microtubule-associated protein, 110K tau - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999

C:Accession: A38235
 R:Goedert, M.; Spillantini, M.G.; Crowther, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 1983-1987, 1992
 A:Title: Cloning of a big tau microtubule-associated protein characteristic of the p
 A:Reference number: A38235; MUID:92179305
 A:Accession: A38235
 A:Molecule type: mRNA
 A:Residues: 1-686 <GOE>
 A:Cross-references: GB:M84156; NID:g207157; PIDN:AAA42204.1; PID:g207158
 A:Note: sequence extracted from NCBI backbone (NCBIN:87358, NCBI:87359)
 C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C:Keywords: alternative splicing; microtubule binding; tandem repeat
 F:497-527/Domain: MAP2/tau repeat homology <MT1>
 F:528-558/Domain: MAP2/tau repeat homology <MT2>
 F:559-589/Domain: MAP2/tau repeat homology <MT3>
 F:590-621/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 2; Length 686;
 Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 YSSPGSPGT 9

DB 442 YSSPGSPGT 450

RESULT 10

A45301

microtubule-associated protein tau - mouse

N:Alternate names: microtubule binding protein tau

C:Species: Mus musculus (house mouse)

C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 13-Aug-1999

C:Accession: A45301; S31658

R:Couchie, D.; Mavilia, C.; Georgieff, I.S.; Liem, R.K.; Shelanski, M.L.; Nunez, J.

Proc. Natl. Acad. Sci. U.S.A. 89, 4378-4381, 1992

A:Title: Primary structure of high molecular weight tau present in the peripheral n

A:Reference number: A45301; MUID:92262443

A:Accession: A45301

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-733 <COU>

A:Note: this sequence is inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:102045, NCBI:102046)

R:Kenner, L.; Forstner, M.; Hutter, H.; Hoefler, G.; Kurzbauer, R.; Zatloukal, K.;

submitted to the EMBL Data Library, May 1992

A:Description: First observation of mRNA for a tau-protein from murine liver and ki

A:Reference number: S31658

A:Accession: S31658

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 'T', 529-651 <KEN>

A:Cross-references: EMBL:Z12133; NID:g54263; PIDN:CAA78121.1; PID:g388534

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: microtubule binding; tandem repeat

F:544-574/Domain: MAP2/tau repeat homology <MT1>

F:575-605/Domain: MAP2/tau repeat homology <MT2>

F:606-636/Domain: MAP2/tau repeat homology <MT3>

F:637-668/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 2; Length 733;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9

DB 489 YSSPGSPGT 497

RESULT 11

T35638

hypothetical protein SC6G9.42c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor
 C:Date: 03-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C:Accession: T35638
 R:Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A:Reference number: Z21584
 A:Accession: T35638
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-150 <SEE>
 A:Cross-references: EMBL:AL079356; PIDN:CAB45633.1; GSPDB:GN00070; SCOEDB:SC6G9.42C
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC6G9.42C

Query Match 78.0%; Score 39; DB 2; Length 150;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 SSPGSPGT 9
 |||||
 Db 3 SSPGKPGT 10

RESULT 12
 T36770
 probable expression regulator - Streptomyces coelicolor (fragment)
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T36770
 R:Saunders, D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, July 1999
 A:Reference number: Z21613
 A:Accession: T36770
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-272 <SAU>
 A:Cross-references: EMBL:AL096849; PIDN:CAB50963.1; GSPDB:GN00070; SCOEDB:SC11.37C
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC11.37C

Query Match 78.0%; Score 39; DB 2; Length 272;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YSPGSPGT 9
 |||||
 Db 170 YAPPGAPGT 178

RESULT 13
 T34434
 hypothetical protein K06A9.1a - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T34434
 R:Gjssel, C.; Gattung, S.
 submitted to the EMBL Data Library, December 1996
 A:Description: The sequence of C. elegans cosmid K06A9.
 A:Reference number: Z21525
 A:Accession: T34434
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2232 <GEI>
 A:Cross-references: EMBL:U08046; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9.1a
 A:Experimental source: strain Bristol N2; clone K06A9
 C:Genetics:
 A:Gene: CESP:K06A9.1a
 A:Map position: X
 A:Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075/1

Query Match 78.0%; Score 39; DB 2; Length 2232;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SPGSPGT 9
 |||||
 Db 886 SPGSPGT 892

RESULT 14
 S72497
 oligopeptide transport protein Pept1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
 C:Accession: S72497; S68161
 R:Miyamoto, K.I.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: S72497
 A:Accession: S72497
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-710 <MIY>
 A:Cross-references: EMBL:D50664; NID:gl384098; PIDN:BAA09318.1; PID:gl212746
 R:Miyamoto, K.; Shiraga, T.; Morita, K.; Yamamoto, H.; Haga, H.; Taketani, Y.; Tamai
 Biochim. Biophys. Acta 1305, 34-38, 1996
 A:Title: Sequence, tissue distribution and developmental changes in rat intestinal o
 A:Reference number: S68161; MUID:96180982
 A:Accession: S68161
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-258, 'E', 260-278, 'MV', 281-710 <MI2>
 A:Cross-references: GB:D50664
 C:Genetics:
 A:Gene: Pept1
 C:Superfamily: peptide transport protein PEPT1
 C:Keywords: oligopeptide transport; transmembrane protein; transport protein

Query Match 76.0%; Score 38; DB 2; Length 710;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSPGSPG 8
 |||||
 Db 441 SSPGSPG 447

RESULT 15
 A55943
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 (valf
 N:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide
 C:Species: Homo sapiens (man)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: A55943
 R:Cheng, H.F.; Jiang, M.J.; Chen, C.L.; Liu, S.M.; Wong, L.P.; Lomasney, J.W.; King,
 J. Biol. Chem. 270, 5495-5505, 1995
 A:Title: Cloning and identification of amino acid residues of human phospholipase Cde
 A:Reference number: A55943; MUID:95197554
 A:Accession: A55943
 A:Molecule type: mRNA
 A:Residues: 1-756 <CHE>
 A:Cross-references: GB:U09117; NID:g483919; PIDN:AAA73567.1; PID:g483920
 A:Experimental source: aortic smooth muscle
 C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-tripho
 C:Genetics:
 A:Gene: GDB:PLCD1
 A:Cross-references: GDB:6075994
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-p
 phosphodiesterase domain Y homology; calmodulin repeat homology; pleckstrin repeat ho
 C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; si
 F;19-128/Domain; pleckstrin repeat homology <PLK>

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F:140-172/Domain: calmodulin repeat homology <EF1>
F:176-208/Domain: calmodulin repeat homology <EF2>
F:298-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom
F:491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y hom
F:614-724/Domain: protein kinase C C2 region homology <KC2>

Query Match 76.0%; Score 38; DB 1; Length 756;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
Db 507 FSSPGTGP 514

RESULT 16
T29090
surface layer-associated STABLE proteinase - Staphylothermus marinus
N:Alternate names: hyperthermostable proteinase
C:Species: Staphylothermus marinus
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T29090
R:Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.
Curr. Biol. 6, 739-749, 1996
A:Title: A hyperthermostable protease of the subtilisin family bound to the surface layer
A:Reference number: Z20559; MUID:96385442
A:Accession: T29090
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1345 <MAY>
A:Cross-references: EMBL:U57968; NID:gl374755; PID:gl374756; PIDN:AAB02323.1
A:Experimental source: strain F1
C:Function:
A:Description: probably serves an exodigestive function related to the organism's energy
A:Note: stoichiometric S-layer component

Query Match 76.0%; Score 38; DB 2; Length 1345;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 596 YSSNGAPGT 604

RESULT 17
T17202
DNA-directed DNA polymerase (BC 2.7.7.7) zeta chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17202
R:Van Sloun, P.P.H.; Romeijn, R.J.; Eeken, J.C.J.
Mutat. Res. 433, 109-116, 1999
A:Title: Molecular cloning, expression and chromosomal localisation of the mouse Rev31
A:Reference number: Z18720; MUID:99202265
A:Accession: T17202
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3122 <VAN>
A:Cross-references: EMBL:AF083464; NID:g4079830; PID:g4079831; PIDN:AAC98785.1
A:Experimental source: strain 129/Ola; testis
C:Genetics:
A:Map position: 10
C:Keywords: nucleotidyltransferase

Query Match 76.0%; Score 38; DB 2; Length 3122;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8

Db 2108 YSSPDSFG 2115

RESULT 18

B88066
protein R52.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bi
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: B88066
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-168 <STO>
A:Cross-references: GB:chr_II; PIDN:AB71062.1; PID:g2429536; GSPDB:GN00020; CESP:R52
C:Genetics:
A:Gene: R52.4
A:Map position: 2

Query Match 74.0%; Score 37; DB 2; Length 168;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
Db 40 TTPGSPGT 47

RESULT 19

T40490
Proteasome 26S proteasome regulatory subunit - fission yeast (Schizosaccharomyces pom
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: T40490
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft,
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21910
A:Accession: T40490
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-302 <WOO>
A:Cross-references: EMBL:AL021730; PIDN:CAAL6829.1; GSPDB:GN00067; SPDB:SPBC4C3.07
A:Experimental source: strain 972h-; cosmid c4C3
C:Genetics:
A:Gene: SPDB:SPBC4C3.07
A:Map position: 2
C:Superfamily: mov-34 protein

Query Match 74.0%; Score 37; DB 2; Length 302;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 123 YASPAEPGT 131

RESULT 20

A40267
interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C:Accession: A40267
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers,
Cell 66, 1175-1184, 1991

A>Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
 A:Reference number: A40267; MUID:92005669
 A:Accession: A40267
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-335 <TAV>
 A:Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
 C:Keywords: cytokine receptor; transmembrane protein

Query Match
 Best Local Similarity 74.0%; Score 37; DB 2; Length 335;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSPGSPGT 9
 Db 119 HAPGSPGT 127

RESULT 21

core protein VP7 - African horse sickness virus (serotype 4, strain Spane)
 C:Species: African horse sickness virus
 C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jun-2000
 C:Accession: JQ1946
 R:Roy, P.; Hirasawa, T.; Fernandez, M.; Blinov, V.M.; Sanchez-Vixcain Rodrique, J.M.
 J. Gen. Virol. 72 1237-1241, 1991
 A>Title: The complete sequence of the group-specific antigen, VP7, of African horsesickn
 A:Reference number: JQ1946; MUID:91259049
 A:Accession: JQ1946
 A:Molecule type: genomic RNA
 A:Residues: 1-353 <ROY>
 A:Cross-references: GB:D12533; NID:g221010; PIDN:BAA02096.1; PID:g221011
 C:Genetics:
 A:Map position: segment 7
 C:Superfamily: bluetongue virus core protein VP7
 C:Keywords: core protein

Query Match
 Best Local Similarity 74.0%; Score 37; DB 1; Length 353;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSPGSPGT 9
 Db 204 SAPGAPGT 211

RESULT 22

conserved hypothetical protein Atu5258 [Imported] - Agrobacterium tumefaciens (strain C5
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: AE3191
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AE3191
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-372 <KUR>
 A:Cross-references: GB:AE008687; PIDN:AAL45947.1; PID:g17743697; GSPDB:GN00188
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu5258
 A:Genome: plasmid

Query Match
 Best Local Similarity 74.0%; Score 37; DB 2; Length 372;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YSPGSPGT 9
 Db 146 YHQPSPGS 154

RESULT 23

titin - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
 C:Accession: S16844
 R:Fritz, J.D.; Greaser, M.L.; Wolff, J.A.
 Nucleic Acids Res. 19, 3747, 1991
 A>Title: A novel 3' extension technique using random primers in RNA-PCR.
 A:Reference number: S16844; MUID:91305130
 A:Accession: S16844
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-393 <PRI>
 A:Cross-references: EMBL:X59596; NID:g1722; PIDN:CAA42165.1; PID:g1723
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1991
 C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology;

Query Match
 Best Local Similarity 74.0%; Score 37; DB 2; Length 393;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 YSPGSPGT 9
 Db 55 YKEPSPGT 63

RESULT 24

W2WLEP
 E2 protein - European elk papillomavirus
 C:Species: European elk papillomavirus
 C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-May-2000
 C:Accession: D29499; D94457; D94506
 R:Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U.
 Gene 50, 195-205, 1986
 A>Title: Organization and expression of the transforming region from the European elk
 A:Reference number: A91567; MUID:87219878
 A:Accession: D29499
 A:Molecule type: DNA
 A:Residues: 1-415 <AHO>
 A:Cross-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
 R:Eriksson, A.
 unpublished results 1987, cited by GenBank
 A:Reference number: A94457
 A:Accession: D94457
 A:Molecule type: DNA
 A:Residues: 1-415 <ERI>
 A:Cross-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
 R:Pettersson, U.
 submitted to GenBank, August 1987
 A:Reference number: A94506
 A:Accession: D94506
 A:Molecule type: DNA
 A:Residues: 1-415 <PET>
 A:Cross-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
 C:Superfamily: papillomavirus E2 protein
 C:Keywords: early protein

Query Match
 Best Local Similarity 74.0%; Score 37; DB 1; Length 415;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YSPGSPGPT 9
Db 268 YSAPSPGS 276

RESULT 25
neurotensin receptor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C:Accession: S29506
R:Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad, M.; Gully, D.; le H
FEBS Lett. 317, 139-142, 1993
A:Title: Cloning and expression of a complementary DNA encoding a high affinity human ne
A:Reference number: S29506; MUID:93154505
A:Accession: S29506
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <VIT>
A:Cross-references: EMBL:X70070; NID:g35020; PIDN:CAA49675.1; PID:g35021
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 74.0%; Score 37; DB 2; Length 418;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGPT 9
Db 6 SAPGTPGT 13

RESULT 26
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored is
S21052
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C:Accession: S21052; S21050; S21053; A46175; S78106; S78107
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.
A:Reference number: S21050; MUID:92121815
A:Accession: S21052
A:Molecule type: DNA
A:Residues: 1-420 <MUR>
A:Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A:Experimental source: clone lambda h5R.12
A:Accession: S21050
A:Molecule type: DNA
A:Residues: 1-395, 'I' <MU2>
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A:Experimental source: clone lambda h5R.27
A:Accession: S21053
A:Molecule type: mRNA
A:Residues: 1-332, 'K' <MU3>
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A:Experimental source: clone lambda h5R.25
R:Tavernier, J.; Tulpens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the human
A:Reference number: A46175; MUID:92357767
A:Accession: A46175
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 333-420 <TAV>
A:Experimental source: HL-60 cells and eosinophils
A:Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIPI:116244)
R:Murata, Y.
submitted to the EMBL Data Library, July 1991
A:Reference number: S78106
A:Accession: S78106
A:Molecule type: DNA

A:Residues: 1-128, 'I', 130-395, 'I' <MUW>
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
R:Murata, Y.
submitted to the EMBL Data Library, September 1991
A:Reference number: S78107
A:Accession: S78107
A:Molecule type: mRNA
A:Residues: 1-128, 'I', 130-332, 'K' <MU4>
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane pro
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>
F:345-365/Domain: transmembrane #status predicted <TMM>
F:35, 131, 137, 142, 216, 244/Binding site: carbohydrate (Asn) (covalent) #status predict
F:35, 131, 137, 142, 216, 244/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 74.0%; Score 37; DB 2; Length 420;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGPT 9
Db 119 HAPGSPGPT 127

RESULT 27
aldehyde dehydrogenase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: H75589
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A:Reference number: A75250; MUID:20036896
A:Accession: H75589
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-515 <WHI>
A:Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12436.1; PID:g6460670;
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0348
A:Map position: 2
C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Query Match 74.0%; Score 37; DB 2; Length 515;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSPGSPGPT 9
Db 13 YANPGTGS 21

RESULT 28
zyxin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Jun-1993 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000
C:Accession: A44358; S30506
R:Sadler, I.; Crawford, A.W.; Michelsen, J.W.; Beckerle, M.C.
J. Cell Biol. 119, 1573-1587, 1992
A:Title: Zyxin and cCRP: two interactive LIM domain proteins associated with the cy
A:Reference number: A44358; MUID:93107157
A:Accession: A44358
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-542 <SAD>
A:Cross-references: EMBL:X69190; NID:g63897; PIDN:CAA48936.1; PID:g63898
```

A:Note: sequence extracted from NCBI backbone (NCBIN:121172, NCBIP:121174)
 C:Superfamily: LIM metal-binding repeat homology
 F:352-404/Domain: LIM metal-binding repeat homology
 F:412-463/Domain: LIM metal-binding repeat homology <LIM1>
 F:472-533/Domain: LIM metal-binding repeat homology <LIM2>

Query Match 74.0%; Score 37; DB 2; Length 542;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||:|
 Db 2 ASPGTPGT 9

RESULT 29
 A53800

mixed-lineage protein kinase (EC 2.7.1.-) 3 - human
 N:Alternate names: protein kinase PTK1; protein kinase SPRK
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A53800; I58395
 R:Gallo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
 J. Biol. Chem. 269, 15092-15100, 1994
 A:Title: Identification and characterization of SPRK, a novel src-homology 3 domain-cont
 A:Reference number: A53800; MUID:94253068
 A:Accession: A53800
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-847 <GAL>
 A:Cross-references: GB:007747; NID:9464027; PIDN:AAA19647.1; PID:9464028
 R:ing, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassam, N.J.
 Oncogene 9, 1745-1750, 1994
 A:Reference number: I58395; MUID:94239734
 A:Title: Mtk-3: identification of a widely-expressed protein kinase bearing an SH3 domain

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-847 <RES>
 A:Cross-references: GB:L32976; NID:9488295; PIDN:AAA59859.1; PID:9488296
 C:Genetics:
 A:Gene: GDB:MLK3; PTK1; SPRK
 A:Cross-references: GDB:134755; OMIM:600050
 A:Map position: llql3.1-llql13.3
 C:Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
 F:48-100/Domain: SH3 homology <SH32>
 F:113-383/Domain: protein kinase homology <KIN>
 F:123-131/Region: protein kinase ATP-binding motif
 F:403-424/Region: leucine zipper motif
 F:438-459/Region: leucine zipper motif
 F:468-482/Region: basic

Query Match 74.0%; Score 37; DB 1; Length 847;
 Best Local Similarity 75.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||:|
 Db 748 SAPGTPGT 755

RESULT 30
 T19140

hypothetical protein C09G5.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19140
 R:Palmer, S.
 submitted to the EMBL Data Library, November 1994

A:Reference number: Z19080
 A:Accession: T19140

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-963 <WIL>
 A:Cross-references: EMBL:Z46791; PIDN:CAA86755.1; GSPDB:GN00020; CESP:C09G5.6
 C:Genetics:
 A:Gene: CESP:C09G5.6
 A:Map position: 2
 A:Introns: 48/3; 862/3; 898/1

Query Match 74.0%; Score 37; DB 2; Length 963;
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||:|
 Db 559 SAPGAPGT 566

RESULT 31
 JC5502

G-protein signaling regulator 12 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
 C:Accession: JC5502
 R:Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, D.P.
 Biochem. Biophys. Res. Commun. 233, 770-777, 1997
 A:Title: Molecular cloning and expression analysis of rat Rgs12 and Rgs14.
 A:Reference number: JC5502; MUID:97312490
 A:Accession: JC5502
 A:Molecule type: mRNA
 A:Residues: 1-1387 <SNO>
 A:Cross-references: GB:U92280; NID:92088557; PIDN:AAC53176.1; PID:92088558
 C:Comment: This protein functions as GTPase activating protein. It interacts with rat

Query Match 74.0%; Score 37; DB 2; Length 1387;
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
 :|||:|
 Db 1296 HSTPGPPT 1304

RESULT 32
 S28353

probable polyketide synthase - Emericella nidulans
 C:Species: Emericella nidulans, Aspergillus nidulans
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-May-2000
 C:Accession: S28353
 R:Mayorga, M.E.; Timberlake, W.F.
 Mol. Gen. Genet. 235, 205-212, 1992
 A:Title: The developmentally regulated Aspergillus nidulans wa gene encodes a polypep
 A:Reference number: S28353; MUID:93101122
 A:Accession: S28353
 A:Molecule type: DNA
 A:Residues: 1-1986 <NAY>
 A:Cross-references: EMBL:X65866; NID:95508; PID:95509
 C:Genetics:
 A:Gene: WA

A:Introns: 96/2; 193/3; 1336/3; 1588/3
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier pro
 C:Keywords: carrier protein

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F;397-805/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F;911-1199/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1648-1718/Domain: acyl carrier protein homology <ACP>
F;1766-1840/Domain: acyl carrier protein homology <ACP1>

Query Match 74.0%; Score 37; DB 2; Length 1986;
Best Local Similarity 87.5%; Pred. No. 5e+02; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSPSPGPGT 9
| | | | |
DB 1749 SSPASPGT 1756

RESULT 33
T09456
intrinsic factor-B12 receptor Cubilin precursor - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09456
R:Koziyaki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998
A:Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterization.
A:Reference number: Z16677; MUID:98241400
A:Accession: T09456
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-3623 <KOZ>
A:CROSS-references: EMBL:AF034611; NID:9329528; PIDN:AC82612.1; PID:9329529
C:Genetics:
A:Map position: 10p12
C:Superfamily: unassigned EGF-related proteins; EGF homology
C:Keywords: receptor; vitamin B12 uptake
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F;436-467/Domain: EGF homology <EGF>

Query Match 74.0%; Score 37; DB 2; Length 3623;
Best Local Similarity 66.7%; Pred. No. 9.2e+02; 1; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGPT 9
| | | | |
DB 3522 FTSPGPGT 3530

RESULT 34
S20901
titin - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C:Accession: S20901; I46520
R:Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A:Title: Towards a molecular understanding of titin.
A:Reference number: S20897; MUID:92258380
A:Accession: S20901
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-6805 <LAB>
A:CROSS-references: EMBL:X64696
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R:Labeit, S.; Barlow, D.P.; Gautel, M.; Gibson, M.; Holt, J.; Hsieh, C.L.; Francke, U.;
Nature 345, 273-276, 1990
A:Title: A regular pattern of two types of 100-residue motif in the sequence of titin.
A:Reference number: I46520; MUID:90238553
A:Accession: I46520
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 4235-5250 <LA2>

A:CROSS-references: EMBL:X17329; NID:g1756; PIDN:CAA35207.1; PID:g930251
C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology;
C:Keywords: muscle

Query Match 74.0%; Score 37; DB 2; Length 6805;
Best Local Similarity 66.7%; Pred. No. 1.7e+03; 3; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YSSPGSPGPT 9
| | | | |
DB 5282 YKEPGPGT 5290

RESULT 35
I38344
titin, cardiac muscle [validated] - human
N:Alternate names: connectin
N:Contains: serine/threonine-specific protein kinase (EC 2.7.1.1.-)
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
C:Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393
R:Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330
A:Accession: I38344
A:Status: nucleic acid sequence not shown; translation not shown; translated from G
A:Molecule type: mRNA
A:Residues: 1-26926 <LAB1>
A:CROSS-references: EMBL:X90568; NID:g1017424; PID:g1017425
R:Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
A:Title: Dissecting titin into its structural motifs: identification of an alpha-h
A:Reference number: I38345; MUID:95119041
A:Accession: I38345
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1977-2014 <MUS>
A:CROSS-references: EMBL:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580
A:Note: conformation and properties are reported for a synthetic peptide correspond
R:Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A:Title: Towards a molecular understanding of titin.
A:Reference number: S20897; MUID:92258380
A:Accession: S20898
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 13597-14200, 'I', 14202-14696 <LAB2>
A:CROSS-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
A:Accession: S20897
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 16330-16382, 'S', 16384-16756, 'F', 16758-16860 <LAB3>
A:CROSS-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191
A:Accession: S20899
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 'P', 22728-22431, 'R', 22433-22448, 'C', 22450-22453, 'O', 22455-22480, 'TR', '2'
A:CROSS-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
R:Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.
J. Mol. Biol. 256, 556-563, 1996
A:Title: Genomic organization of M line titin and its tissue-specific expression i
A:Reference number: S63665; MUID:96177761
A:Accession: S63665
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 26729-26825 <KOL>
A:CROSS-references: EMBL:X92412; NID:g1236761
R:Gautel, M.; Leonard, K.; Labeit, S.
EMBO J. 12, 3827-3834, 1993
A:Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differ
A:Reference number: S37393; MUID:94008990

A:Accession: S37393
 A:Molecule type: mRNA
 A:Residues: 26831-26926 <GAU>
 R:Impronta, S.; Politou, A.S.; Pastore, A.
 submitted to the Brookhaven Protein Data Bank, February 1996
 A:Reference number: A66736; PDB:1IIT
 A:Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
 R:Pfuhl, M.; Pastore, A.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A66201; PDB:1NCT
 A:Contents: annotation; conformation by (1)H-NMR, residues 5' , 26059-26155
 C:Genetics:
 A:Gene: GDB:TTN
 A:Cross-references: GDB:127867; OMIM:188840
 A:Map position: 2q31-2q32
 C:Function:
 A:Description: structural protein forming filaments in striated muscle
 C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; pro
 C:Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glyco
 structural protein
 F:24752-25008/Domain: protein kinase homology <KIN>
 F:84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068,
 98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,1
 6780,16976,17579,17602,17667,17681,17845,17899,18121,18188,18209,18336,18670,18680,18
 ,21900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,248
 F:26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 74.0%; Score 37; DB 1; Length 26926;
 Best Local Similarity 66.7%; Pred. No. 6.7e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 YSSPGSPGT 9
 | |||||
 Db 16923 YKEPGPGT 16931

RESULT 36
 T17003
 dormancy-associated protein [similarity] - apple tree
 C:Species: Malus domestica (apple tree)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
 C:Accession: T17003
 R:Lee, S.A.; Gardner, R.C.; Lay-Yee, M.
 Plant Physiol. 103, 1017, 1993
 A:Title: An apple gene highly expressed in fruit.
 A:Reference number: 218646; MUID:94294548
 A:Accession: T17003
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-119 <LEE>
 A:Cross-references: EMBL:L15194; NID:q439878; PIDN:AAAT1994.1; PID:q439879
 A:Experimental source: cultivar Golden delicious; fruit cortical

Query Match 72.0%; Score 36; DB 2; Length 119;
 Best Local Similarity 85.7%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SPGSPGT 9
 |||||
 Db 51 SPGTPGT 57

RESULT 37
 S41860
 gene Nkx-1.1 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S41860
 R:Schubert, F.R.; Gruss, P.
 submitted to the EMBL Data Library, October 1993

A:Description: Expression of the novel Murine homeobox gene Nkx-1.1 in the developing
 A:Reference number: S41860
 A:Accession: S41860
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-305 <SCH>
 A:Cross-references: EMBL:X75384; NID:q453171; PIDN:CAA53153.1; PID:q453172
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:157-213/Domain: homeobox homology <HOX>

Query Match 72.0%; Score 36; DB 2; Length 305;
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSFGSPGT 9
 :|||||
 Db 134 ASFGSPGS 141

RESULT 38
 A55983
 microtubule-associated protein MAP2 - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 23-Aug-1997
 C:Accession: A55983; A41011; A33734
 R:Coffey, R.L.; Joly, J.C.; Cain, B.D.; Purich, D.L.
 Biochemistry 33, 13199-13207, 1994
 A:Title: Exploring the microtubule-binding region of bovine microtubule-associated pr
 A:Reference number: A55983; MUID:95034751
 A:Accession: A55983
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-323 <COF>
 A:Cross-references: GB:S74025
 R:Dingus, J.; Obar, R.A.; Hyams, J.S.; Goedert, M.; Vallee, R.B.
 J. Biol. Chem. 266, 18854-18860, 1991
 A:Title: Use of a heat-stable microtubule-associated protein class-specific antibody
 A:Reference number: A41011; MUID:92011652
 A:Accession: A41011

A:Molecule type: protein
 A:Residues: 227-258 <DIN>
 R:Joly, J.C.; Flynn, G.; Purich, D.L.
 J. Cell Biol. 109, 2289-2294, 1989
 A:Title: The microtubule-binding fragment of microtubule-associated protein-2: locali
 A:Reference number: A33734; MUID:90037224
 A:Accession: A33734
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 121-139 <JOL>
 C:Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
 C:Keywords: microtubule binding; tandem repeat
 F:165-195/Domain: MAP2/tau repeat homology <MT1>
 F:227-258/Domain: MAP2/tau repeat homology <MT2>

Query Match 72.0%; Score 36; DB 2; Length 323;
 Best Local Similarity 72.7%; Pred. No. 1.2e+02;
 Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 QY 1 YSS--PGSPGT 9
 ||| ||||
 Db 105 YSSRTPGTPGT 115

RESULT 39
 T32783
 hypothetical protein C50b2.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T32783
 R:Sammons, L.; Wohldmann, P.; Bauer, C.

Wed May 22 11:04:42 2002

us-09-734-281-2.rpr

submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C50D2.
A;Reference number: Z21224

A;Accession: T32783

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-329 <SAM>

A;Cross-references: EMBL:AF040642; PIDN:AAB94952.1; GSPDB:GN000020; CESP:C50D2.4

A;Experimental source: strain Bristol N2; clone C50D2

C;Genetics:

A;Gene: CESP:C50D2.4

A;Map position: 2

A;Introns: 27/1; 59/3; 76/3; 237/1

C;Superfamily: unassigned collagens

Query Match 72.0%; Score 36; DB 2; Length 329;

Best Local Similarity 85.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9

|||:||||

Db 160 SPGNPGT 166

RESULT 40

A75621

Tors-related protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C;Accession: A75621

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.N.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896

A;Accession: A75621

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-351 <WHI>

A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12581.1; PID:g6460877; TIGR:DRB00

A;Experimental source: strain R1

C;Genetics:

A;Gene: DRB0027

A;Map position: megaplasmid

A;Genome: plasmid

A;Note: plasmid MP1

Query Match

Best Local Similarity 72.0%; Score 36; DB 2; Length 351;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9

|||:||||

Db 95 YSTAGTPGT 103

Search completed: May 21, 2002, 11:19:11

Job time: 206 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2002, 11:24:11 ; Search time 13.48 seconds
(without alignments)
25.851 Million cell updates/sec

Title: US-09-734-281-2

Perfect score: 50

Sequence: 1 YSPGSPCT 9

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	382	TAU_PAPHA	G9myx8 papio hamad
2	50	100.0	402	TAU_CAPHI	O02828 capra hircu
3	50	100.0	447	TAU_BOVIN	P29172 bos taurus
4	50	100.0	458	TAU_MACMU	P57786 macaca mula
5	50	100.0	732	TAU_MOUSE	P10637 mus musculus
6	50	100.0	751	TAU_RAT	P19332 rattus norv
7	50	100.0	757	TAU_HUMAN	P10636 homo sapien
8	39	78.0	639	P2BI_CRYNE	O42773 cryptococcu
9	38	76.0	710	P2BI_RAT	P51178 rattus norv
10	38	76.0	756	P2BI_HUMAN	P51178 homo sapien
11	38	76.0	756	P2BI_HUMAN	O19002 felis silve
12	37	74.0	3122	DPOZ_MOUSE	O9eqn3 mus musculus
13	37	74.0	164	CDN1_FELCA	P11329 european el
14	37	74.0	387	TI22_MOUSE	P30989 homo sapien
15	37	74.0	395	TI22_HUMAN	O01344 homo sapien
16	37	74.0	415	VE2_PAPVE	O9ryg9 delnococcu
17	37	74.0	418	NTB1_HUMAN	O04584 gallus gall
18	37	74.0	420	ILSR_HUMAN	O08774 caenorhabdi
19	37	74.0	515	DHAL_DEIRA	O08774 ratu norv
20	37	74.0	542	ZYA_CHICK	O03149 emericella
21	37	74.0	963	YQ36_CAEEL	P42580 mus musculus
22	37	74.0	1387	RGSC_RAT	O58626 methanococc
23	36	72.0	1986	WA_EMENI	P18126 pseudomonas
24	36	72.0	305	SAXL_MOUSE	P41698 saccharomyc
25	36	72.0	501	PVCA_METJA	O05305 mus musculus
26	36	72.0	511	GUNB_PSEFL	O9rk9 streptomyce
27	36	72.0	603	BUD8_YEAST	P11337 homo sapien
28	36	72.0	680	CAIA_MOUSE	P20357 mus musculus
29	36	72.0	1171	TR12_STRCO	P15146 rattus norv
30	36	72.0	1827	MAP2_HUMAN	P39689 mus musculus
31	36	72.0	1828	MAP2_MOUSE	P49684 rattus norv
32	35	70.0	1861	MAP2_RAT	
33	35	70.0	159	CDN1_MOUSE	
34	35	70.0	386	UR2R_RAT	

34	35	70.0	415	1	ILSR_MOUSE	P21183 mus musculu
35	35	70.0	495	1	HXKG_ASPNG	Q92407 aspergillus
36	35	70.0	573	1	AMH2_HUMAN	Q16671 homo sapien
37	35	70.0	828	1	MRKC_KLEPN	P21647 klebsiella
38	35	70.0	903	1	VGLB_HSVIF	P06436 herpes simp
39	35	70.0	904	1	VGLB_HSV11	P10211 herpes simp
40	35	70.0	904	1	VGLB_HSV1P	P08665 herpes simp
41	35	70.0	956	1	RRPO_SBMV	P21405 southern be
42	35	70.0	1464	1	CA13_MOUSE	P08121 mus musculu
43	35	70.0	1690	1	CA44_HUMAN	P53420 homo sapien
44	35	70.0	1835	1	CCAT_RAT	Q920y8 rattus norv
45	34	68.0	114	1	ET3_RABIT	P19998 cryptotagus
46	34	68.0	238	1	ET3_HUMAN	P14138 homo sapien
47	34	68.0	239	1	CALD_MELGA	P13505 meleagris g
48	34	68.0	239	1	MABA_MOUSE	P39039 mus musculu
49	34	68.0	249	1	PSPA_PIG	P49874 sus scrofa
50	34	68.0	298	1	34KD_MVCPA	Q04959 mycobacteri
51	34	68.0	467	1	RPB1_CRIGR	P11414 cricetus
52	34	68.0	492	1	DY22_HUMAN	O43237 homo sapien
53	34	68.0	508	1	CILA_KLEPN	P45413 klebsiella
54	34	68.0	520	1	MRCO_HUMAN	Q9uew3 homo sapien
55	34	68.0	547	1	CD19_MOUSE	P25918 mus musculu

ALIGNMENTS

RESULT 1

ID	TAU_PAPHA	STANDARD	PRT	382 AA
AC	Q9MYX8			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Microtubule-associated protein tau (Neurofibrillary tangle protein)			
DE	(Paired helical filament-tau) (PHF-tau).			
GN	MAPT OR TAU			
OS	Papio hamadryas (Hamadryas baboon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OX	Cercopithecoidea; Papio.			
RP	NCBI_TaxID=9557;			
RP	[1]			
CC	SEQUENCE FROM N.A.			
CC	TISSUE=Frontal cortex;			
CC	Wang X.L., Wang J., Schultz C., Hubbard G.B.;			
CC	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT			
CC	BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL			
CC	POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-			
CC	TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT			
CC	TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH AXONAL POLARITY IS			
CC	PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE			
CC	DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE			
CC	CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS (BY			
CC	SIMILARITY).			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.			
CC	-!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN.			
CC	-!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN			
CC	S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,			
CC	CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN			
CC	MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY			
CC	MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).			
CC	-!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			

```

CC EMBL; AF281310; AAF97596.1;
CC InterPro; IPR002955; tau_protein.
CC InterPro; IPR001084; tubulin-bind.
CC Pfam; PF00418; tubulin-binding; 4.
CC PRINTS; PR01261; TAUPTROTEIN.
CC PROSITE; PS00229; TAU_MAP; 4.
CC Microtubules; Cytoskeleton; Repeat; Acetylation; Phosphorylation.
CC INIT_MET 0 BY SIMILARITY.
CC REPEAT 185 215 TAU/NAF MOTIF 1.
CC REPEAT 216 246 TAU/NAF MOTIF 2.
CC REPEAT 247 277 TAU/NAF MOTIF 3.
CC REPEAT 278 309 TAU/NAF MOTIF 4.
CC MOD_RES 1. 1 ACETYLATION (BY SIMILARITY).
CC DISULFID 232 263 BY SIMILARITY.
CC SEQUENCE 382 AA; 39879 MW; D2D15A53AA00B8E7 CRC64;

Query Match 100.0%; Score 50; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 138 YSSPGSPGT 146

RESULT 2
TAU_BOVIN
ID TAU_CAPHI STANDARD; PRT; 402 AA.
AC Q02828;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE (paired helical filament-tau) (PHF-tau).
GN MAPT OR TAU.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC TISSUE=Brain cortex;
RX MEDLINE=97012131; PubMed=8858947;
RA Nelson P.T., Stefansson K., Gulcher J., Saper C.B.;
RT "Molecular evolution of tau protein: implications for Alzheimer's
RT disease."
RL J. Neurochem. 67:1622-1632(1996).
CC -1- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH AXONAL POLARITY IS
CC PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC -1- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; TAU-A (SHOWN HERE) AND
CC TAU-B; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER FROM EACH
CC OTHER BY THE PRESENCE OR ABSENCE OF TWO EXONS. ONE OF THESE
CC OPTIONAL EXONS CONTAINS THE ADDITIONAL TAU/NAF REPEAT.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC -1- DOMAIN: THE TAU/NAF REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC -1- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC MITOSIS). AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).

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CC -1- SIMILARITY: CONTAINS 4 TAU/NAF REPEATS.
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CC EMBL; S83347; AAB50785.1;
CC InterPro; IPR002955; tau_protein.
CC InterPro; IPR001084; tubulin-bind.
CC Pfam; PF00418; tubulin-binding; 4.
CC PRINTS; PR01261; TAUPTROTEIN.
CC PROSITE; PS00229; TAU_MAP; 4.
CC Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
CC Phosphorylation.
CC INIT_MET 0 BY SIMILARITY.
CC REPEAT 205 235 TAU/NAF MOTIF 1.
CC REPEAT 236 266 TAU/NAF MOTIF 2.
CC REPEAT 267 297 TAU/NAF MOTIF 3.
CC REPEAT 298 329 TAU/NAF MOTIF 4.
CC MOD_RES 1. 1 ACETYLATION (BY SIMILARITY).
CC DISULFID 252 283 BY SIMILARITY.
CC VARSPLIC 33 61 MISSING (IN ISOFORM TAU-B).
CC SEQUENCE 402 AA; 41716 MW; 3E623B684E9F8AEF CRC64;

Query Match 100.0%; Score 50; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 158 YSSPGSPGT 166

RESULT 3
TAU_BOVIN
ID TAU_BOVIN STANDARD; PRT; 447 AA.
AC P29172; P29173; Q28185; Q28186; Q28187; Q28188; Q28189; Q28190;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE (paired helical filament-tau) (PHF-tau).
GN MAPT OR TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS TAU-A; TAU-B; TAU-G AND TAU-H).
RC TISSUE=Brain;
RX MEDLINE=89261765; PubMed=2498649;
RA Himmler A., Drechsel D., Kirschner M.W., Martin D.W. Jr.;
RT "Tau consists of a set of proteins with repeated C-terminal
RT microtubule-binding domains and variable N-terminal domains."
RL Mol. Cell. Biol. 9:1381-1388(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS TAU-A TO TAU-F AND TAU-I TO TAU-T).
RC TISSUE=Brain;
RX MEDLINE=89261766; PubMed=2498650;
RA Himmler A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts
RT generate a protein family."
RN Mol. Cell. Biol. 9:1389-1396(1989).
RP GLYCOSYLATION.
RX MEDLINE=97067111; PubMed=8910513;

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RA Arnold C.S., Johnson G.V.W., Cole R.N., Dong D.L.-Y., Lee M.,
 RA "The microtubule-associated protein tau is extensively modified with
 RT O-linked N-acetylglucosamine";
 RL J. Biol. Chem. 271:28741-28744(1996).
 CC -1- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
 CC BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
 CC POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
 CC TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
 CC TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
 CC DETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
 CC DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
 CC ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
 CC ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
 CC -1- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS. IN THE
 CC CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS. IN THE
 CC ALTERNATIVE PRODUCTS: AT LEAST 20 ISOFORMS: TAU-A/PBT43112 (SHOWN
 CC HERE), TAU-B/PBT43-12, TAU-C, TAU-D, TAU-E, TAU-F, TAU-G/PBT4,
 CC TAU-H/PBT7, TAU-I, TAU-J, TAU-K, TAU-L, TAU-M, TAU-N, TAU-O, TAU-
 CC P, TAU-Q, TAU-R, TAU-S AND TAU-T; ARE PRODUCED BY ALTERNATIVE
 CC SPLICING. THEY DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE
 CC OF UP TO 6 OF THE 14 EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS
 CC THE ADDITIONAL TAU/MAP REPEAT. TAU-A CDNA HAS BEEN CONSTRUCTED
 CC FROM TWO OVERLAPPING CDNAS BY THE AUTHORS OF REF.1. TAU-G AND TAU-
 CC H SEQUENCES BEGIN WITH EXON 6 OR A PART OF IT (EXON 6 IS MISSING
 CC IN ISOFORMS THAT BEGIN WITH EXON 1). 3 DIFFERENT C-TERMINI ARE
 CC OBTAINED EITHER BY THE RETENTION OR THE SPLICING OF INTRON 13/14
 CC (2 DIFFERENT 5' SPLICE DONORS).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
 CC -1- INDUCTION: DURING NEURITE OUTGROWTH.
 CC -1- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
 CC CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
 CC -1- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
 CC S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK; CDC2,
 CC CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
 CC MITOSIS). AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
 CC MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
 CC -1- PTM: O-LINKED N-ACETYLGLUCOSAMINATION AT MORE THAN 4 SITES PER
 CC PROTEIN. SITE-SPECIFIC OR STOICHIOMETRIC CHANGES IN GLYCOSYLATION
 CC MAY MODULATE TAU FUNCTION AND ALSO PLAY A ROLE IN PHF'S FORMATION.
 CC -1- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
 CC -----
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 CC EMBL; L35318; AAA51609.1; JOINED.
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 CC EMBL; L35328; AAA51609.1; JOINED.
 CC EMBL; L35329; AAA51609.1; JOINED.
 CC EMBL; L3

RX MEDLINE-88099510; PubMed-3122323;
 RA Lee G., Cowan N.J., Kirschner M.;
 RT "The primary structure and heterogeneity of tau protein from mouse
 RL brain.";
 RN Science 239:285-288 (1988).
 RP [4]
 RC PARTIAL SEQUENCE FROM N.A. (ISOFORM B).
 RA STRAIN=ICR; TISSUE=Brain;
 RX MEDLINE-95182802; PubMed-7877441;
 RA Sawa A., Oyama F., Matsushita M., Ihara Y.;
 RT "Molecular diversity at the carboxyl terminus of human and rat tau.";
 RL Brain Res. Mol. Brain Res. 27:111-117 (1994).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE-94005827; PubMed-8402267;
 RA Couchie D., Gache Y., Mavilla C., Guilleminot J., Bridoux A.-M.,
 RA Navez M.-P., Nunez J.;
 RT "High molecular weight tau proteins and acquisition of neuronal
 RL polarity in peripheral nervous system.";
 RN C. R. Acad. Sci. III. Sci. Vie 316:404-409 (1993).
 RP [4]
 RC FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
 BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
 POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
 TERMINUS BINDS NEURONAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
 TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
 PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
 DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
 ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
 ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
 [1]
 CC SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS. IN THE
 CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS. IN THE
 [2]
 CC ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; PNS-TAU (SHOWN HERE),
 TAU-A, TAU-B, TAU-C, TAU-D AND TAU-E; ARE PRODUCED BY ALTERNATIVE
 SPLICING. THEY DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE
 OF UP TO 5 OF THE 14 EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS
 THE ADDITIONAL TAU/MAP REPEAT. TWO DIFFERENT C-TERMINI ARE
 OBTAINED EITHER BY THE RETENTION OR THE SPLICING OF INTRON 13/14.
 [3]
 CC TISSUE SPECIFICITY: EXPRESSED IN NEURONS AND AT A LOWER LEVEL IN
 THE LIVER AND KIDNEY. PNS-TAU IS EXPRESSED IN THE PERIPHERAL
 NERVOUS SYSTEM WHILE THE OTHERS ARE EXPRESSED IN THE CENTRAL
 NERVOUS SYSTEM.
 [4]
 CC DEVELOPMENTAL STAGE: SHORTER FORMS OR LOW MOLECULAR WEIGHT TAU
 (LMW-TAU) ARE GENERALLY EXPRESSED AT EARLY DEVELOPMENT STAGES AND
 LONGER FORMS OR HIGH MOLECULAR WEIGHT TAU (HMW-TAU) IN THE ADULT
 BRAIN.
 [5]
 CC DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
 CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
 [6]
 CC PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
 S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
 CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
 MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
 MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
 [7]
 CC DISEASE: MAY BE INVOLVED IN THE PATHOGENESIS OF CYTOPLASMIC
 INCLUSIONS (AS MALLORY BODIES) IN LIVERS OF MICE CHRONICALLY
 INTOXICATED WITH GRISEOFULVIN OR DDC (3,5-DIETHOXYCARBONYL-2,4-
 DIHYDROCOLIDINE), A MODEL FOR HUMAN ALCOHOLIC HEPATITIS.
 [8]
 CC ALTERATION OF TAU (ABNORMAL PHOSPHORYLATION AND CROSSLINKING)
 COULD CONTRIBUTE TO MALLORY BODIES FORMATION AND DISTURBANCE OF
 MICROTUBULE FUNCTION IN ALCOHOLIC LIVER DISEASE.
 [9]
 CC SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
 [10]
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 or send an email to license@isb-sib.ch).
 [11]
 EMBL; U12914; AAA58343.1; -
 EMBL; U12915; AAA58344.1; -
 EMBL; U12916; AAA58345.1; -
 EMBL; Z12133; CAA78121.1; -

DR EMBL; M93266; -; NOT_ANNOTATED_CDS.
 DR EMBL; M18775; AAA40165.1; -
 DR EMBL; M18776; AAA40166.1; -
 DR EMBL; D30627; BAA18878.1; -
 DR PIR; A28820; A28820.
 DR PIR; B28820; B28820.
 DR MGI; 97180; Mapt.
 DR InterPro; IPR002955; Tau_protein.
 DR InterPro; IPR001084; Tubulin-bind.
 DR Pfam; PF00418; tubulin-binding; 7.
 DR PRINTS; PR01261; TAUPROTEIN.
 DR PROSITE; PS00229; TAU_MAP; 3.
 KW Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
 KW phosphorylation.
 FT INIT_MET 0 0
 FT REPEAT 535 565
 FT REPEAT 566 596
 FT REPEAT 597 627
 FT REPEAT 628 659
 FT MOD_RES 1 1
 FT DISULFID 582 613
 FT VARSPLIC 33 90
 FT VARSPLIC 91 112
 FT VARSPLIC 113 349
 FT VARSPLIC 367 432
 FT VARSPLIC 566 596
 FT VARSPLIC 732 732
 FT CONFLICT 2 2
 FT CONFLICT 8 8
 FT CONFLICT 527 527
 FT CONFLICT 671 671
 FT CONFLICT 732 732
 FT SEQUENCE 732 AA; 76112 MW; BFDFO767E41C7A3A CRC64;
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 Query Match 100.0%; Score 50; DB 1; Length 732;
 Best Local Similarity 100.0%; Pred. No. 0.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSPGSPGT 9
 Db 488 YSSPGSPGT 496
 RESULT 6
 TAU_RAT
 ID TAU_RAT STANDARD; PRT; 751 AA.
 AC P19332; Q63567; O9QW06; Q63677;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Microtubule-associated protein tau (Neurofibrillary tangle protein)
 DE (Paired helical filament-tau) (PHF-tau).
 GN MAPT OR MTAPT OR TAU.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM TAU-B).
 RC TISSUE=Phenochromocytoma;
 RX MEDLINE-92179305; PubMed-1542696;
 RA Goedert M., Spillantini M.G., Crowther R.A.;
 RT "Cloning of a big tau microtubule-associated protein characteristic of
 the peripheral nervous system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1983-1987 (1992).
 RN [2]

ISOFORMS MAY PREPREFERENTIALLY EXPRESSED IN THE AXONS OF NEURONS, IN THE
 -! SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
 CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
 -! ALTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS; TAU-A/SC1 (SHOWN HERE),
 TAU-B/BIG-TAU/HW-TAU, TAU-C, TAU-D/SC2, TAU-E, TAU-F, TAU-
 G/FETAL-TAU AND TAU-H; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY
 DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF UP TO 4 OF
 THE 14 EXONS. TWO DIFFERENT C-TERMINI ARE OBTAINED EITHER BY THE
 RETENTION OR THE SPLICING OF INTRON 13/14.
 -! TISSUE SPECIFICITY: EXPRESSED IN NEURONS. THE LARGER FORMS (TAU-A
 AND TAU-B) ARE PREPREFERENTIALLY EXPRESSED IN THE PERIPHERAL NERVOUS
 SYSTEM WHILE THE OTHERS ARE EXPRESSED IN THE CENTRAL NERVOUS
 SYSTEM. LOW AMOUNTS OF THE LARGER FORMS ARE ALSO FOUND IN LIMITED
 AREAS OF THE CNS.
 -! DEVELOPMENTAL STAGE: DURING THE IMMEDIATE POSTNATAL PERIOD, THE
 DORSAL ROOT GANGLIA EXPRESS ALL ISOFORMS WHEREAS ONLY THE LARGER
 FORMS PERSIST IN THE ADULTS.

protein tau gene with familial frontotemporal dementia and parkinsonism.";
Hum. Mol. Genet. 7:1825-1829(1998).

[19] VARIANTS FTDP17 VAL-588; LEU-617 AND TRP-722.
MEDLINE=98303385; PubMed=9641683;
Hutton M., Lendon C.L., Rizzu P., Baker M., Froelich S., Houiden H., Pickering-Brown S., Chakraverty S., Isaacs A., Grover A., Hackett J., Adamson J., Lincoln S., Dickson S., Davies P., Petersen R.C., Stevens M., Kwon J.M., Nowotny P., Che L.K., Norton J., Morris J.C., Reed L.A., Trojanowski J., Basun H., Lannfelt L., Neystat M., Fahn S., Dark F., Tannenberg T., Dodd P.R., Hayward N., Kwok J.B.J., Schofield P.R., Andreadis A., Snowden J., Craufurd D., Neary D., Owen F., Oostra B.A., Hardy J., Goate A., van Swieten J., Mann D., Lynch T., Heutink P.;
"Association of missense and 5'-splice-site mutations in tau with the inherited dementia FTDP-17.";
Nature 393:702-705(1998).

[20] VARIANT PPND LYS-595, AND VARIANT FTDP17 LEU-617.
MEDLINE=99007274; PubMed=9789048;
Clark L.N., Pookraj P., Wazolek Z., Geschwind D.H., Nasreddine Z.S., Miller B., Li D., Payami H., Avert F., Markopoulou K., Andreadis A., D'Souza I., Lee V.M.-Y., Reed L.A., Trojanowski J.O., Zhukareva V., Bird T., Schellenberg G., Wilhelmsen K.C.;
"Pathogenic implications of mutations in the tau gene in pallido-ponto-nigral degeneration and related neurodegenerative disorders linked to chromosome 17.";
Proc. Natl. Acad. Sci. U.S.A. 95:13103-13107(1998).

[21] VARIANTS FTDP17 VAL-588; LYS-596 DEL; LEU-617 AND TRP-722.
MEDLINE=99138654; PubMed=9973279;
Rizzu P., Van Swieten J.C., Joosse M., Hasegawa M., Stevens M., Tibben A., Niermeijer M.F., Hillebrand M., Ravid R., Oostra B.A., Goedert M., van Duijn C.M., Heutink P.;
"High prevalence of mutations in the microtubule-associated protein tau in a population study of frontotemporal dementia in the Netherlands.";
Am. J. Hum. Genet. 64:414-421(1999).

[22] VARIANTS FTDP17 LEU-617; MET-653 AND TRP-722.
MEDLINE=99229757; PubMed=10214944;
Nacharaju P., Lewis J., Easson C., Yen S., Hackett J., Hutton M., Yen S.H.;
"Accelerated filament formation from tau protein with specific FTDP-17 missense mutations.";
FEBS Lett. 447:195-199(1999).

[23] VARIANT FTDP17/CBD SER-617.
Query Match 100.0%; Score 50; DB 1; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 513 YSSPGSPGT 521
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RESULT 8
P2B1_CRYNE STANDARD; PRT; 639 AA.
ID P2B1_CRYNE
AC C42773;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Serine/threonine protein phosphatase 2B catalytic subunit A1 (EC 3.1.3.16) (Calcineurin A1).
GN CNAL.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellales; Tremellaceae; Filobasidiella.

RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney;
 RX MEDLINE-96108664; PubMed-8531138;
 RA Saito H., Okuda M., Terada T., Sasaki S., Inui K.;
 RT "Cloning and characterization of a rat H+/peptide cotransporter
 RT mediating absorption of beta-lactam antibiotics in the intestine and
 RT kidney.";
 RL J. Pharmacol. Exp. Ther. 278:1631-1637(1995).
 CC -!- FUNCTION: PROTON-COUPLED INTAKE OF OLIGOPEPTIDES OF 2 TO 4
 CC AMINO ACIDS WITH A PREFERENCE FOR DIPEPTIDES. MAY CONSTITUTE
 CC A MAJOR ROUTE FOR THE ABSORPTION OF PROTEIN DIGESTION END-
 CC PRODUCTS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D50664; BAA09318.1; -;
 CC EMBL; D50306; BAA08844.1; -;
 CC InterPro; IPR000109; PTR2.
 CC Pfam; PF00854; PTR2; 2.
 CC PROSITE; PS01022; PTR2_1; 1.
 CC PROSITE; PS01023; PTR2_2; 1.
 CC Peptide transport; Transport; Transmembrane; Symport; Glycoprotein.
 FT TRANSMEM 1 21
 FT DOMAIN 22 53
 FT TRANSMEM 54 74
 FT DOMAIN 75 82
 FT TRANSMEM 83 103
 FT DOMAIN 104 118
 FT TRANSMEM 119 139
 FT DOMAIN 140 161
 FT TRANSMEM 162 182
 FT DOMAIN 183 198
 FT TRANSMEM 199 219
 FT DOMAIN 220 276
 FT TRANSMEM 277 297
 FT DOMAIN 298 327
 FT TRANSMEM 328 348
 FT DOMAIN 349 361
 FT TRANSMEM 362 382
 FT DOMAIN 383 586
 FT TRANSMEM 587 607
 FT DOMAIN 608 621
 FT TRANSMEM 622 642
 FT DOMAIN 643 647
 FT TRANSMEM 648 688
 FT DOMAIN 689 710
 FT CARBOHYD 710 710
 FT CARBOHYD 415 415
 FT CARBOHYD 439 439
 FT CARBOHYD 510 510
 FT CARBOHYD 532 532
 FT CARBOHYD 539 539
 FT CONFLICT 241 241
 FT CONFLICT 259 259
 FT CONFLICT 279 280
 FT SEQUENCE 710 AA; 78928 MW; 435727A6C76F2D7B CRC64;

Query Match 76.0%; Score 38; DB 1; Length 710;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 SSPGSPG 8
 Db 441 SSPGSPG 447
 |||||

RESULT 10
 PIDL_HUMAN
 ID PIDL_HUMAN STANDARD; PRT; 756 AA.
 AC PS1178;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
 DE (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III).
 GN PLCD1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RX MEDLINE=95197554; PubMed=7890667;
 RA Cheng H.F., Jiang M.J., Chen C.L., Liu S.M., Wong L.P.,
 RA Lomasney J.W., King K.;
 RT "Cloning and identification of amino acid residues of human
 RT phospholipase C delta 1 essential for catalysis.";
 RL J. Biol. Chem. 270:5495-5505(1995).
 CC -!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -!- COFACTOR: REQUIRES CALCIUM.
 CC -!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC -----
 CC EMBL; U09117; AAA73567.1; -;
 CC HSP; P10688; 1MA1.
 CC MTM; 602142; -;
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR02048; EF-hand.
 CC InterPro; IPR001849; PH.
 CC InterPro; IPR001192; PI-PLC.
 CC InterPro; IPR000909; PI-PLC-X.
 CC InterPro; IPR001711; PI-PLC-Y.
 CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00036; ehand; 2.
 CC Pfam; PF00169; PH; 1.
 CC Pfam; PF00388; PI-PLC-X; 1.
 CC Pfam; PF00387; PI-PLC-Y; 1.
 CC PRINTS; PR00360; C2DOMAIN.
 CC PRINTS; PR00390; PHPLIPASEC.
 CC PRODOM; PD001202; PI-PLC-Y; 1.
 CC SMART; SM00239; C2; 1.
 CC SMART; SM00233; PH; 1.
 CC SMART; SM00148; PLCX; 1.
 CC SMART; SM00149; PLCYC; 1.
 CC PROSITE; PS00018; EF_HAND; 2.
 CC PROSITE; PS00003; PH_DOMAIN; 1.
 CC PROSITE; PS00004; C2_DOMAIN_2; 1.
 CC PROSITE; PS00007; PIPLC_X_DOMAIN; 1.
 CC PROSITE; PS00008; PIPLC_Y_DOMAIN; 1.
 KW Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat.
 FT DOMAIN 21 130
 FT PH.

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FT CA_BIND 153 164 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 189 200 EF-HAND 2 (POTENTIAL).
 FT DOMAIN 296 440 DOMAIN X.
 FT DOMAIN 492 609 DOMAIN Y.
 FT DOMAIN 616 720 C2 DOMAIN.
 FT ACT_SITE 311 311 BY SIMILARITY.
 FT ACT_SITE 356 356 BY SIMILARITY.
 SQ SEQUENCE 756 AA; 85763 MW; AD9A4251C5EBADF8 CRC64;

Query Match 76.0%; Score 38; DB 1; Length 756;
 Best Local Similarity 75.0%; Pred. No. 56;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
 :||||:|
 Db 507 FSSPGTGP 514

RESULT 11

DPOZ_MOUSE STANDARD; PRT; 3122 AA.
 AC Q61493; Q9QWX6; Q9JMD6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (Seizure related protein 4).
 DE REV3L OR POLZ OR SEZ4.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/OLA; TISSUE=Testis;
 RX MEDLINE=99202265; PubMed=10102037;
 RA Van Sloun P.P.H., Romeijn R.J., Eken J.C.J.;
 RT "Molecular cloning, expression and chromosomal localisation of the mouse Rev3l gene, encoding the catalytic subunit of polymerase zeta.";
 RL Mutat. Res. 433:109-116(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kajiwara K.;
 RT "Molecular analyses of Sez4 encoding murine homologue of yeast REV3 in brain neurons.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 2368-3122 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryonic brain;
 RX MEDLINE=96216731; PubMed=8645260;
 RA Kajiwara K., Nagawara H., Shimizu-Nishikawa K., Ookura T., Kimura M., Sugaya E.;
 RT "Molecular characterization of seizure-related genes isolated by differential screening.";
 RL Biochem. Biophys. Res. Commun. 219:795-799(1996).
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate + [DNA](N)
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.

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 CC -----
 CC EMBL; AF083464; AAC98785.1; -.
 CC EMBL; AB031049; BAA90768.1; -.
 CC EMBL; D78644; BAA11461.1; -.
 CC MGD; MGI:1337131; Rev31.

DR InterPro: IPR002064; DNA_pol_B.
 DR Pfam: PF00136; DNA_pol_B; 2.
 DR Pfam: PF03104; DNA_pol_B_exo; 1.
 DR PRINTS; PR00106; DNAPOLB.
 DR SMART; SM00486; POLBC; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 KW Transferase: DNA-directed DNA polymerase; DNA replication;
 KW DNA-binding; DNA repair; Nuclear protein; Zinc-finger.
 FT ZN_FING 3034 3049 C4-TYPE (POTENTIAL).
 FT ZN_FING 3078 3096 C4-TYPE (POTENTIAL).
 FT CONFLICT 92 92 G -> A (IN REF. 2).
 FT CONFLICT 294 294 A -> T (IN REF. 2).
 FT CONFLICT 578 578 E -> Q (IN REF. 2).
 FT CONFLICT 609 609 R -> Q (IN REF. 2).
 FT CONFLICT 1278 1278 L -> P (IN REF. 2).
 FT CONFLICT 1298 1298 L -> F (IN REF. 2).
 FT CONFLICT 1416 1416 P -> L (IN REF. 2).
 FT CONFLICT 1848 1848 A -> T (IN REF. 2).
 FT CONFLICT 2368 2368 V -> G (IN REF. 3).
 SQ SEQUENCE 3122 AA; 350654 MW; A39846CAF7365BA8 CRC64;

Query Match 76.0%; Score 38; DB 1; Length 3122;
 Best Local Similarity 87.5%; Pred. No. 2.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
 :||||:|
 Db 2108 YSSPDSPG 2115

RESULT 12

CDNL_FELCA STANDARD; PRT; 164 AA.
 ID CDNL_FELCA
 AC O19002;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1 (p21) (CDK-interacting protein 1).
 GN CDKN1A OR CIP1 OR WAF1.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=98036042; PubMed=9370275;
 RA Okuda M., Minehata K., Setoguchi A., Cho K.-W., Nakamura N., Nishigaki K., Watari T., Cevario S., O'Brien S.J., Tsujimoto H., Hasegawa A.;
 RT "Cloning and chromosome mapping of the feline genes p21WAF1 and p27Kip1.";
 RL Gene 198:141-147(1997).
 CC -!- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.

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 CC -----
 CC EMBL; D84650; BAA23168.1; -.
 CC HSSP; P46527; 1JSU.

DR InterPro: IPR003175; CDI.
 DR Pfam: PF02234; CDI; 1.
 KW Cell cycle; Nuclear protein; zinc-finger.
 FT ZN_FING 13 41 C4-TYPE (POTENTIAL);
 FT DOMAIN 141 156 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 164 AA; 18315 MW; 0F7912A76C78BF38 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 164;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPG 9
 :|||:||||
 Db 129 ASPGAPCT 136

RESULT 13
 T122_MOUSE STANDARD; PRT; 387 AA.
 AC O9EQN3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE TSC22-related inducible leucine zipper protein 2.
 GN TILZ2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ershler M.A., Belyavsky A.V., Visser J.W.M.;
 RT "Identification and characterization of a family of leucine zipper
 genes related to TSC22";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR (BY SIMILARITY).
 CC -!- SUBUNIT: FORMS HOMODIMER OR HETERODIMER. CAN FORM AN HETERODIMER
 WITH TSC-22.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.

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 EMBL; AF201286; AAG41219.1;
 DR InterPro: IPR000580; TSC-22_Dip_Bun.
 DR Pfam: PF01166; TSC22; 1.
 DR ProDom: PD007152; TSC-22_Dip_Bun; 1.
 DR PROSITE; PS01289; TSC22; 1.
 KW Transcription regulation; Repressor; Nuclear protein.
 FT DOMAIN 336 357 LEUCINE-ZIPPER.
 SQ SEQUENCE 387 AA; 39987 MW; C78BB96B5B2DFB90 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 387;
 Best Local Similarity 75.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YSSPGSPG 8
 :|||||
 Db 19 YEGPGSPG 26

RESULT 14
 T122_HUMAN STANDARD; PRT; 395 AA.
 ID T122_HUMAN
 AC Q9Y3Q8;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE TSC22-related inducible leucine zipper protein 2 (Tsc-22-like protein
 THG-1).
 DE TILZ2.
 GN Homo sapiens (Human).
 OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99419018; PubMed=10488076;
 RA Kester H.A., Blanchetot C., den Hertog J., van der Saag P.T.,
 van der Burg B.;
 RT "Transforming growth factor-beta-stimulated clone-22 is a member of a
 family of leucine zipper proteins that can homo- and heterodimerize
 and has transcriptional repressor activity.";
 RL J. Biol. Chem. 274:27439-27447(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR.
 CC -!- SUBUNIT: FORMS HOMODIMER OR HETERODIMER. CAN FORM AN HETERODIMER
 WITH TSC-22.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.

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 EMBL; AJ133115; CAB43491.1;
 DR EMBL; BC001966; AAH01966.1;
 DR InterPro: IPR000580; TSC-22_Dip_Bun.
 DR Pfam: PF01166; TSC22; 1.
 DR ProDom: PD007152; TSC-22_Dip_Bun; 1.
 DR PROSITE; PS01289; TSC22; 1.
 KW Transcription regulation; Repressor; Nuclear protein.
 FT DOMAIN 344 365 LEUCINE-ZIPPER.
 FT CONFLICT 355 356 NA -> KR (IN REF. 1).
 SQ SEQUENCE 395 AA; 41026 MW; DA08B5617C9BB151 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 395;
 Best Local Similarity 75.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YSSPGSPG 8
 :|||||
 Db 19 YEGPGSPG 26

RESULT 15
 VE2_PAPVE STANDARD; PRT; 415 AA.
 ID VE2_PAPVE
 AC P11329;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Probable regulatory protein E2.
 GN E2.
 OS European elk papillomavirus (EEPV).
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10565;
 RN [1]

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us-09-734-281-2.rsp

SEQUENCE FROM N.A.
 RP MEDLINE-87219878; PubMed-3034730;
 RA Ahola H., Bergman P., Strom A.C., Moreno-Lopez J., Petterson U.;
 RT "Organization and expression of the transforming region from the
 RT European elk papillomavirus (EEPV).";
 RL Gene 50:195-205(1986).
 CC -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
 CC IT BINDS TO THE E2 RESPONSE ELEMENT (5'-ACNNNNNGGT-3') PRESENT
 CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
 CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING ON E2RE'S POSITION
 CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
 CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
 CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
 CC REPLICATION.
 CC -1- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
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 CC EMBL; M15953; AAA66854.1; -;
 DR F1R; D29499; W2WLEP.
 DR HSP; P03122; 2BOP.
 DR InterPro; IPR001866; E2_N.
 DR InterPro; IPR000427; Early2_C.
 DR Pfam; PF00511; E2_C; 1.
 DR Pfam; PF00508; E2_N; 1.
 DR ProDom; PD000672; Early2_C; 1.
 DR ProDom; PD000678; E2_N; 1.
 DR Early protein; transcription regulation; Activator; DNA-binding;
 KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
 SQ SEQUENCE 415 AA; 46245 MW; 0B7BF6AE0AC80C CRC64;

Query Match 74.0%; Score 37; DB 1; Length 415;
 Best Local Similarity 66.7%; Pred. No. 43;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YSPSPGPGT 9
 Db 268 YSAPSPGSGS 276
 ||| |||
 ||| |||

RESULT 16
 NTRL_HUMAN STANDARD; PRT; 418 AA.
 ID NTRL_HUMAN
 AC P30989; Q9H4T5; Q9H4H1.
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Neurotensin receptor type 1 (NT-R-1) (High-affinity leucobastine-
 DE insensitive neurotensin receptor) (NTRH).
 GN NTSR1 OR NTRR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE-93154505; PubMed-8381365;
 RA Vita N., Laurent P., Lefort S., Chalou P., Dumont X., Kaghad M.,
 RA Gully D., le Fur G., Ferrara P., Caput D.;
 RT "Cloning and expression of a complementary DNA encoding a high
 RT affinity human neurotensin receptor."
 RL FEBS Lett. 317:139-142(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
 Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
 Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 Hammond E., Hunt A.R., Hunt S.E., Jekosch K., Johnson J.L., Howden P.J.,
 Huckle M.P., Kimberley A.M., King A., Knights A., Laird G.K., Johnson S.,
 Kay M.P., Kimberley M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
 Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
 Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 Rice C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -1- FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS
 CC ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCULIN SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC HIGHEST TO TACHYKININS RECEPTORS.
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 CC EMBL; X70070; CAA49675.1; -;
 DR EMBL; AL357033; CAC14923.1; -;
 DR EMBL; AL035669; CAC12747.1; -;
 DR F1R; S29506; S29506.
 DR GCRdb; GCR_0577; -;
 DR GCRdb; GCR_2067; -;
 DR MIN; 162651; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR003985; NTL_rec.
 DR InterPro; IPR003984; NTL_rec.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01479; NEUROTENSINR.
 DR PRINTS; PR01480; NEUROTENSINR.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 63
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 64 86
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 87 95
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 96 120
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 121 142
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 143 164
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 165 187
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 188 209
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 210 234
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 235 259
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 260 303
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 304 325
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 326 343
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 344 367
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 368 418


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FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 141 224 BY SIMILARITY.
FT LIPID 383 383 PALMITATE (POTENTIAL).
FT CONFLICT 200 200 T -> A (IN REF. 2).
SQ SEQUENCE 418 AA; 46288 MW; BBBDEEC2B5E390 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 418;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
DB 6 SAPGTGT 13

RESULT 17
IL5R_HUMAN
ID IL5R_HUMAN STANDARD; PRT; 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE Interleukin-5 receptor alpha chain precursor (IL-5R-alpha) (CD125
DE antigen).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetnick G., Verhee A., Fiers W.,
RA Devos R.;
RT "Molecular basis of the membrane-anchored and two soluble isoforms of
RT the human interleukin 5 receptor alpha subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
RN [3]
SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=92005669; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA Fiers W., Plaetnick G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of
RT an IL5-specific alpha chain and a beta chain shared with the receptor
RT for GM-CSF.";
RL Cell 66:1175-1184(1991).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SURCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CDw125 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M96652; AAA59152.1; -
DR EMBL; M96651; AAA59151.1; -
DR EMBL; M75914; AAA36110.1; -
DR EMBL; A26249; CAA01793.1; -
DR EMBL; A24587; CAA01731.1; -
DR EMBL; A26251; CAA01794.1; -
DR PIR; A40267; A40267.
DR MIM; I47851; -
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003532; Hematopo_receptor_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT DOMAIN 21 342 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 343 362 POTENTIAL.
FT DOMAIN 363 420 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 333 335 NDE -> FSR (IN SOLUBLE ISOFORM S1).
FT VARSPPLIC 336 420 MISSING (IN SOLUBLE ISOFORM S1).
FT VARSPPLIC 333 333 N -> K (IN SOLUBLE ISOFORM S2).
FT VARSPPLIC 334 420 MISSING (IN SOLUBLE ISOFORM S2).
SQ SEQUENCE 420 AA; 47700 MW; 420681FBC6B51700 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 420;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
DB 119 HAPGSPGT 127

RESULT 18
DHAL_DEIRA
ID DHAL_DEIRA STANDARD; PRT; 515 AA.
AC Q9RYG9; O32502;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Aldehyde dehydrogenase (EC 1.2.1.3).
GN ALDA OR DRA0348.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=RI;
RX MEDLINE=20036996; PubMed=10567266;
RA White O., Eissen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Yamahirovan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Aravind L., Smith H.O., Salzberg S., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI.";
RL Science 286:1571-1577(1999).
RN [2]
SEQUENCE OF 1-258 FROM N.A.
RP STRAIN=KD301;
RA Narumi I., Du Z., Alatas Z., Kitayama S., Watanabe H.;
RT "Isolation and characterization of pBRA, a novel Deinococcus
RT radiodurans gene involved in DNA repair.";

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Wed May 22 11:04:43 2002

us-09-734-281-2.rsp

Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
 -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

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 EMBL: AE001963; AAF12436.1; -
 EMBL: AB003475; BAA21372.1; -
 HSP: P05091; ICW3.
 TIGR: DRA0348; -
 InterPro: IPR002086; Aldehyde_dehydr.
 Pfam: PF00171; aldedh; 1.
 PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 Oxidoreductase; NAD; Complete proteome.
 NP_BIND 228 234 NAD (ADP PART) (BY SIMILARITY).
 FT ACT_SITE 272 272 BY SIMILARITY.
 FT ACT_SITE 311 311 BY SIMILARITY.
 FT ACT_SITE 311 311 BY SIMILARITY.
 SQ SEQUENCE 515 AA; 56409 MW; DBB5DDF7D2DBBC0 CRC64;

 Query Match 74.0%; Score 37; DB 1; Length 515;
 Best Local Similarity 55.6%; Pred. No. 54;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 1 YSPGSPGT 9
 DB 13 YANPGTGS 21

 RESULT 19
 ZYX_CHICK
 ID ZYX_CHICK STANDARD; PRT; 542 AA.
 AC 004584;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zyxin.
 GN Zyxin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93107157; PubMed=1469049;
 RA Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
 RT "Zyxin and cCRP: two interactive LIM domain proteins associated with the cytoskeleton."
 RL J. Cell Biol. 119:1573-1587(1992).
 CC -1- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN CYTOSKELETON NEAR THE ADHESION PLAQUES.
 CC -1- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC IONS.

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EMBL: X69190; CAA48936.1; -
 PIR: A44358; A44358.
 InterPro: IPR001781; LIM.
 InterPro: IPR001841; Znf_ring.
 Pfam: PF00412; LIM; 3.
 ProDom: PD000094; LIM; 3.
 SMART: SM00132; LIM; 3.
 SMART: SM00184; RING; 1.
 PROSITE: PS00478; LIM_DOMAIN_1; 2.
 PROSITE: PS00023; LIM_DOMAIN_2; 3.
 Repeat: LIM domain; Metal-binding; Zinc; Cell adhesion.
 FT DOMAIN 83 90 PRO-RICH.
 FT DOMAIN 103 130 PRO-RICH.
 FT DOMAIN 352 411 LIM 1.
 FT DOMAIN 412 471 LIM 2.
 FT DOMAIN 472 538 LIM 3.
 FT VARIANT 463 463 D -> V.
 SQ SEQUENCE 542 AA; 58537 MW; 9D898AC180C680FC CRC64;

 Query Match 74.0%; Score 37; DB 1; Length 542;
 Best Local Similarity 75.0%; Pred. No. 57;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 2 SSPGSPGT 9
 DB 2 ASPGTPGT 9

 RESULT 20
 YQ36_CAEEL
 ID YQ36_CAEEL STANDARD; PRT; 963 AA.
 AC Q09457;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative cuticle collagen C09G5.6.
 GN C09G5.6
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Palmer S.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).
 CC -1- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-LINKS (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE COLLAGENS.

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 EMBL: Z46791; CAA86755.1; -
 WormPep: C09G5.6; CE01486.
 InterPro: IPR002486; Col_cuticle_N.
 InterPro: IPR000087; Collagen.
 Pfam: PF01391; Collagen; 2.
 Pfam: PF01484; Col_cuticle_N; 1.
 Hypothetical protein; Cuticle; Connective tissue; Repeat;
 KW Multigene family; 392
 FT DOMAIN 392 423 TRIPLE-HELICAL REGION.

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FT DOMAIN 441 503 TRIPLE-HELICAL REGION.
FT DOMAIN 506 567 TRIPLE-HELICAL REGION.
FT DOMAIN 563 666 POLY-PRO.
FT DOMAIN 685 688 POLY-PRO.
SQ SEQUENCE 963 AA; 107031 MW; AFT6895A75909F66E CRC64;

Query Match 74.0%; Score 37; DB 1; Length 963;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
D 1:1:1:1:1
Db 559 SAPGAPGT 566

RESULT 21
RSCG_RAT
ID RGSC_RAT STANDARD; PRT; 1387 AA.
AC O08774; O88383;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Regulator of G-protein signaling 12 (RGS12).
GN RGS12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97312490; PubMed=9168931;
RA Snow B.E., Antonio L., Suggs S., Gutstein H.B., Siderovski D.P.;
RT "Molecular cloning and expression analysis of rat Rgs12 and Rgs14.";
RL Biochem. Biophys. Res. Commun. 233:770-777(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98316347; PubMed=9651375;
RA Snow B.E., Hall R.A., Krumins A.M., Brothers G.M., Bouchard D.,
RA Brothers C.A., Chung S., Mangion J., Gilman A.G., Lefkowitz R.J.,
RA Siderovski D.P.;
RT "GTPase activating specificity of RGS12 and binding specificity of an
alternatively spliced PDZ (PSD-95/Dlg/ZO-1) domain.";
RL J. Biol. Chem. 273:17749-17755(1998).
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
THEIR INACTIVE GDP-BOUND FORM.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO ISOFORMS THAT ARISE
FROM ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN AND LUNG
AND LOWER LEVELS IN TESTIS, HEART, AND SPLEEN.
CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 PID DOMAIN.
CC -----
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CC -----
CC EMBL; U92280; AAC53176.1;
CC EMBL; AF035151; AAC40154.1;
CC HSP; P49799; IAGR.
CC InterPro; IPR003109; GoLoco.
CC InterPro; IPR001478; PDZ.
CC InterPro; IPR000050; PID_domain.
CC InterPro; IPR003116; RBD.
CC -----

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DR InterPro; IPR000342; RGS.
DR Pfam; PF02188; GoLoco; 1.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00640; PID; 1.
DR Pfam; PF02196; RBD; 2.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS/PROTEIN.
DR PRODOM; PD001580; RGS; 1.
DR SMART; SM00390; GoLoco; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00462; PTB; 1.
DR SMART; SM00455; RBD; 2.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS50106; PDZ; 1.
DR PROSITE; PS01179; PID; 1.
DR PROSITE; PS50132; RGS; 1.
KW Signal transduction inhibitor; Nuclear protein; Alternative splicing.
FT DOMAIN 21 97 PDZ.
FT DOMAIN 227 339 PID.
FT DOMAIN 715 832 RGS.
FT DOMAIN 1368 1373 POLY-PRO.
FT VARSPLIC 1 648 MISSING (IN ISOFORM PDZ-LESS).
FT VARSPLIC 649 666 SFGRRRSLRSLDDLE -> MNLEKGLSDSDVFDIDQO
(IN ISOFORM PDZ-LESS).
SQ SEQUENCE 1387 AA; 150468 MW; 958047D106B08310 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 1387;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
D 1:1:1:1:1
Db 1296 HSTPGPPT 1304

RESULT 22
WA_EMENI
ID WA_EMENI STANDARD; PRT; 1986 AA.
AC Q03149;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Conidial green pigment synthase (EC 2.3.1.-).
GN WA.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93101122; PubMed=1465094;
RA Mayorga M.E., Timberlake W.E.;
RT "The developmentally regulated Aspergillus nidulans WA gene encodes a
polypeptide homologous to polyketide and fatty acid synthases.";
RL Mol. Gen. Genet. 235:205-212(1992).
CC -!- FUNCTION: THIS PROTEIN CONDENSES CARBON UNITS TO FORM AN
INTERMEDIATE YELLOW POLYKETIDE PIGMENT THAT IS POLYMERIZED
BY CONIDIAL LACCASE TO FORM THE GREEN PIGMENT IN MATURE
ASEXUAL SPORES (CONIDIA).
CC -!- COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTHETINES
(POTENTIAL).
CC -!- PATHWAY: BIOSYNTHESIS OF CONIDIAL GREEN PIGMENT.
CC -!- SIMILARITY: CONTAINS 2 ACYL CARRIER DOMAINS.
CC -----
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CC -----

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CC EMBL; X75384; CAA53153.1; -
CC EMBL; U58137; AAB06948.1; -
CC HSP; P02836; 3HDD.
DR MGD; MGI:104806; Saxl.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein.
KW DOMAIN 88 96 POLY-GLU.
FT DOMAIN 143 148 POLY-ARG.
FT DNA_BIND 156 215 HOMEBOX.
FT DOMAIN 239 242 POLY-GLY.
SQ SEQUENCE 305 AA; 32012 MW; E02E09A40453FF1B CRC64;

Query Match 72.0%; Score 36; DB 1; Length 305;
Best Local Similarity 75.0%; Pred. No. 45; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0;

QY 2 SSPGSPGT 9
DB 134 ASPGSPGS 141

RESULT 24
PYCA.METJA STANDARD; PRT; 501 AA.
ID PYCA.METJA
AC Q58626;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
GN PYCA OR MJ1229.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A. DSM 2661 / ATCC 43067;
RC STRAIN=JAL-1 / DSM 2661; PubMed=8688087;
RX MEDLINE=96337999; PubMed=1195096;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Adams M.D., Reich C.I.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Overbeek R., Kirkness E.F., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Scott J.L., Geohagen N.S.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Utterback T.R., Kelley J.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Cotton M.D., Roberts K.M., Smith H.O., Woese C.R., Venter J.C.;
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
ET "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii".
RL Science 273:1058-1073(1996).
RN [2]
RP SEQUENCE OF 1-12, AND FUNCTION.
RX MEDLINE=21034791; PubMed=1195096;
RA Mukhopadhyay B., Patel V.J., Wolfe R.S.;
ET "A stable archaeal pyruvate carboxylase from the hyperthermophile Methanococcus jannaschii".
RL Arch. Microbiol. 174:406-414(2000).
CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
CC GROUP TO PYRUVATE IN THE SECOND.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +

DR EMBL; X65866; CAA46695.1; -
DR PTR; S28353; S28353.
DR InterPro; IPR001227; Acyltransf_domain.
DR InterPro; IPR000794; Ketoacyl-synt.
DR InterPro; IPR003880; Phosphopant_attch.
DR Pfam; PF00698; Acyl_transf; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt_C; 1.
DR Pfam; PF00550; pp-binding; 2.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
DR PROSITE; PS00606; B.KETOACYL SYNTHASE; 1.
DR PROSITE; PS00075; ACP_DOMAIN; 2.
KW Transferase; Phosphopantetheine; Multifunctional enzyme; Repeat.
FT DOMAIN 529 582 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT DOMAIN 991 1024 ACYL/MALONYL TRANSFERASES (BY SIMILARITY).
FT DOMAIN 1650 1719 ACYL CARRIER (ACP) 1.
FT DOMAIN 1772 1841 ACYL CARRIER (ACP) 2.
FT ACT_SITE 548 548 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT ACT_SITE 1001 1001 ACYL/MALONYL TRANSFERASES (BY SIMILARITY).
FT BINDING 1682 1682 PHOSPHOPANTETHEINE (BY SIMILARITY).
FT BINDING 1804 1804 PHOSPHOPANTETHEINE (BY SIMILARITY).
SQ SEQUENCE 1986 AA; 216634 MW; 74EF0940FF40EE9A CRC64;

Query Match 74.0%; Score 37; DB 1; Length 1986;
Best Local Similarity 87.5%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1;

QY 2 SSPGSPGT 9
DB 1749 SSPASPGT 1756

RESULT 23
SAX1_MOUSE STANDARD; PRT; 305 AA.
ID SAX1_MOUSE
AC P42580;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Homeobox protein SAX-1 (NKX-1.1).
GN SAX1 OR NKX1-1 OR NKX-1.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=95399317; PubMed=7669696;
RA Schubert F.R., Fainsod A., Gruenbaum Y., Gruss P.;
RT "Expression of the novel murine homeobox gene Sax-1 in the developing nervous system".
RL Mech. Dev. 51:99-114(1995).
RN [2]
RP SEQUENCE OF 289-305 FROM N.A.
RC STRAIN=BALB/C;
RA Hong S.B., Kim S.J., Noh M.J., Lee Y.M., Kim Y.S., Yoo O.J.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY FUNCTION IN CELL SPECIFICATION, PARTICULARLY IN THE CNS.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING POSTERIOR CENTRAL NERVOUS SYSTEM. FIRST SEEN IN THE ECTODERM LATERAL TO THE PRIMITIVE STREAM, LATER IT ENCOMPASSES THE NEURAL PLATE. STARTING AT DAY 9.5 PC, IT IS EXPRESSED IN DISTINCT AREAS OF SPINAL CORD, HINDBRAIN, MIDBRAIN AND FOREBRAIN.
CC -!- SIMILARITY: BELONGS TO THE NK-1 FAMILY OF HOMEBOX PROTEINS.
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CC CC oxaloacetate.
 CC CC COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
 CC CC BICARBONATE.
 CC CC -1- ENZYME REGULATION: INHIBITED BY MAGNESIUM, WHEN ITS CONCENTRATION
 CC CC EXCEEDED THE ATP ONE, AND BY HIGH CONCENTRATION OF ATP AND ALPHA-
 CC CC KETOGLUTARATE.
 CC CC -1- PATHWAY: GLUCONEOGENESIS.
 CC CC -1- SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS.
 CC CC -1- MASS SPECTROMETRY: MW=55500; METHOD=MALDI.
 CC CC -1- MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE
 CC CC IS 80-90 DEGREES CELSIUS.
 CC CC -1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
 CC CC AND CARBAMYL PHOSPHATE SYNTHETASES.
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 CC CC EMBL: U67563; AAB99432.1;
 CC CC HSSP: P24182; 1BNC.
 CC CC TIGR: MJ1229;
 CC CC InterPro: IPR000901; CPSase.
 CC CC Pfam: PF02785; Biotin_carb.C; 1.
 CC CC Pfam: PF00289; CPSase_Lchain; 1.
 CC CC Pfam: PF02786; CPSase_LD2; 1.
 CC CC PROSITE: PS00866; CPSase_1; 1.
 CC CC PROSITE: PS00867; CPSase_2; 1.
 CC CC Lgase: Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
 CC CC ATP-binding; Complete proteome.
 CC CC NP_BIND 162 167 ATP (POTENTIAL).
 CC CC ACT_SITE 291 291 POTENTIAL.
 CC CC SEQUENCE 501 AA; 55402 MW; 04D2E401892F872F CRC64;

Query Match 72.0%; Score 36; DB 1; Length 501;
 Best Local Similarity 75.0%; Pred. No. 77;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSPSPGPG 8 72.0%; Score 36; DB 1; Length 501;
 Best Local Similarity 75.0%; Pred. No. 77;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 357 YRSPGPG 364
 RESULT 25
 GUNB_PSEFL STANDARD; PRT; 511 AA.
 ID GUNB_PSEFL STANDARD; PRT; 511 AA.
 AC P18126;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Endoglucanase B precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
 DE (Cellulase) (ECB).
 GN CELB.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 CC NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-48.
 RC STRAIN=SP. CELLULOSA;
 RX MEDLINE=90355836; PubMed=2117693;
 RA Gilbert H.J., Hall J., Hazlewood G.P., Ferreira L.M.A.;
 RT "The N-terminal region of an endoglucanase from Pseudomonas
 RT fluorescens subspecies cellulosa constitutes a cellulose-binding
 RT domain that is distinct from the catalytic centre.";
 RL Mol. Microbiol. 4:759-767(1990).
 CC -1- FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF 1,4-BETA-
 CC GLUCOSIDIC LINKAGES IN CELLULOSE, LICHENIN AND CEREAL BETA-D-
 CC GLUCANS. EGB IS MOST ACTIVE AGAINST BARLEY BETA-GLUCAN, BUT SHOWED

CC CC SIGNIFICANT ACTIVITY AGAINST AMORPHOUS AND CRISTALLINE CELLULOSE.
 CC CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC CC linkages in cellulose.
 CC CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC CC -1- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
 CC CC (CBD).
 CC CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
 CC CC HYDROLASES).
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 CC CC or send an email to license@isb-sib.ch).
 CC CC EMBL: X52615; CAA36844.1;
 CC CC PIR: S10527; S10527.
 CC CC HSSP: P43316; 2ENG.
 CC CC InterPro: IPR001919; CBD_2.
 CC CC InterPro: IPR002883; CBD_5.
 CC CC InterPro: IPR000334; Glyco_hydro_45.
 CC CC Pfam: PF00553; CBD_2; 1.
 CC CC Pfam: PF02013; CBD_5; 1.
 CC CC Pfam: PF02015; Glyco_hydro_45; 1.
 CC CC PROSITE: PS00561; CBD_BACTERIAL; 1.
 CC CC PROSITE: PS01140; GLYCOSYL_HYDROL_F45; 1.
 CC CC Cellulose degradation; Hydrolase; Glycosidase; Signal; Periplasmic.
 CC CC SIGNAL 1 29
 CC CC CHAIN 30 511 ENDOGLUCANASE B.
 CC CC DOMAIN 30 131 CELLULOSE-BINDING (BY SIMILARITY).
 CC CC DOMAIN 132 173 SER-RICH (LINKER).
 CC CC DOMAIN 223 259 SER-RICH.
 CC CC DISULFID 32 127 BY SIMILARITY.
 CC CC ACT_SITE 276 276 NUCLEOPHILE (BY SIMILARITY).
 CC CC ACT_SITE 393 393 PROTON DONOR (BY SIMILARITY).
 CC CC SEQUENCE 511 AA; 52078 MW; 3C3119D998291D8E CRC64;

Query Match 72.0%; Score 36; DB 1; Length 511;
 Best Local Similarity 55.6%; Pred. No. 78;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPSPGPG 9
 Best Local Similarity 55.6%; Pred. No. 78;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 360 YNAPGDPGS 368
 RESULT 26
 BUD8_YEAST STANDARD; PRT; 603 AA.
 ID BUD8_YEAST STANDARD; PRT; 603 AA.
 AC P41698; Q06482;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Bud site selection protein BUD8.
 GN BUD8 OR YLR353W OR L9638.3.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harkins H.A., Pringle J.R.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Meneses S.,

Wed May 22 11:04:43 2002

Cloning of the human and mouse type X collagen genes and mapping of the mouse type X collagen gene to chromosome 10.
Eur. J. Biochem. 206:217-224(1992).

(4) SEQUENCE OF 385-627 FROM N.A.

STRAIN=CS57BL;
MEDLINE=92182017; PubMed=1543751;
Elma K., Metsaranta M., Kallio J., Perälä M., Eerola I.,
Garofalo S., de Crombrughe B., Vuorio E.;
"Specific hybridization probes for mouse alpha 2(IX) and alpha 1(X)
collagen mRNAs";
Biochim. Biophys. Acta 1130:78-80(1992).
CC -!- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHERMIC
CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.

CC -!- SUBUNIT: HOMOTRIMER.
CC -!- PIV: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -!- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

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CC EMBL: X67348; CAA47763.1; -
CC EMBL: X65121; CAA46237.1; -
CC EMBL: X63013; CAA44741.1; -
CC EMBL: Z21610; CAA79736.1; -
CC PIR: S28807; S28807.
CC PIR: S31216; S31216.
CC PIR: S22215; S22215.
CC MGD: MGI:88445; Col10a1.
CC InterPro: IPR001073; C1q.
CC InterPro: IPR000087; Collagen.
CC Pfam: PF00386; C1q; 1.
CC PRINTS: PR00007; COMPLEMENTC1Q.
CC SMART: SM00110; C1Q; 1.
CC PROSITE: PS01113; C1Q; 1.
CC Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
CC Cartilage; Collagen; signal.
CC SIGNAL 18
CC CHAIN 19 680
CC DOMAIN 19 56
CC DOMAIN 57 519
CC DOMAIN 520 680
CC DOMAIN 545 680
CC CONFLICT 248 248
CC CONFLICT 286 286
CC CONFLICT 306 306
CC CONFLICT 417 417
CC CONFLICT 451 451
CC CONFLICT 500 500
CC CONFLICT 567 567
CC CONFLICT 569 569
CC CONFLICT 571 572
CC CONFLICT 571 635
CC SEQUENCE 680 AA; 66775 MW; FE984CA99AF708E2 CRC64;
POTENTIAL.
COLLAGEN ALPHA 1(X) CHAIN.
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
C1Q.
P -> L (IN REF. 3).
A -> S (IN REF. 2).
L -> F (IN REF. 3).
T -> S (IN REF. 3).
R -> K (IN REF. 4).
H -> L (IN REF. 3).
A -> C (IN REF. 3).
I -> H (IN REF. 3).
FD -> Y (IN REF. 3).
Q -> T (IN REF. 3).

Query Match 72.0%; Score 36; DB 1; Length 680;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSPSPGSPG 8
Db 193 YGSPGPRPG 200

RA Miller N., Nhan M., Pauley A., Peluso D., Rifkin L., Riles L.,
RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., Waterston R.;
RA Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST BUD9.
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CC EMBL: L37016; AAA64518.1; -
CC EMBL: U19102; AAB67749.1; -
CC SGD: S0004345; BUD9.
CC DOMAIN 84 95
CC CONFLICT 140 140
CC CONFLICT 145 145
CC CONFLICT 221 221
CC CONFLICT 350 350
CC CONFLICT 354 354
CC CONFLICT 422 422
CC CONFLICT 602 602
CC SEQUENCE 603 AA; 66288 MW; 83F8843CA47656C4 CRC64;
POLY-SER.
R -> W (IN REF. 1).
V -> M (IN REF. 1).
Y -> C (IN REF. 1).
S -> N (IN REF. 1).
T -> M (IN REF. 1).
MISSING (IN REF. 1).
R -> L (IN REF. 1).

Query Match 72.0%; Score 36; DB 1; Length 603;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
Db 299 SPGAPGT 305

RESULT 27
ID CAIA_MOUSE STANDARD; PRT; 680 AA.
AC Q05306;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Collagen alpha 1(X) chain precursor.
GN COL10A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=BALB/C;
MEDLINE=93143676; PubMed=8424763;
Elma K., Eerola I., Rosati R., Metsaranta M., Garofalo S., Perälä M.,
de Crombrughe B., Vuorio E.;
"The mouse collagen X gene: complete nucleotide sequence, exon
structure and expression pattern";
Biochem. J. 289:247-253(1993).
[2]
SEQUENCE FROM N.A.
STRAIN=129/SV; TISSUE=Liver;
MEDLINE=93238750; PubMed=8477738;
Kong R.Y.C., Kwan K.M., Lau E.T., Thomas J.T., Boot-Handford R.P.,
Grant M.E., Cheah K.S.E.;
"Intron-exon structure, alternative use of promoter and expression of
the mouse collagen X gene, Col10a1";
Eur. J. Biochem. 213:99-111(1993).
[3]
SEQUENCE OF 51-680 FROM N.A.
STRAIN=DRA/2J;
MEDLINE=92267014; PubMed=1587271;
Apte S.S., Seldin M.F., Hayashi M., Olsen B.R.;

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RESULT 28
TRI2_STRCO
ID TRI2_STRCO STANDARD; PRT; 1171 AA.
AC Q9RKB9;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Putative tricorn protease homolog 2 (EC 3.4.21.-).
GN TRI2 OR SCE87.19.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D., Thomson N.R., Parkhill J., Barrell B.G.,
RA Rejandream M.A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Degrades oligopeptides in a sequential manner
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S41 (SERINE PROTEASE).
CC
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CC
CC EMBL: AL132674; CAB59664.1;
CC DR MEROPS; S41A;
CC DR InterPro: IPR003581; TSPC.
CC DR SMART; SM00245; TSPC.1.
CC KW Hydrolase; Serine protease.
FT DOMAIN 842 941
FT SITE 1022 1022 PD2-LIKE.
FT FT SUBSTRATE SPECIFICITY SWITCH (BY
FT FT SIMILARITY).
FT ACT_SITE 827 827 BY SIMILARITY.
FT ACT_SITE 1051 1051 SUBSTRATE-BINDING (BY SIMILARITY).
FT ACT_SITE 1052 1052 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 1171 AA; 125660 MW; 9C53019CEC0B0A25 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 1171;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
Db 487 TPGSPGT 493

RESULT 29
MAP2_HUMAN
ID MAP2_HUMAN STANDARD; PRT; 1827 AA.
AC P11137; Q99975;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE Microtubule-associated protein 2 (MAP 2) (MAP2B) [Contains: MAP2C].
GN MAP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Price R.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.

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[2]
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP TISSUE=Brain;
RC MEDLINE=941124038; PubMed=8294038;
RA Albala J.S., Kalcheva N., Shafit-Zagardo B.;
RT "Characterization of the transcripts encoding two isoforms of human
RL microtubule-associated protein-2 (MAP-2).";
RN Gene 136:377-378(1993).
RP SEQUENCE OF 493-1562 FROM N.A.
RC MEDLINE=88274407; PubMed=2455776;
RA Kosik K.S., Orecchio L.D., Bakalis S., Duffy L., Neve R.L.;
RT "Partial sequence of MAP2 in the region of a shared epitope with
RL J. Neurochem. 51:587-598(1988).
CC -1- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
CC ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
CC FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC
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CC
CC EMBL: U01828; AAA03354.1;
CC DR EMBL; U89330; AAB48098.1;
CC DR EMBL; U89329; AAB48097.1;
CC DR EMBL; M25668; AAA59552.1;
CC DR PIR; P10024; QRHUMT.
CC DR MIN; 157130;
CC DR InterPro: IPR001084; Tubulin-bind.
CC DR Pfam: PF00418; tubulin-binding; 3.
CC DR PROSITE; PS00229; TAU_MAP; 2.
CC KW Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
FT DOMAIN 1447 1467 CALMODULIN-BINDING (POTENTIAL).
FT REPEAT 1661 1691 TAU/MAP MOTIF.
FT REPEAT 1692 1722 TAU/MAP MOTIF.
FT REPEAT 1723 1754 TAU/MAP MOTIF.
FT VARSPLIC 152 1507 MISSING (IN ISOFORM MAP2C).
FT CONFLICT 9 9 A -> G (IN REF. 2).
FT CONFLICT 37 37 R -> A (IN REF. 2).
FT CONFLICT 108 108 A -> G (IN REF. 2).
FT CONFLICT 152 155 MISSING (IN REF. 2).
FT CONFLICT 187 187 S -> K (IN REF. 2).
FT CONFLICT 1655 1655 A -> GL (IN REF. 2).
FT CONFLICT 1736 1736 V -> A (IN REF. 2).
SQ SEQUENCE 1827 AA; 199610 MW; BAC36D0030F5F455 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 1827;
Best Local Similarity 72.7%; Pred. No. 3e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 1 YSS--PGSPGT 9
Db 1609 YSSRTPTGTPGT 1619

RESULT 30
MAP2_MOUSE
ID MAP2_MOUSE STANDARD; PRT; 1828 AA.
AC P20357;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Microtubule-associated protein 2 (MAP 2).

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us-09-734-281-2.rsp

Wed May 22 11:04:43 2002

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GN MAP2 OR MTAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=89083571; PubMed=3205744;
RX Wang D., Lewis S.A., Cowan N.J.;
RA "Complete sequence of a cDNA encoding mouse MAP2.";
RL Nucleic Acids Res. 16:11369-11370(1988).
RN [2]
RP MEDLINE=90043973; PubMed=3142041;
RX Lewis S.A., Wang D., Cowan N.J.;
RA "Microtubule-associated protein MAP2 shares a microtubule binding
  motif with tau protein.";
RL Science 242:936-939(1988).
RN [3]
RP MEDLINE=9365159; PubMed=2770869;
RX Papadimitrakopoulou A., Doll T., Tucker R.P., Garner C.C., Matus A.;
RA "Embryonic MAP2 lacks the cross-linking sidearm sequences and
  dendritic targeting signal of adult MAP2.";
RL Nucleic Acids Res. 18:361-361(1990).
RN [4]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=94110302; PubMed=8282767;
RX Doll T., Meichsner M., Riederer B.M., Honegger P., Matus A.;
RA "An isoform of microtubule-associated protein 2 (MAP2) containing
  four repeats of the tubulin-binding motif.";
RL Cell Sci. 106:633-640(1993).
RN [5]
RP SEQUENCE OF 1695-1725 FROM N.A.
RX MEDLINE=94110302; PubMed=8282767;
RX Doll T., Meichsner M., Riederer B.M., Honegger P., Matus A.;
RA "An isoform of microtubule-associated protein 2 (MAP2) containing
  four repeats of the tubulin-binding motif.";
RL Cell Sci. 106:633-640(1993).
RN [6]
RP FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
  STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
  SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
RN [7]
RP ALTERNATIVE SPLICING: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
  ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
  FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
RN [8]
RP DEVELOPMENTAL STAGE: MAP2C IS EXPRESSED DURING EMBRYONIC BRAIN
  DEVELOPMENT AND UNTIL POSTNATAL DAY 10. MAP2B IS EXPRESSED
  THROUGHOUT BRAIN DEVELOPMENT.
RN [9]
RP SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
RN [10]
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RN [11]
RP EMBL; M21041; AAA39490.1;
RP PIR; S06467; S06467.
RP MGI; 97175; Mtap2.
RP InterPro; IPR001084; Tubulin-bind.
RP Pfam; PF00418; tubulin-binding; 3.
RP PROSITE; PS00229; TAU_MAP; 2.
RN [12]
RP Microtubules; Repeat; Calmodulin-binding.
KW DOMAIN 1452 1472 CALMODULIN-BINDING (POTENTIAL).
FT REPEAT 1662 1692 TAU/MAP MOTIF.
FT REPEAT 1693 1723 TAU/MAP MOTIF.
FT REPEAT 1724 1755 TAU/MAP MOTIF.
SQ SEQUENCE 1828 AA; 198980 MW; 200BC59E360538CA CRC64;

Query Match 72.0%; Score 36; DB 1; Length 1828;
Best Local Similarity 72.7%; Pred. No. 3e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 1 YSS--PGSPGT 9
DB 1613 YSSRTPGTPGT 1623

RESULT 31
MAP2_RAT STANDARD; PRT; 1861 AA.
AC P15146;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Microtubule-associated protein 2 (MAP 2) (MAP2B) [Contains: MAP2C].
GN MAP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
RX STRAIN-WISTAR; TISSUE=Brain;
RL MEDLINE=90251471; PubMed=2339070;
RX Kindler S., Schwanke B., Schulz B., Garner C.C.;

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RT "Complete cDNA sequence encoding rat high and low molecular weight
  MAP2.";
RL Nucleic Acids Res. 18:2822-2822(1990).
RN [2]
RP SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
RX STRAIN-WISTAR; TISSUE=Brain;
RL MEDLINE=91060576; PubMed=2174050;
RX Kindler S., Schulz B., Goedert M., Garner C.C.;
RA "Molecular structure of microtubule-associated protein 2b and 2c from
  rat brain.";
RL J. Biol. Chem. 265:19679-19684(1990).
RN [3]
RP SEQUENCE OF 1-151; 1515-1694 AND 1726-1861 FROM N.A.
RX MEDLINE=90221819; PubMed=2326166;
RX Doll T., Papadimitrakopoulou A., Matus A.;
RA "Nucleotide and amino acid sequences of embryonic rat MAP2c.";
RL Nucleic Acids Res. 18:361-361(1990).
RN [4]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=89365159; PubMed=2770869;
RX Papadimitrakopoulou A., Doll T., Tucker R.P., Garner C.C., Matus A.;
RA "Embryonic MAP2 lacks the cross-linking sidearm sequences and
  dendritic targeting signal of adult MAP2.";
RL Nature 340:650-652(1989).
RN [5]
RP SEQUENCE OF 1695-1725 FROM N.A.
RX MEDLINE=94110302; PubMed=8282767;
RX Doll T., Meichsner M., Riederer B.M., Honegger P., Matus A.;
RA "An isoform of microtubule-associated protein 2 (MAP2) containing
  four repeats of the tubulin-binding motif.";
RL Cell Sci. 106:633-640(1993).
RN [6]
RP FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
  STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
  SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
RN [7]
RP ALTERNATIVE SPLICING: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
  ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
  FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
RN [8]
RP DEVELOPMENTAL STAGE: MAP2C IS EXPRESSED DURING EMBRYONIC BRAIN
  DEVELOPMENT AND UNTIL POSTNATAL DAY 10. MAP2B IS EXPRESSED
  THROUGHOUT BRAIN DEVELOPMENT.
RN [9]
RP SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
RN [10]
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
RN [11]
RP EMBL; X51842; CAA36135.1;
RP EMBL; X17682; CAA35667.1;
RP EMBL; X71487; CAA50588.1;
RP PIR; S07887; S07887.
RP PIR; S10003; S10003.
RP InterPro; IPR001084; Tubulin-bind.
RP Pfam; PF00418; tubulin-binding; 4.
RP PROSITE; PS00229; TAU_MAP; 3.
RN [12]
RP Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
KW DOMAIN 1454 1474 CALMODULIN-BINDING (POTENTIAL).
FT REPEAT 1664 1694 TAU/MAP MOTIF.
FT REPEAT 1695 1725 TAU/MAP MOTIF.
FT REPEAT 1726 1756 TAU/MAP MOTIF.
FT REPEAT 1757 1788 TAU/MAP MOTIF.
FT VARSPLIC 152 1514 MISSING (IN ISOFORM MAP2C).
FT VARSPLIC 1695 1725 MISSING (IN ISOFORM WITH 3 TAU/MAP
  REPEATS).
SQ SEQUENCE 1861 AA; 202409 MW; 42DCF116D21EF54E CRC64;

Query Match 72.0%; Score 36; DB 1; Length 1861;
Best Local Similarity 72.7%; Pred. No. 3.1e+02;

```


Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 QY 1 YSS--PGSPGT 9
 DB 1615 YSSRTGTGTGT 1625

RESULT 32
 CDNL_MOUSE
 ID CDNL_MOUSE STANDARD; PRT; 159 AA.
 AC P39689;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1 (Melanoma differentiation
 associated protein) (P21) (CDK-interacting protein 1).
 GN CDRN1A OR CIP1 OR WAF1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BXSB; TISSUE=Spleen;
 RA Huppi K., Siwarski D., Dosik J., Michieli P., Chedid M., Reed S.,
 Mock B., Givol D., Mushinski J.F.,
 RT "Molecular cloning, sequencing, chromosomal localization and
 expression of mouse p21 (Waf1)."
 RL Oncogene 9:3017-3020(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95316868; PubMed=7796420;
 RA El-Deiry W.S., Tokino T., Waldman T., Velculescu V., Oliner J.D.,
 Burrell M., Hill D.E., Rees J.L., Hamilton S.R., Kinzler K.W.,
 RT Vogelstein B.;
 RT "Topological control of p21WAF1/CIP1 expression in normal and
 neoplastic tissues."
 RL Cancer Res. 55:2910-2919(1995).
 RN [3]
 RP SEQUENCE OF 1-143 FROM N.A.
 RX MEDLINE=94061997; PubMed=824752;
 RA El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons R.,
 Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;
 RT "WAF1, a potential mediator of p53 tumor suppression."
 RL Cell 75:817-825(1993).
 CC -!- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
 ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
 DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
 ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
 KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- INDUCTION: BY P53, MEZEREIN (ANTILEUKEMIC COMPOUND) AND INTERFERON
 BETA.
 CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
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 or send an email to license@isb-sib.ch).
 CC EMBL; U09507; AAB60456.1; -;
 DR EMBL; U24173; AAC52220.1; -;
 DR PIR; A49438; A49438.
 DR HSSP; P46527; IJUS.
 DR MGI; MGI:104556; Cdkn1a.
 DR InterPro; IPR003175; Cdi.
 DR Pfam; PF02234; Cdi; 1.
 KW Cell cycle; Nuclear protein; Zinc-finger.
 FT ZN_FING 12 40 C4-TYPE (POTENTIAL).

FT CONFLICT 30 30 R -> S (IN REF. 3).
 FT CONFLICT 56 57 TP -> RQ (IN REF. 3).
 SQ SEQUENCE 159 AA; 17785 MW; 37B7C22B9A2FD089 CRC64;
 Query Match 70.0%; Score 35; DB 1; Length 159;
 Best Local Similarity 85.7%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SPGSPGT 9
 DB 125 SPGPGGT 131
 III III
 RESULT 33
 UR2R_RAT
 ID UR2R_RAT STANDARD; PRT; 386 AA.
 AC P49684; P48041;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urotensin II receptor (UR-II-R) (G protein-coupled sensory epithelial
 neuro peptide-like receptor) (SENR).
 GN GPR14.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96115583; PubMed=8666380;
 RA Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R.,
 Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
 O'Dowd B.F., Docherty J.M.;
 RT "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
 and GPR14, encoding receptors related to interleukin 8, neuropeptide
 Y, and somatostatin receptors."
 RL Genomics 29:335-344(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Circumvallate papillae;
 MEDLINE=95251679; PubMed=7733947;
 RA Tal M., Ammar D.A., Karpuz M., Krizhanovsky V., Naim M.,
 Thompson D.A.;
 RT "A novel putative neuropeptide receptor expressed in neural tissue,
 including sensory epithelia."
 RL Biochem. Biophys. Res. Commun. 209:752-759(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=WISTAR; TISSUE=Urinary bladder;
 Suga H., Takao K.;
 RT "Expression of the rat SENR in the urinary bladder tissues."
 Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR UROSENSIN II. THE ACTIVITY OF
 THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A
 PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (BY
 SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein
 CC -!- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN NEURAL AND SENSORY
 CC TISSUES.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 or send an email to license@isb-sib.ch).
 CC EMBL; U32673; AAC52593.1; -;
 DR EMBL; U23483; AAA80111.1; -;
 DR EMBL; AB012210; BAA25251.1; -;

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DR EMBL: D90205; BAA14231.1; -

DR PIR: S12357; S12357

DR MGD: MGI:96558; IL5ra

DR InterPro: IPR002996; CRLA

DR InterPro: IPR003532; Hematopoietic_receptor_S_F2

DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1

DR Receptor; Transmembrane; Glycoprotein; Signal

DR SIGNAL 1 17

FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN

FT DOMAIN 18 339 EXTRACELLULAR (POTENTIAL)

FT TRANSMEM 340 361 POTENTIAL

FT DOMAIN 362 415 CYTOPLASMIC (POTENTIAL)

FT DISULFID 131 152 BY SIMILARITY

FT CARBOHYD 32 32 N-LINKED (GLCNAC. .) (POTENTIAL)

FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL)

FT CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL)

FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL)

SQ SEQUENCE 415 AA; 46989 MW; A4326D292571C08 CRC64;

Query Match 70.0%; Score 35; DB 1; Length 415;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGSPT 9

DB 119 PGSPT 124

RESULT 35

HXKG_ASPNG STANDARD; PRT; 495 AA.

AC Q92407; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Glucokinase (EC 2.7.1.2) (Glucose kinase) (GLK)

GN GLKA.

OS Aspergillus niger

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX NCBI_TaxID=5061;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CHS 120.49 / N400;

RX MEDLINE=97008939; PubMed=8856049;

RA Panneman H., Ruljter G.J.G., van den Broeck H.C., Driever E.T.M., Visser J.;

RT "Cloning and biochemical characterisation of an Aspergillus niger glucokinase. Evidence for the presence of separate glucokinase and hexokinase enzymes."

RT Eur. J. Biochem. 240:518-525(1996).

CC -1- FUNCTION: THE ENZYME HAS GREAT AFFINITY FOR GLUCOSE. MANNOSE, 2-DEOXYGLUCOSE AND GLUCOSAMINE CAN SERVE AS SUBSTRATES. ACTIVITY IS RELATIVELY CONSTANT BETWEEN PH 7.5 AND PH 9.0. BELOW PH 7.5, THE ACTIVITY DECREASES WITH PH.

CC -1- CATALYTIC ACTIVITY: ATP + D-glucose -> ADP + D-glucose 6-phosphate.

CC -1- SUBUNIT: MONOMER (PROBABLE).

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QY 3 SPGSPT 9

DB 341 SPGSPTS 347

RESULT 34

IL5R_MOUSE STANDARD; PRT; 415 AA.

AC P21183; 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Interleukin-5 receptor alpha chain precursor (IL-5R-alpha)

GN IL5RA OR IL5R.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91092260; PubMed=2265612;

RA Takaki S., Tomimaga A., Mita S., Sonoda E., Yamaguchi N., Takatsu K.; cloning and expression of the murine interleukin-5 receptor."

RT "Molecular cloning and expression of the murine interleukin-5 receptor."

RT EMBO J. 9:4367-4374(1990).

CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN BINDS TO IL-5.

CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO ON B-CELLS.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.

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SEQUENCE FROM N.A.
TISSUE-Testis;
MEDLINE=20035680; PubMed=10589763;
Masiakos P.T., MacLaughlin D.T., Maheswaran S., Teixeira J.,
Fuller A.F. Jr., Shah P.C., Ketas D.J., Kenneally M.K.,
Dombkowski D.M., Ha T.U., Preffer F.I., Donahoe P.K.:
"Human ovarian cancer, cell lines, and primary ascites cells express
the human Mullerian inhibiting substance (MIS) type II receptor,
bind, and are responsive to MIS".
Clin. Cancer Res. 5:3488-3499(1999).
-|- FUNCTION: RECEPTOR FOR ANTI-MULLERIAN HORMONE.
-|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-|- SUBCELLULAR LOCATION: Type I membrane protein.
-|- DISEASE: DEFECTS IN AMHR2 ARE THE CAUSE OF PERSISTENT MULLERIAN
DUCT SYNDROME TYPE II (PMDS-2); A FORM OF MALE
PSEUDOHERMAPHRODITISM CHARACTERIZED BY A FAILURE OF MUELLERIAN

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Query Match          70.0%; Score 35; DB 1; Length 573;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PGSPGT 9
        |||||
Db       126 PGSPGT 131

RESULT 37
MRKC_KLEPN
ID MRKC_KLEPN STANDARD; PRT; 828 AA.
AC 221647;
DDT 01-MAY-1991 (Rel. 18, Created)
DDT 01-MAY-1991 (Rel. 18, Last sequence update)
DDT 01-NOV-1995 (Rel. 32, Last annotation update)
DDE Outer membrane usher protein mrkc precursor.
MRKC.
SS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
NCBI_TaxID=573;
OX

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Wed May 22 11:04:43 2002

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[1]
RN SEQUENCE FROM N.A.
RC STRAIN=IA565; PubMed=1670938;
RX MEDLINE=91100388; G-F., Clegg S.;
RA Allen B.L., Gerlach G.-F., Clegg S.;
RT "Nucleotide sequence and functions of mrk determinants necessary for
RT expression of type 3 fimbriae in Klebsiella pneumoniae.";
RL J. Bacteriol. 173:916-920(1991).
CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF THE TYPE 3
CC FIMBRIAL SUBUNIT (MRKA).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (By similarity).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC
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CC
CC EMBL; M55912; AAA25095.1; -.
CC PIR; D39142; D39142.
CC InterPro: IPR00015; Fimb_usher.
CC Pfam: PF00577; Usher; 1.
CC PROSITE; PS01151; FIMBRIAL_USHER; 1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 828 OUTER MEMBRANE USHER PROTEIN MRKC.
FT DISULFID 813 827 POTENTIAL.
FT SEQUENCE 828 AA; 91049 MW; B30EDF3798249FC9 CRC64;
SQ
Query Match 70.0%; Score 35; DB 1; Length 828;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGSPGT 9
Db 693 PGSPGT 698
RESULT 38
VGLB_HSVIF STANDARD; PRT; 903 AA.
ID VGLB_HSVIF
AC P06436;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein B precursor.
DE GB OR UL27.
GN Herpes simplex virus (type 1 / strain F).
OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10304;
RN [1]
RP MEDLINE=85083254; PubMed=2981343;
RA Pellett P.E., Kousoulas K.G., Pereira L., Roizman B.;
RT "Anatomy of the herpes simplex virus 1 strain F glycoprotein B gene:
RT primary sequence and predicted protein structure of the wild type and
RT of monoclonal antibody-resistant mutants.";
RL J. Virol. 53:243-253(1985).
RN [2]
RP SEQUENCE OF 1-176 FROM N.A.
RP MEDLINE=88306232; PubMed=2457278;
RX Hammerschmidt W., Conraths F., Mankertz J., Buhk H.-J., Pauli G.,
RA Ludwig H.;
RT "Common epitopes of glycoprotein B map within the major DNA-binding
RT proteins of bovine herpesvirus type 2 (BHV-2) and herpes simplex
RT virus type 1 (HSV-1).";
RL Virology 165:406-418(1988).

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CC -1- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC GB, GC, GG, GD, GI, AND GE.
CC -1- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC REQUIRED FOR VIRAL GROWTH.
CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M4164; AAA45776.1; -.
CC EMBL; M21633; AAA45788.1; -.
CC PIR; A03750; VGBEB1.
CC InterPro: IPR000234; Glycoprot_B.
CC Pfam: PF00606; Glycoprotein_B; 1.
CC ProDom: PD000693; Glycoprot_B; 1.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 903 GLYCOPROTEIN B.
FT DOMAIN 21 729 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 730 745 POTENTIAL.
FT TRANSMEM 751 770 POTENTIAL.
FT DOMAIN 774 794 POTENTIAL.
FT DOMAIN 795 903 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 673 673 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 903 AA; 100104 MW; 73BDCA7813DB35E8 CRC64;
SQ
Query Match 70.0%; Score 35; DB 1; Length 903;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSPGSPG 8
Db 32 SSPGTPG 38
RESULT 39
VGLB_HSV11 STANDARD; PRT; 904 AA.
ID VGLB_HSV11
AC P10211;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein B precursor.
DE GB OR UL27.
GN Herpes simplex virus (type 1 / strain 17).
OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10299;
RN [1]
RP MEDLINE=88274327; PubMed=2839594;
RX McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA McNab D., Perry L.J., Scott J.E., Taylor P.;
RT "The complete DNA sequence of the long unique region in the genome of
RT herpes simplex virus type 1";
RL J. Gen. Virol. 69:1531-1574(1988).
CC -1- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC GB, GC, GG, GD, GI, AND GE.
CC -1- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC REQUIRED FOR VIRAL GROWTH.

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CC CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR DR EMBL: D10879; BAA01673.1; -
DR DR EMBL: X14112; CAA32320.1; -
DR DR PIR: I30084; VGBEW7.
DR DR InterPro: IPR000234; Glycoprot_B.
DR DR Pfam: PF00606; Glycoprotein_B; 1.
DR DR ProDom: PD000693; Glycoprot_B; 1.
KW KW Glycoprotein; Transmembrane; Signal.
FT FT SIGNAL 1 30
FT FT CHAIN 31 904 GLYCOPROTEIN B.
FT FT DOMAIN 31 730 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 731 746 POTENTIAL.
FT FT TRANSMEM 752 771 POTENTIAL.
FT FT TRANSMEM 775 795 POTENTIAL.
FT FT DOMAIN 796 904 CYTOPLASMIC (POTENTIAL).
FT FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SQ SEQUENCE 904 AA; 100292 MW; 2C14E8B1284C1E3A CRC64;

Query Match 70.0%; Score 35; DB 1; Length 904;
Best Local Similarity 85.7%; Pred. No. 2.le+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPG 8
DB 33 SSPGTPG 39

RESULT 40
VGLB_HSV1P
ID VCLB_HSV1P STANDARD; PRT; 904 AA.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein B precursor.
DE GB OR UL27.
OS Herpes simplex virus (type 1 / strain Patton).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10308;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87112925; PubMed=3027364;
RA Stuve L.L., Brown-Shimer S., Fachi C., Najarian R., Dina D.,
RA Burke R.L.;
RT "Structure and expression of the herpes simplex virus type 2
RT glycoprotein gb gene."
RL J. Virol. 61:326-335(1987).
CC CC -1- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC CC GB, CC, GG, GD, GI, AND GE.
CC CC -1- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC CC REQUIRED FOR VIRAL GROWTH.
CC CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC CC -----
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CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR DR EMBL: K03541; AAA45778.1; -
DR DR InterPro: IPR000234; Glycoprot_B.
DR DR Pfam: PF00606; Glycoprotein_B; 1.
DR DR ProDom: PD000693; Glycoprot_B; 1.
KW KW Glycoprotein; Transmembrane; Signal.
FT FT SIGNAL 1 30
FT FT CHAIN 31 904 GLYCOPROTEIN B.
FT FT DOMAIN 31 730 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 731 746 POTENTIAL.
FT FT TRANSMEM 752 772 POTENTIAL.
FT FT TRANSMEM 775 795 POTENTIAL.
FT FT DOMAIN 796 904 CYTOPLASMIC (POTENTIAL).
FT FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SQ SEQUENCE 904 AA; 100115 MW; 7825E1DC830A626F CRC64;

Query Match 70.0%; Score 35; DB 1; Length 904;
Best Local Similarity 85.7%; Pred. No. 2.le+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPG 8
DB 33 SSPGTPG 39

```

Search completed: May 21, 2002, 11:24:11
Job time: 331 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2002, 11:23:51 ; Search time 41.2 Seconds
(without alignments)
37.790 Million cell updates/sec

Title: US-09-734-281-2

Perfect score: 50

Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database : SPTREMBL19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	372	11 Q91WK4	Q91WK4 mus musculus
2	42	84.0	641	3 Q9Y879	Q9Y879 cryptococcus
3	41	82.0	15	6 Q9TR5	Q9TR5 bos taurus
4	41	82.0	626	10 Q9ZRY1	Q9ZRY1 glycine max
5	40	80.0	376	4 Q96CK9	Q96CK9 homo sapien
6	40	80.0	435	2 Q68641	Q68641 oerskovia x
7	39	78.0	150	2 Q9XAE0	Q9XAE0 streptomyce
8	39	78.0	272	2 Q9S283	Q9S283 streptomyce
9	39	78.0	389	6 Q9BEG5	Q9BEG5 bos taurus
10	39	78.0	391	6 Q9BEG6	Q9BEG6 bos taurus
11	39	78.0	405	4 Q9NMV9	Q9NMV9 homo sapien
12	39	78.0	424	4 Q9UKS6	Q9UKS6 homo sapien
13	39	78.0	424	4 Q9H331	Q9H331 homo sapien
14	39	78.0	513	4 Q9BRM0	Q9BRM0 homo sapien
15	39	78.0	651	4 Q9P2L4	Q9P2L4 homo sapien
16	39	78.0	2232	5 P91365	P91365 caenorhabdi

17	38	76.0	280	5	Q95TC5	Q95TC5 drosophila
18	38	76.0	453	11	Q63422	Q63422 rattus norv
19	38	76.0	517	17	Q974W1	Q974W1 sulfolobus
20	38	76.0	711	5	Q9U5M3	Q9U5M3 podocoryne
21	38	76.0	1019	5	Q961C7	Q961C7 drosophila
22	38	76.0	1345	1	Q54437	Q54437 staphylothe
23	37	74.0	168	5	Q17289	Q17289 caenorhabdi
24	37	74.0	238	4	Q9H4T5	Q9H4T5 homo sapien
25	37	74.0	302	3	Q43060	Q43060 schizosacch
26	37	74.0	333	4	Q15469	Q15469 homo sapien
27	37	74.0	387	11	Q9D2V9	Q9D2V9 mus musculu
28	37	74.0	387	11	Q99PD5	Q99PD5 mus musculu
29	37	74.0	393	6	Q99147	Q99147 oryctolagus
30	37	74.0	396	4	Q14631	Q14631 homo sapien
31	37	74.0	406	3	Q74658	Q74658 candida alb
32	37	74.0	407	3	Q74661	Q74661 candida alb
33	37	74.0	407	3	Q74661	Q74661 candida alb
34	37	74.0	407	3	Q74661	Q74661 candida alb
35	37	74.0	420	4	Q14633	Q14633 homo sapien
36	37	74.0	539	4	Q95196	Q95196 mus musculu
37	37	74.0	539	11	Q9Y332	Q9Y332 mus musculu
38	37	74.0	541	6	Q01106	Q01106 oryctolagus
39	37	74.0	723	11	Q9D677	Q9D677 mus musculu
40	37	74.0	734	4	Q75112	Q75112 homo sapien
41	37	74.0	742	11	Q9CW54	Q9CW54 mus musculu
42	37	74.0	847	4	Q16584	Q16584 homo sapien
43	37	74.0	850	11	Q9JJ15	Q9JJ15 mus musculu
44	37	74.0	1523	3	Q9HF4	Q9HF4 candida alb
45	37	74.0	3494	4	Q96RU9	Q96RU9 homo sapien
46	37	74.0	3620	6	Q9TU53	Q9TU53 canis fami
47	37	74.0	3623	4	Q60494	Q60494 homo sapien
48	37	74.0	6875	6	Q28733	Q28733 oryctolagus
49	36	72.0	26926	4	Q10466	Q10466 homo sapien
50	36	72.0	114	10	Q9ATC9	Q9ATC9 malus comes
51	36	72.0	119	10	Q43548	Q43548 malus comes
52	36	72.0	149	11	Q9JXX0	Q9JXX0 mus musculu
53	36	72.0	179	11	Q9JKW9	Q9JKW9 mus musculu
54	36	72.0	209	16	Q98K79	Q98K79 rhizobium l
55	36	72.0	216	11	Q9JXX1	Q9JXX1 mus musculu
			221	2	Q9RJC5	Q9RJC5 streptomyce

ALIGNMENTS

RESULT 1					
Q91WK4					
ID	Q91WK4	PRELIMINARY;	PRT;	372	AA.
AC	Q91WK4				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	MICROTUBULE-ASSOCIATED PROTEIN TAU.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=EYE, AND RETINA;				
RA	Strausberg R.;				
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC014748; AAI14748.1; ..				
SQ	SEQUENCE 372 AA; 38861 MW; B027745D23BC62A2 CRC64;				

Query Match 100.0%; Score 50; DB 11; Length 372;
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
QY 1 YSSPGSPGT 9
DB 128 YSSPGSPGT 136

us-09-734-281-2.ispt

Wed May 22 11:04:45 2002

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QY 1 YSPGSPG 8
Db 3 YSPGSPG 10

RESULT 4
Q9ZRY1 PRELIMINARY; PRT; 626 AA.
ID Q9ZRY1
AC Q9ZRY1; 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE NDX1 HOMEBOX PROTEIN (FRAGMENT).
GN NDX1
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
SEQUENCE FROM N.A.
RP Jorgensen J.E., Gronlund M., Pallisgaard N., Larsen K., Marcher K.A.,
RA Jensen E.;
RT "A new class of plant homeobox genes is expressed in specific regions
of determinate symbiotic root nodules.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ011831; CAA09794.1; -.
DR InterPro; IPR001356; Homeobox.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR Homeobox; DNA-binding; Nuclear protein.
KW NON_TER 1
FT SEQUENCE 626 AA; 69101 MW; 0D8F8C371CD61B11 CRC64;
SQ SEQUENCE 626 AA; 69101 MW; 0D8F8C371CD61B11 CRC64;

Query Match 82.0%; Score 41; DB 10; Length 626;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPG 8
Db 498 YSPGSPG 505

RESULT 5
Q96CK9 PRELIMINARY; PRT; 376 AA.
ID Q96CK9
AC Q96CK9; 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SIMILAR TO ZINC FINGER PROTEIN 16 (K0X 9).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE-LUNG CARCINOMA;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC014165; AAH14165.1; -.
SQ SEQUENCE 376 AA; 41145 MW; 68B1A638CC0758BC CRC64;

Query Match 80.0%; Score 40; DB 4; Length 376;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPG 9
Db 20 SSPGSPG 27

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RESULT 6
O88641 ID O68641 PRELIMINARY; PRT; 435 AA.
AC O68641;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE BEVA-1,3-GLUCANASE II.
GN BGLII.
OS Oerskovia xanthineolytica.
OC Bacteria; Firmicutes; Actinobacteridae;
OC Actinomycetales; Micrococineae; Cellulomonadaceae; Oerskovia.
OX NCBI_TaxID=1826;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LL G109;
RA Ventom A.M., Asenjo J.A.;
RT "Characterization of yeast lytic enzymes from Oerskovia
xanthineolytica LL-G109.";
RL Enzyme Microb. Technol. 13:71-75(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LL G109;
RA Parrado J., Escudero P.R., Conejero-Lara F., Kotlik M., Ponting C.P.,
Asenjo J.A., Dobson C.M.;
RT "Molecular characterization of a thermoactive beta-1,3-glucanase from
Oerskovia xanthineolytica.";
RL Blochm. Biophys. Acta 1296:145-151(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=LL G109;
RA Ferrer P., Hedegaard L., Diers I.;
RT "BglII codes for a yeast-lytic beta-1,3-glucanase from Oerskovia
xanthineolytica LL G109 (Cellulomonas cellulans) having a mannose-
binding domain.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052745; AAC38290.1;
DR HSSP; P23904; 1AJK.
DR InterPro; IPR000757; Glyco_hydro_16.
DR Pfam; PF00722; Ricin_B_lectin.
DR Pfam; PF00852; Glyco_hydro_16; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
DR PROSITE; PS0231; RICIN_B_LLECTIN; 1.
SQ SEQUENCE 435 AA; 46037 MW; 00F087BE644C0F58 CRC64;

Query Match 80.0%; Score 40; DB 2; Length 435;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SSPGSPGT 9
Db 297 SSPGNPGT 304

RESULT 7
O9XAE0 ID O9XAE0 PRELIMINARY; PRT; 150 AA.
AC O9XAE0;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)

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DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE HYPOTHETICAL 16.1 KDA PROTEIN.
GN SC6G9.42C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL079356; CAB45633.1; -.
KW Hypothetical protein.
SQ SEQUENCE 150 AA; 16072 MW; 7A8D93D1C6A48A0D CRC64;

Query Match 78.0%; Score 39; DB 2; Length 150;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 SSPGSPGT 9
Db 3 SSPGKPGT 10

RESULT 8
O9S283 ID O9S283 PRELIMINARY; PRT; 272 AA.
AC Q9S283;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE PUTATIVE EXPRESSION REGULATOR (FRAGMENT).
GN SC111.37C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D., Harris D.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL096849; CAB50963.1; -.

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RC InterPro: IPR001450; 4Fe4S_ferredoxin.
 RA InterPro: IPR000561; EGF-like.
 RT PROSITE: PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
 RL PROSITE: PS00222; EGF_1; UNKNOWN_1.
 FT NON_TER
 SQ SEQUENCE 272 AA; 27508 MW; 6E8523635D929BB5 CRC64;

Query Match 78.0%; Score 39; DB 2; Length 272;
 Best Local Similarity 66.7%; Pred. No. 25;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
 : | | | | |
 Db 170 YAPGAPGT 178

RESULT 9
 Q9BEG5 PRELIMINARY; PRT; 389 AA.

AC Q9BEG5
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE ECTODYSPLASIN 1, ISOFORM A2.

GN ED1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;

RP SEQUENCE FROM N.A.
 RC STRAIN-HOLSTEIN;
 RA Drogenmuller C., Distl O., Leeb T.;
 RT "Identification of a highly polymorphic microsatellite within the
 bovine ectodysplasin A (ED1) gene on BTA Xq22-24.";

RL Anlm. Genet. 31:416-416(2000).
 DR EMBL; AJ300468; CAC29152.1;
 DR EMBL; AJ300469; CAC29152.1; JOINED.
 DR EMBL; AJ278907; CAC29152.1; JOINED.
 DR InterPro: IPR000087; Collagen.
 DR InterPro: IPR000478; TNF_family.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS50049; TNF 2; 1.
 SQ SEQUENCE 389 AA; 41339 MW; 60BE0077C7C83986 CRC64;

Query Match 78.0%; Score 39; DB 6; Length 389;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
 : | | | | |
 Db 78 FSGPGTGT 86

RESULT 10
 Q9BEG6 PRELIMINARY; PRT; 391 AA.

AC Q9BEG6
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE ECTODYSPLASIN 1, ISOFORM A1.

GN ED1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-HOLSTEIN;
 RA Drogenmuller C., Distl O., Leeb T.;
 RT "Identification of a highly polymorphic microsatellite within the
 bovine ectodysplasin A (ED1) gene on BTA Xq22-24.";
 RL Anlm. Genet. 31:416-416(2000).
 DR EMBL; AJ300468; CAC29151.1;
 DR EMBL; AJ300469; CAC29151.1; JOINED.
 DR EMBL; AJ278907; CAC29151.1; JOINED.
 DR InterPro: IPR000087; Collagen.
 DR InterPro: IPR000478; TNF_family.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS50049; TNF 2; 1.
 SQ SEQUENCE 391 AA; 41567 MW; 1F87AD67A04EB7AA CRC64;

Query Match 78.0%; Score 39; DB 6; Length 391;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
 : | | | | |
 Db 78 FSGPGTGT 86

RESULT 11
 Q9NWV9 PRELIMINARY; PRT; 405 AA.

AC Q9NWV9
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE CDNA FLJ20570 FIS, CLONE REC00956 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
 RA Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T.,
 RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK005077; BAA91267.1;
 DR InterPro: IPR001060; FCH.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00611; FCH; 1.
 DR SMART: SM00055; FCH; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR NON_TER 405 405
 SQ SEQUENCE 405 AA; 46494 MW; 6EA81D7782B53D92 CRC64;

Query Match 78.0%; Score 39; DB 4; Length 405;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 : | | | | |
 Db 341 SPGSPGT 347

RESULT 12
 Q9UKS6 PRELIMINARY; PRT; 424 AA.
 ID Q9UKS6
 AC Q9UKS6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE SH3 DOMAIN-CONTAINING PROTEIN 6511.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2002705; PubMed=10531379;
 RA Howard L., Nelson K.K., Maciewicz R.A., Blobel C.P.;
 RT "Interaction of the metalloprotease disintegrins MDC9 and MDC15 with
 RL two SH3 domain-containing proteins, endophilin I and SH3PX1.";
 J. Biol. Chem. 274:31693-31699(1999).
 DR EMBL; AF130979; AAF04472.1; -;
 DR HSSP; P29355; ISEM.
 DR InterPro; IPR001060; FCH.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00611; FCH; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR SMART; SM00055; FCH; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 SQ SEQUENCE 424 AA; 48515 MW; 924A7BF79C8DC395 CRC64;
 Query Match 78.0%; Score 39; DB 4; Length 424;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SPGSPGT 9
 Db 341 SPGSPGT 347
 RESULT 13
 O9H331 PRELIMINARY; PRT; 424 AA.
 AC O9H331;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PACSIN3 (PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE 3) (UNKNOWN)
 DE (PROTEIN FOR MGC:19935) (PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE
 DE IN NEURONS 3).
 GN PACSIN3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11082044;
 RA Modregger J., Ritter B., Witter B., Paulsson M., Plomann M.;
 RT "All three PACSIN isoforms bind to endocytic proteins and inhibit
 RL endocytosis.";
 J. Cell Sci. 113:4511-4521(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21100457; PubMed=11179684;
 RA Sunoy L., Pluvinet R., Andreu N., Estivill X., Escarceller M.;
 RT "PACSIN 3 is a novel SH3 domain cytoplasmic adapter protein of the
 RL pacsin-syndapin-FAP52 gene family.";
 Gene 262:199-205(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MELANOMA;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-UTERUS; LEIOMYOSARCOMA;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF149825; AAG31023.1; -;
 DR EMBL; AF242530; AAK29207.1; -;
 DR EMBL; BC011889; AAL11889.1; -;

DR EMBL; BC007914; AAH07914.1; -;
 DR HSSP; P29355; ISEM.
 DR InterPro; IPR001060; FCH.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00611; FCH; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR SMART; SM00055; FCH; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Kinase.
 SQ SEQUENCE 424 AA; 48486 MW; 6DBD940AE6D1F352 CRC64;
 Query Match 78.0%; Score 39; DB 4; Length 424;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SPGSPGT 9
 Db 341 SPGSPGT 347
 RESULT 14
 O9BRM0 PRELIMINARY; PRT; 513 AA.
 ID O9BRM0
 AC O9BRM0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE HYPOTHETICAL PROTEIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-UTERUS; AND LEIOMYOSARCOMA;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006174; AAH06174.1; -;
 DR InterPro; IPR001798; Kelch.
 DR Pfam; PF01344; Kelch; 1.
 FT NON_TER 1
 SQ SEQUENCE 513 AA; 54599 MW; 21FD050215015520 CRC64;
 Query Match 78.0%; Score 39; DB 4; Length 513;
 Best Local Similarity 87.5%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSPGSPGT 9
 Db 379 SSPGSPGT 386
 RESULT 15
 O9P2L4 PRELIMINARY; PRT; 651 AA.
 ID O9P2L4
 AC O9P2L4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE KIAA1332 PROTEIN (FRAGMENT).
 GN KIAA1332.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K., Hirokawa M., Ohara O.;

ID Q974W1 PRELIMINARY; PRT; 517 AA.
AC 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN SF0549.
GN SF0549.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545
RX PubMed=11572479;
RA Kawaiyabashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7.";
RL DNA Res. 8:123-140(2001).
DR EMBL: AP000982; BAB5546.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 517 AA; 57965 MW; E129448C73A27A24 CRC64;

Query Match 76.0%; Score 38; DB 17; Length 517;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPCT 9
I: I I I I I I I I
DB 204 YASPSTPGT 212

RESULT 20
Q9U5M3
ID Q9U5M3 PRELIMINARY; PRT; 711 AA.
AC Q9U5M3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PAIRED BOX PROTEIN.
GN PAX-B.
OS Podocoryne carnea.
OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
OC Hydractiniidae; Podocoryne.
OX NCBI_TaxID=6096;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20302558; PubMed=10842067;
RX Groeger H., Callaerts P., Gehring W.J., Schmid V.;
RT "Characterization and expression analysis of an ancestor-type Pax gene
RT in the hydrozoan jellyfish Podocoryne carnea.";
RL Mech. Dev. 94:157-169(2000).
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -|- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
CC EMBL: AJ249563; CAB61522.1;
DR HSSP; P26367; 6PAX.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001523; Paired_box.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00292; PAX; 1.
DR PRINTS; PR00027; PAIREDBOX.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00351; PAX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00034; PAIRED_BOX; 1.
KW DNA-binding; Developmental protein; Homeobox; Nuclear protein;

RW Paired box: Transcription regulation.
SQ SEQUENCE 711 AA; 79326 MW; AC1D909E252549B1 CRC64;

Query Match 76.0%; Score 38; DB 5; Length 711;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPG 8
I: I I I I I I I I
DB 211 SSPGSPG 217

RESULT 21
Q961G7
ID Q961G7 PRELIMINARY; PRT; 1019 AA.
AC Q961G7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GH23906P.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celisner S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY051598; AAK93022.1;
SQ SEQUENCE 1019 AA; 112156 MW; 207885C035945EAF CRC64;

Query Match 76.0%; Score 38; DB 5; Length 1019;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPG 8
I: I I I I I I I I
DB 864 YNPGSPG 871

RESULT 22
Q54437
ID Q54437 PRELIMINARY; PRT; 1345 AA.
AC Q54437
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE STABLE PROTEASE PRECURSOR.
OS Staphylothermus marinus.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Staphylothermus.
OX NCBI_TaxID=2280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F1;
RX MEDLINE=95139068; PubMed=7837271;
RA Peters J., Nitsch M., Kuhlmoegen B., Golbik R., Lupas A.,
RA Kellermann J., Engelhardt H., Pfander J.-P., Muller S., Goldie K.,
RA Engel A., Stetter K.-O., Baumeister W.;
RT "Tetrabrachion: a filamentous archaeobacterial surface protein assembly
RT of unusual structure and extreme stability.";
RL J. Mol. Biol. 245:385-401(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F1;

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RA Mayr J., Lupas A., Kellermann J., Eckerskorn C., Baumeister W.,
 RA Peters J.;
 RT "A hyperthermostable protease of the subtilisin family bound to the
 RT surface layer of the archaeon *Staphylothermus marinus*.";
 RL Curr. Biol. 0:0-0(1996).
 DR EMBL: U57968; AAB02323.1; -.
 DR MF000082; S08.096; -.
 DR InterPro: IPR000209; Peptidase_S8.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR Pfam: PF00082; Peptidase_S8; 3.
 DR PRINTS: PR00723; SUBTILISIN.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
 DR PROSITE: PS00136; SUBTILASE_ASP; UNKNOWN_1.
 DR PROSITE: PS00138; SUBTILASE_SER; UNKNOWN_1.
 DR Signal: Protease.
 KW SIGNAL
 FT SIGNAL
 SQ SEQUENCE 1345 AA; 148446 MW; D40878E437A52EC3 -CRC64;

Query Match 76.0%; Score 38; DB 1; Length 1345;
 Best Local Similarity 77.8%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
 ||| |
 DB 596 YSSNGAPGT 604

RESULT 23
 OI7289 PRELIMINARY; PRT; 168 AA.
 AC OI7289;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 18.6 KDA PROTEIN.
 OS Caenorhabditis elegans.
 GN Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderiinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Du Z., Goela D., Ozersky P.;
 RT "The sequence of *C. elegans* cosmid R52.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston K.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF025471; AAB71062.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 168 AA; 18604 MW; 4D72C56A94F38F88 -CRC64;

Query Match 74.0%; Score 37; DB 5; Length 168;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPSGSPGT 9
 :|:|:|:|:|
 DB 40 TTPGSPGT 47

RESULT 24
 Q9H4T5 PRELIMINARY; PRT; 238 AA.
 ID Q9H4T5;
 AC Q9H4T5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE BA93B14.3 (NEUROTENSIN RECEPTOR 1 (HIGH AFFINITY)(NTR))
 DE (FRAGMENT).
 DE (FRAGMENT).
 GN NTSR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Heath P.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL357033; CAC14923.1; -.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_2; 1.
 DR Receptor.
 KW NON_TER
 FT NON_TER
 SQ SEQUENCE 238 AA; 25503 MW; 258BE57EACCF6EF0 -CRC64;

Query Match 74.0%; Score 37; DB 4; Length 238;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPSGSPGT 9
 |:|:|:|:|
 DB 6 SAPGTPGT 13

RESULT 25
 O43060 PRELIMINARY; PRT; 302 AA.
 ID O43060;
 AC O43060;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE HYPOTHETICAL 33.3 KDA PROTEIN C4C3.07 IN CHROMOSOME II.
 GN SPBC4C3.07.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Wood V., Rajandream M.A., Barrell B.G., Lauber J., Hilbert H.,
 RA Duesterhoeft A.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO PROTEASOME REGULATORY SUBUNIT S12/MOV-34.
 DR EMBL: AL021730; CAA16829.1; -.
 DR InterPro: IPR000555; Mov34.
 DR InterPro: IPR003640; Mov34_2.
 DR Pfam: PF01398; Mov34; 1.
 DR ProDom: PD005425; Mov34_2; 1.
 DR SMART: SM00232; JAB_MPN; 1.
 DR Hypothetical protein.
 KW SEQUENCE 302 AA; 33251 MW; A046E087CF083D84 -CRC64;

Query Match 74.0%; Score 37; DB 3; Length 302;
 Best Local Similarity 66.7%; Pred. No. 63;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 123 YASPAEPT 131

RESULT 26
Q15469
ID Q15469 PRELIMINARY; PRT; 333 AA.
AC Q15469;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSIL5R4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RX MEDLINE=92121815; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.,
RT "Molecular cloning and expression of the human interleukin 5
receptor.";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL; X62156; CAA44081.1; -
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003532; Hematopo_receptor_SF2.
DR PROSITE; PS01356; HEMATOPO_REC_SF2; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;

Query Match 74.0%; Score 37; DB 4; Length 333;
Best Local Similarity 56.7%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 27
Q9D2V9
ID Q9D2V9 PRELIMINARY; PRT; 387 AA.
AC Q9D2V9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 0610009M14RIK PROTEIN.
GN 0610009M14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21083660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Query Match 74.0%; Score 37; DB 11; Length 387;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSSPGSPG 8
Db 19 YEGPGSPG 26

RESULT 28
Q99PD5
ID Q99PD5 PRELIMINARY; PRT; 387 AA.
AC Q99PD5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LEUCINE ZIPPER PROTEIN THG-1PIT.
GN 0610009M14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX "Thg-1pit, a putative Lhx3 target gene.";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF315352; AAK02018.1; -
DR HSSP; P80220; 1DIP.
DR MGD; MGI:1926079; 0610009M14RIK.
DR InterPro: IPR000580; TSC-22_Dip_Bun.
DR InterPro: IPR000580; TSC-22_Dip_Bun.
DR Pfam; PF01166; TSC22; 1.
DR ProDom; PD007152; TSC-22_Dip_Bun; 1.
DR PROSITE; PS01289; TSC22; 1.
SQ SEQUENCE 387 AA; 39978 MW; D4160FA3AB2DFB90 CRC64;

Query Match 74.0%; Score 37; DB 11; Length 387;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSSPGSPG 8
Db 19 YEGPGSPG 26

RESULT 29
Q99147
ID Q99147 PRELIMINARY; PRT; 393 AA.
AC Q99147;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

us-09-734-281-2.rspt

Wed May 22 11:04:45 2002

Db 119 HAPGSPGT 127

01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
TITIN (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
[1]
SEQUENCE FROM N.A.
STRAIN=NEW ZEALAND WHITE; TISSUE=HEART;
MEDLINE=91305130; PubMed=1712941;
Fritz J.D.; Greaser M.L.; Wolff J.;
"A novel 3' Extension Technique using Random Primers in RNA-PCR.";
Nucleic Acids Res. 19:3747-3747(1991).
ENBL; X59596; CAA42165.1;
InterPro: IPR003962; FNIII_repeat.
InterPro: IPR003961; FNIII.
InterPro: IPR003600; Ig-like.
Pfam: PF00041; fn3; 2.
PRINTS; PR00014; FNTPPIII.
SMART; SM00060; FN3; 2.
SMART; SM00410; IG-like; 1.
Repeat.
NON_TER 1
NON_TER 393
SEQUENCE 393 AA; 43475 MW; 0672492F4091CBE7 CRC64;

Query Match 74.0%; Score 37; DB 6; Length 393;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
Db 55 YKEPGPGT 63

RESULT 30
Q14631 PRELIMINARY; PRT; 396 AA.
AC Q14631;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.
GN HSILSR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=PERIPHERAL BLOOD;
MEDLINE=92121815; PubMed=1732409;
Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
"Molecular cloning and expression of the human interleukin 5
receptor.";
J. Exp. Med. 175:341-351(1992).
ENBL; X61177; CAA43484.1;
InterPro: IPR002996; CRIA.
InterPro: IPR003532; Hematopo_receptor_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN1.
Signal; Receptor.
FT SIGNAL 20 POTENTIAL.
FT CHAIN 1 INTERLEUKIN-5 RECEPTOR TYPE 2.
FT SEQUENCE 396 AA; 44998 MW; 1AB60619842ACDA5 CRC64;

Query Match 74.0%; Score 37; DB 4; Length 396;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9

RESULT 31
O74658 PRELIMINARY; PRT; 406 AA.
ID O74658;
AC O74658;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN ALS2.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
[1]
SEQUENCE FROM N.A.
STRAIN=1161;
MEDLINE=98440424; PubMed=9765564;
Hoyer L.L.; Payne T.L.; Hecht J.E.;
"Identification of Candida albicans ALS2 and ALS4 and localization of
als proteins to the fungal cell surface.";
J. Bacteriol. 180:5334-5343(1998).
ENBL; AF024581; AAC64236.1;
NON_TER 1
NON_TER 1
SEQUENCE 406 AA; 40585 MW; 9A6C92C1B2A93A81 CRC64;

Query Match 74.0%; Score 37; DB 3; Length 406;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
Db 189 SNPGAPGT 196

RESULT 32
Q9URP9 PRELIMINARY; PRT; 406 AA.
ID Q9URP9;
AC Q9URP9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN ALS4.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
[1]
SEQUENCE FROM N.A.
STRAIN=1161;
MEDLINE=98440424; PubMed=9765564;
Hoyer L.L.; Payne T.L.; Hecht J.E.;
"Identification of Candida albicans ALS2 and ALS4 and localization of
als proteins to the fungal cell surface.";
J. Bacteriol. 180:5334-5343(1998).
ENBL; AF024585; AAC64240.1;
NON_TER 1
NON_TER 1
SEQUENCE 406 AA; 40592 MW; E0117B4CE4ECB4C3 CRC64;

Query Match 74.0%; Score 37; DB 3; Length 406;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
Db 189 SNPGAPGT 196

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RESULT 33
074661 ID 074661 PRELIMINARY; PRT; 407 AA.
AC 074661
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN ALS4
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=98440424; PubMed=9765564;
RX MEDLINE=98440424; PubMed=9765564;
RA Hoyer L.L., Payne T.L., Hecht J.E.;
RT "Identification of Candida albicans ALS2 and ALS4 and localization of
RT als proteins to the fungal cell surface.";
RL J. Bacteriol. 180:5334-5343(1998).
DR EMBL; AF024587; AAC64242.1; -.
FT NON_TER 1
SQ SEQUENCE 407 AA; 40649 MW; FC846B7A1640CF44 CRC64;

Query Match 74.0%; Score 37; DB 3; Length 407;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
I:|||||
DB 189 SNPGAPGT 196

RESULT 34
014633 ID 014633 PRELIMINARY; PRT; 420 AA.
AC 014633
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSIL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=PERIPHERAL BLOOD;
RX MEDLINE=92121815; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5
RT receptor.";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL; X611176; CAA43483.1; -.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003532; Hematopo_receptor_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 420 AA; 47670 MW; 8DC56DFC8BEFF524 CRC64;

Query Match 74.0%; Score 37; DB 4; Length 420;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
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Db 119 HAPPGSPGT 127

RESULT 35
095196 ID 095196 PRELIMINARY; PRT; 539 AA.
AC 095196
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NEUROGLYCAN C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=BRAIN;
RX MEDLINE=99133557; PubMed=9950058;
RA Yasuda Y., Tokita Y., Aono S., Matsui F., Ono T., Sonta S.,
RA Watanabe E., Nakanishi Y., Oohira A.;
RT "Cloning and chromosomal mapping of the human gene of neuroglycan C
RT (NGC), a neural transmembrane chondroitin sulfate proteoglycan with an
RT EGF module.";
RL Neurosci. Res. 32:313-322(1998).
DR EMBL; AF059274; AAC69612.1; -.
DR InterPro; IPR000561; EGF-like.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 539 AA; 57024 MW; 5B22E9E8DE34290E CRC64;

Query Match 74.0%; Score 37; DB 4; Length 539;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
I:|||||
DB 227 SPPGSPGT 234

RESULT 36
090Y32 ID 090Y32 PRELIMINARY; PRT; 539 AA.
AC 090Y32
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NEUROGLYCAN C.
GN CSPG5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=BRAIN;
RX MEDLINE=20085050; PubMed=10617623;
RA Aono S., Keino H., Ono T., Yasuda Y., Tokita Y., Matsui F.,
RA Taniguchi M., Sonta S.-I., Oohira A.;
RT "Genomic Organization and Expression Pattern of Mouse Neuroglycan C in
RT the Cerebellar Development.";
RL J. Biol. Chem. 275:337-342(2000).
DR EMBL; AF133700; AAF23362.1; -.
DR MGI; MGI:1352747; Cspg5.
DR InterPro; IPR000561; EGF-like.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 539 AA; 57352 MW; 7D566881555460ED CRC64;

Query Match 74.0%; Score 37; DB 11; Length 539;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
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Wed May 22 11:04:45 2002

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QY      2  SSGSPGCT 9
DB      228  SFGSPGCT 235

RESULT 37
ID Q01106 PRELIMINARY; PRT; 541 AA.
AC Q01106;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TIPIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX MEDLINE=92258380; PubMed=1582406;
RA Labelit S., Gautel M., Lakey A., Trinick J.;
RT "Towards a molecular understanding of titin.";
RL EMBO J. 11:1711-1716(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RA Fritz J.D., Greaser M.L., Wolff J.;
RT "A novel 3' extension method using random primers.";
RL Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M98338; AAA31480.1; -.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 4.
DR PRINTS; PRO0014; ENTPEI11.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00409; IG; 1.
KW Repeat.
FT NON_TER
FT SEQUENCE 541 AA; 60088 MW; 0DAA2541E1318B99 CRC64;

Query Match 74.0%; Score 37; DB 6; Length 541;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  YSSPGSPGCT 9
DB      55  YKEGPPGCT 63

RESULT 38
ID Q9D677 PRELIMINARY; PRT; 723 AA.
AC Q9D677;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 4632412M04RIK PROTEIN.
GN 4632412M04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SKIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa K., Kiyosawa H., Nishi K., Kiyosawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz K., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC EMBL; AK014569; BAB29434.1; -.
DR HSP; P49799; IAGR.
DR MGD; MG1:1924302; 4632412M04RIK.
DR InterPro: IPR003109; GoLoco.
DR InterPro: IPR003116; RBD.
DR InterPro: IPR000342; RGS.
DR Pfam; PF02188; GoLoco; 1.
DR Pfam; PF02196; RBD; 2.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS/PROTEIN.
DR PRODOM; PD001580; RGS; 1.
DR SMART; SM00390; GoLoco; 1.
DR SMART; SM00455; RBD; 2.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS50132; RGS; 1.
DR SEQUENCE 723 AA; 78539 MW; EBCBFD7D5A56BF51 CRC64;

Query Match 74.0%; Score 37; DB 11; Length 723;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  YSSPGSPGCT 9
DB      632  HSTPGPPGCT 640

RESULT 39
ID Q75112 PRELIMINARY; PRT; 734 AA.
AC Q75112;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE KIAA0613 PROTEIN (FRAGMENT).
GN KIAA0613.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BRIN;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
CC -1- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC EMBL; AB014513; BAA31588.1; -.
DR HSP; Q05158; 10LI.
DR InterPro: IPR003006; IQ_MHC.
DR InterPro: IPR001781; LIM.

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DR InterPro: IPR001478; PDZ.
 DR InterPro: IPR002965; P-rich_extensn.
 DR Pfam: PF00412; LIM; 3.
 DR Pfam: PF00595; PDZ; 1.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR ProDom: PD000094; LIM; 3.
 DR SMART: SM00132; LIM; 3.
 DR SMART: SM00228; PDZ; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE: PS00223; LIM_DOMAIN_2; 3.
 DR PROSITE: PS0106; PDZ; 1.
 KW LIM domain; Metal-binding; zinc.
 FT NON_TER 1.
 SQ SEQUENCE 734 AA; 77738 MW; 5CB9AC39CC690FB8 CRC64;

Query Match 74.0%; Score 37; DB 4; Length 734;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
 :|||:|
 Db 135 ASPGTPGT 142

RESULT 40

Q9CW54
 ID Q9CW54 PRELIMINARY; PRT; 742 AA.
 AC Q9CW54
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE I200016K18RIK PROTEIN (FRAGMENT).
 GN I200016K18RIK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=LUNG;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikolaev I., Pesole G., Quackenbush J.,
 RA Sakai K., Okido T., Furuno M., Tomita M., Wagner L., Washio T.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC EMBL: AK004813; BAB23584.1; -
 DR HSSP; P49799; IAGR.
 DR MGD; MGI:1918979; I200016K18RIK.
 DR InterPro: IPR000634; dehydrtse_ser_thr.
 DR InterPro: IPR003109; GoLoco.
 DR InterPro: IPR003116; RBD.
 DR InterPro: IPR000342; RGS.
 DR Pfam: PF02188; GoLoco; 1.
 DR Pfam: PF02196; RBD; 2.

DR Pfam: PF00615; RGS; 1.
 DR PRINTS: PR01301; RGSPTOTIN.
 DR ProDom: PD001580; RGS; 1.
 DR SMART: SM00390; GoLoco; 1.
 DR SMART: SM00455; RBD; 2.
 DR SMART: SM00315; RGS; 1.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR; UNKNOWN_1.
 DR PROSITE: PS0132; RGS; 1.
 FT NON_TER 1.
 SQ SEQUENCE 742 AA; 80828 MW; ACAPE5225ECBE74D CRC64;

Query Match 74.0%; Score 37; DB 11; Length 742;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 :|||:|
 Db 651 HSTPGPPGT 659

Search completed: May 21, 2002, 11:23:51
 Job time: 341 sec

us-09-734-281-2.rspt

Wed May 22 11:04:45 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2002, 11:18:35 ; Search time 21.42 seconds
(without alignments)
10.263 Million cell updates/sec

Title: US-09-734-281-2
Perfect score: 50
Sequence: 1 YSSPGSPCT 9

Scoring table:
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	4	US-08-617-987A-1
2	50	100.0	9	4	US-08-617-987A-2
3	50	100.0	27	2	US-08-244-951A-5
4	50	100.0	31	2	US-08-244-951A-4
5	50	100.0	34	2	US-08-602-264A-10
6	50	100.0	34	3	US-08-461-018A-10
7	50	100.0	37	2	US-09-216-958-10
8	50	100.0	64	4	US-08-244-951A-1
9	50	100.0	67	2	US-08-389-011-1
10	50	100.0	67	3	US-08-403-917A-1
11	50	100.0	67	3	US-09-348-952A-1
12	50	100.0	106	3	US-08-776-404B-1
13	50	100.0	112	3	US-08-666-360-1
14	50	100.0	351	1	US-08-159-969-2
15	50	100.0	352	1	US-08-726-306A-17
16	50	100.0	391	2	US-08-244-951A-10
17	50	100.0	391	2	US-08-389-011-23
18	50	100.0	391	3	US-08-403-917A-23
19	50	100.0	391	4	US-09-348-952A-23
20	50	100.0	441	4	US-08-244-951A-1
21	40	80.0	263	4	US-09-159-106-2
22	40	80.0	435	4	US-09-159-106-11
23	39	78.0	23	2	US-08-244-951A-3
24	39	78.0	33	2	US-08-244-951A-2
25	39	78.0	33	2	US-08-389-011-2
26	39	78.0	33	3	US-08-403-917A-2
27	39	78.0	33	4	US-09-348-952A-2

28	39	78.0	35	2	US-08-244-951A-6
29	37	74.0	313	3	US-08-836-561-106
30	37	74.0	335	1	US-07-947-130-2
31	37	74.0	335	1	US-08-421-822-2
32	37	74.0	335	1	US-08-421-823-2
33	37	74.0	396	1	US-07-757-390-14
34	37	74.0	396	1	US-08-442-282-14
35	37	74.0	396	1	US-08-442-281-14
36	37	74.0	420	1	US-08-939-727-14
37	37	74.0	420	1	US-07-757-390-13
38	37	74.0	420	1	US-08-442-282-13
39	37	74.0	420	1	US-08-442-281-13
40	37	74.0	420	1	US-08-939-727-13
41	36	72.0	61	1	US-08-175-155-67
42	36	72.0	61	2	US-08-477-509B-102
43	36	72.0	61	2	US-08-707-237A-74
44	36	72.0	61	3	US-08-482-085B-102
45	36	72.0	62	1	US-09-444-791A-102
46	36	72.0	62	1	US-08-642-255-100
47	36	72.0	63	1	US-08-397-633A-43
48	36	72.0	63	1	US-08-642-255-121
49	36	72.0	63	1	US-08-397-633A-32
50	36	72.0	65	1	US-08-642-255-125
51	36	72.0	65	1	US-08-397-633A-46
52	36	72.0	71	1	US-08-642-255-108
53	36	72.0	71	1	US-08-642-255-115
54	36	72.0	71	1	US-08-397-633A-21
55	36	72.0	71	1	US-08-397-633A-27

ALIGNMENTS

RESULT 1

US-08-617-987A-1

; Sequence 1, Application US/08617987A

; Patent No. 6238892

; GENERAL INFORMATION:

; APPLICANT: MERCKEN, MARC

; APPLICANT: MANDELKOW, EVA-MARIA

; APPLICANT: VANDEMEEREN, MARC

; APPLICANT: VANMECHELEN, EUGEN

; APPLICANT: VAN DE VOORDE, ANDRE

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED AGAINST THE

; FILE REFERENCE: MICROBUTULE-ASSOCIATED PROTEIN TAU

; CURRENT FILING DATE: 1996-03-15

; PRIOR FILING DATE: 1993-09-02

; PRIOR FILING DATE: 1993-09-02

; PRIOR FILING DATE: 1991-10-25

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (3)

; OTHER INFORMATION: No. 6238892e = "S is phosphorylated"

US-08-617-987A-1

; Sequence 1, Application US/08617987A

; Patent No. 6238892

; GENERAL INFORMATION:

; APPLICANT: MERCKEN, MARC

; APPLICANT: MANDELKOW, EVA-MARIA

; APPLICANT: VANDEMEEREN, MARC

; APPLICANT: VANMECHELEN, EUGEN

; APPLICANT: VAN DE VOORDE, ANDRE

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED AGAINST THE

; FILE REFERENCE: MICROBUTULE-ASSOCIATED PROTEIN TAU

; CURRENT FILING DATE: 1996-03-15

; PRIOR FILING DATE: 1993-09-02

; PRIOR FILING DATE: 1993-09-02

; PRIOR FILING DATE: 1991-10-25

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (3)

; OTHER INFORMATION: No. 6238892e = "S is phosphorylated"

; LOCATION: (6)

; OTHER INFORMATION: No. 6238892e = "S is phosphorylated"

US-08-617-987A-1

; Sequence 1, Application US/08617987A

; Patent No. 6238892

; GENERAL INFORMATION:

; APPLICANT: MERCKEN, MARC

; APPLICANT: MANDELKOW, EVA-MARIA

; APPLICANT: VANDEMEEREN, MARC

; APPLICANT: VANMECHELEN, EUGEN

; APPLICANT: VAN DE VOORDE, ANDRE

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED AGAINST THE

; FILE REFERENCE: MICROBUTULE-ASSOCIATED PROTEIN TAU

; CURRENT FILING DATE: 1996-03-15

; PRIOR FILING DATE: 1993-09-02

; PRIOR FILING DATE: 1993-09-02

; PRIOR FILING DATE: 1991-10-25

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

Sequence 6, Appl1

Sequence 106, App

Sequence 2, Appl1

Sequence 2, Appl1

Sequence 2, Appl1

Sequence 14, Appl1

Sequence 14, Appl1

Sequence 14, Appl1

Sequence 13, Appl1

Sequence 13, Appl1

Sequence 67, Appl1

Sequence 102, App

Sequence 102, App

Sequence 102, App

Sequence 100, App

Sequence 43, Appl1

Sequence 121, App

Sequence 32, Appl1

Sequence 125, App

Sequence 46, Appl1

Sequence 108, App

Sequence 115, App

Sequence 21, Appl1

Sequence 27, Appl1

Query Match 100.0%; Score 50; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 1 YSSPGSPCT 9

PRESENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/244,951A
 FILING DATE: 19-JAN-1995

TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-244-951A-4

Query Match 100.0%; Score 50; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

RESULT 5
US-08-602-264A-10
; Sequence 10, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: AKIHKO TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-602-264A-10

Query Match 100.0%; Score 50; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

US-08-602-264A-10
; Sequence 10, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: AKIHKO TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-602-264A-10

Query Match 100.0%; Score 50; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

RESULT 6
US-08-461-018A-10
; Sequence 10, Application US/08461018A
; Patent No. 6071694
; GENERAL INFORMATION:
; APPLICANT: AKIHKO TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,018A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-461-018A-10

Query Match 100.0%; Score 50; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

US-08-461-018A-10
; Sequence 10, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: AKIHKO TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,018A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-461-018A-10

Query Match 100.0%; Score 50; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

US-09-216-958-10
; Sequence 10, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: AKIHKO TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:

Query Match 100.0%; Score 50; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

Wed May 22 11:04:36 2002

us-09-734-281-2.rai

MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216.958
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461.018
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-216-958-10

Query Match 100.0%; Score 50; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13; 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 1 YSSPGSPGT 9
DB 7 YSSPGSPGT 15

RESULT 8
US-08-244-951A-1
Sequence 1, Application US/08244951A
Patent No. 5843779
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERMEEREN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244.951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6

FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
FEATURE: human tau protein 155-211
NAME/KEY: human tau protein 155-211
US-08-244-951A-1

Query Match 100.0%; Score 50; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25; 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 1 YSSPGSPGT 9
DB 43 YSSPGSPGT 51

RESULT 9
US-08-389-011-1
Sequence 1, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERMEEREN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389.011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403.917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403.916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244.951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: linear
US-08-389-011-1

Query Match 100.0%; Score 50; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 43 YSSPGSPGT 51

RESULT 10
US-08-403-917A-1
Sequence 1, Application US/08403917A
Patent No. 6010913
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-403-917A-1

Query Match 100.0%; Score 50; DB 3; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 43 YSSPGSPGT 51

RESULT 11
US-09-348-952A-1
Sequence 1, Application US/09348952A
Patent No. 6232437
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/348,952A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown

us-09-734-281-2.ra1

Wed May 22 11:04:36 2002

```
US-09-348-952A-1
Query Match      100.0%; Score 50; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
    |||||
Db 43 YSSPGSPGT 51

RESULT 12
US-08-776-404B-1
; Sequence 1, Application US/08776404B
; Patent No. 6121003
; GENERAL INFORMATION:
; APPLICANT: VANMECHELEN, EUGEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR AN EPITOPE OF
; TITLE OF INVENTION: A PARTICULAR SUBCLASS OR FORM OF PHOSPHORYLATED TAU,
; TITLE OF INVENTION: HYBRIDOMAS SECRETING THEM, ANTIGEN RECOGNITION OF THESE
; TITLE OF INVENTION: ANTIBODIES AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,404B
; FILING DATE: 27 Jan 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03032
; FILING DATE: 31 Jul 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870131.3
; FILING DATE: 29 Jul 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:003
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-776-404B-1

Query Match      100.0%; Score 50; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
    |||||
Db 52 YSSPGSPGT 60

RESULT 13
US-08-666-360-1
; Sequence 1, Application US/08666360
; Patent No. 6008024
; GENERAL INFORMATION:
; APPLICANT: Monoclonal antibodies specific for PHF-tau,
; TITLE OF INVENTION: hybridomas secreting them, antigen recognition of these
; TITLE OF INVENTION: antibodies and their applications
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,360
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-666-360-1

Query Match      100.0%; Score 50; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
    |||||
Db 55 YSSPGSPGT 63

RESULT 14
US-08-159-969-2
; Sequence 2, Application US/08159969
; Patent No. 5492812
; GENERAL INFORMATION:
; APPLICANT: Voorheis, Paul H.
; TITLE OF INVENTION: Diagnostic Method for Alzheimer's
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,969
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/738,778
; FILING DATE: 01-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MISTOCK, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 4697-040
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```


MOLECULE TYPE: protein
US-08-159-969-2

Query Match 100.0%; Score 50; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 139 YSSPGSPGT 147

RESULT 15
US-08-726-306A-17
Sequence 17, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/087726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-726-306A-17

Query Match 100.0%; Score 50; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 139 YSSPGSPGT 147

RESULT 16
US-08-244-951A-10
Sequence 10, Application US/08244951A

Patent No. 5843779
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 391
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
FEATURE:
NAME/KEY: mTHMPH-tau1 fusion protein
US-08-244-951A-10

Query Match 100.0%; Score 50; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 178 YSSPGSPGT 186

RESULT 17
US-08-389-011-23
Sequence 23, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

us-09-734-281-2.ra1

Wed May 22 11:04:36 2002

STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
FILING DATE: 19-JAN-1995
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 391
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-403-917A-23

Query Match 100.0%; Score 50; DB 3; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 178 YSSPGSPGT 186

RESULT 19
US-09-348-952A-23
Sequence 23, Application US/09348952A
Patent No. 6232437
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERMEEREN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
PROTEIN TAU, HYBRIDOMAS SECRETING BY THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 391
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-389-011-23

Query Match 100.0%; Score 50; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 178 YSSPGSPGT 186

RESULT 18
US-08-403-917A-23
Sequence 23, Application US/08403917A
Patent No. 6010913
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERMEEREN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
PROTEIN TAU, HYBRIDOMAS SECRETING BY THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK

```

; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/348,952A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-09-348-952A-23

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```

Query Match      100.0%; Score 50; DB 4; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGPT 9
Db 178 YSSPGSPGPT 186

```

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RESULT 20
US-08-244-603A-1
; Sequence 1, Application US/08244603A
; Patent No. 6200768
; GENERAL INFORMATION:
; APPLICANT: Mandelkow, Eva-Maria
; APPLICANT: Mandelkow, Eckhard
; APPLICANT: Lichtenberg-Kraag, Birgit
; APPLICANT: Biernat, Jacek
; APPLICANT: Drewes, Gerard
; APPLICANT: Steiner, Barbara
; TITLE OF INVENTION: No. 6200768el Tools For The Diagnosis And
; TITLE OF INVENTION: Treatment Of Alzheimer's Disease
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,603A
; FILING DATE:

```

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph A. Williams, Jr.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 28384/32778
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-484-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-244-603A-1

```

```

Query Match      100.0%; Score 50; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGPT 9
Db 197 YSSPGSPGPT 205

```

```

RESULT 21
US-09-159-106-2
; Sequence 2, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Ferrer, Pau
; APPLICANT: Diers, Ivan
; APPLICANT: Halkier, Torben
; APPLICANT: Hedegaard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159,106
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-2

```

```

Query Match      80.0%; Score 40; DB 4; Length 263;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGPT 9
Db 244 SSPGSPGPT 251

```

```

RESULT 22
US-09-159-106-11
; Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Ferrer, Pau
; APPLICANT: Diers, Ivan

```

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Wed May 22 11:04:36 2002

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23

; TYPE: Amino Acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Unknown

; FEATURE:

; NAME/KEY: human tau protein 199-221

; US-08-244-951A-3

Query Match 78.0%; Score 39; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9

Db 1 SPGSPGT 7

RESULT 24

US-08-244-951A-2

; Sequence 2, Application US/08244951A

; Patent No. 5843779

; GENERAL INFORMATION:

; APPLICANT: VANDEMEEREN, MARC; MERCKEN, MARC;

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE

; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN & MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/244,951A

; FILING DATE: 19-JAN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION NUMBER: PCT/EP93/03499

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP/92/403403.6

; FILING DATE: 14-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410.003A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000

; TELEFAX: (212) 661-8002

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33

; TYPE: Amino Acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Unknown

; FEATURE: human tau protein 199-231

; US-08-244-951A-2

APPLICANT: Halkier, Torben
APPLICANT: Hedegaard, Lisbeth
TITLE OF INVENTION: An Enzyme with -1,3-Glucanase

; TITLE OF INVENTION: Activity

; FILE REFERENCE: 4693.204-US

; CURRENT APPLICATION NUMBER: US/09/159,106

; CURRENT FILING DATE: 1998-09-23

; EARLIER APPLICATION NUMBER: 0427/96

; EARLIER FILING DATE: 1996-12-04

; EARLIER APPLICATION NUMBER: 0885/96

; EARLIER FILING DATE: 1996-08-23

; EARLIER APPLICATION NUMBER: PCT/DK97/00160

; EARLIER FILING DATE: 1997-04-14

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 11

; LENGTH: 435

; TYPE: PRT

; ORGANISM: Oerskovia xanthineolytica

; US-09-159-106-11

Query Match 80.0%; Score 40; DB 4; Length 435;

Best Local Similarity 87.5%; Pred. No. 56;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9

Db 297 SSPGSPGT 304

RESULT 23

US-08-244-951A-3

; Sequence 3, Application US/08244951A

; Patent No. 5843779

; GENERAL INFORMATION:

; APPLICANT: VANDEMEEREN, MARC; MERCKEN, MARC;

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE

; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN & MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/244,951A

; FILING DATE: 19-JAN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION NUMBER: PCT/EP93/03499

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP/92/403403.6

; FILING DATE: 14-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410.003A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000

; TELEFAX: (212) 661-8002

Query Match 78.0%; Score 39; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 |||||
 Db 1 SPGSPGT 7

RESULT 25
 US-08-389-011-2
 ; Sequence 2, Application US/08389011
 ; Patent No. 5861257
 ; GENERAL INFORMATION:
 ; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
 ; APPLICANT: VANMECHELEN, EUGEN;
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
 ; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 ; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIERMAN & MUSERLIAN
 ; STREET: 600 THIRD AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10016
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/389,011
 ; FILING DATE: 15-FEB-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/403,917
 ; FILING DATE: 19-JAN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/403,916
 ; FILING DATE: 19-JAN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/244,951
 ; FILING DATE: 13-JUN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/03499
 ; FILING DATE: 10-DEC-1993
 ; APPLICATION NUMBER: EP/92/403403.6
 ; FILING DATE: 14-DEC-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CHARLES A. MUSERLIAN
 ; REGISTRATION NUMBER: 19,683
 ; REFERENCE/DOCKET NUMBER: 410.003-1-CON
 ; TELEPHONE: (212) 661-8000
 ; TELEFAX: (212) 661-8002
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; US-08-389-011-2

Query Match 78.0%; Score 39; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 |||||
 Db 1 SPGSPGT 7

RESULT 26
 US-08-403-917A-2
 ; Sequence 2, Application US/08403917A
 ; Patent No. 6010913
 ; GENERAL INFORMATION:
 ; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
 ; APPLICANT: VANMECHELEN, EUGEN;
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
 ; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 ; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIERMAN & MUSERLIAN
 ; STREET: 600 THIRD AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10016
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,917A
 ; FILING DATE: 19-JAN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/256,167
 ; FILING DATE: 27-JUN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/244,951
 ; FILING DATE: 13-JUN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/03499
 ; FILING DATE: 10-DEC-1993
 ; APPLICATION NUMBER: EP/92/403403.6
 ; FILING DATE: 14-DEC-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CHARLES A. MUSERLIAN
 ; REGISTRATION NUMBER: 19,683
 ; REFERENCE/DOCKET NUMBER: 410.003-1
 ; TELEPHONE: (212) 661-8000
 ; TELEFAX: (212) 661-8002
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; US-08-403-917A-2

Query Match 78.0%; Score 39; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
 |||||
 Db 1 SPGSPGT 7

RESULT 27
 US-09-348-952A-2

Sequence 2, Application US/09348952A
Patent No. 6232437
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDEHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/348,952A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
APPLICATION DATA: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-09-348-952A-2

Query Match 78.0%; Score 39; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 3 SPGSPT 9
Db 1 SPGSPT 7
|||||||

RESULT 28
US-08-244-951A-6
; Sequence 6, Application US/08244951A
; Patent No. 5843779
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANDEHELEN, EUGEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/348,952A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; APPLICATION DATA: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; US-09-348-952A-2

Query Match 78.0%; Score 39; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.1; Indels 0;
Matches 7; Conservative 0; Mismatches 0;

QY 3 SPGSPT 9
Db 3 SPGSPT 9
|||||||

RESULT 29
US-08-836-561-106
; Sequence 106, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY

```

; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-561-106

```

```

Query Match          74.0%; Score 37; DB 3; Length 313;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
Db 99 HAPGSPGT 107

```

```

RESULT 30
US-07-947-130-2
; Sequence 2, Application US/07947130
; Patent No. 5455337
; GENERAL INFORMATION:
; APPLICANT: Devos, Rene
; APPLICANT: Fiers, Walter
; APPLICANT: Tavernier, Jan
; TITLE OF INVENTION: Chimeric Interleukin-5
; TITLE OF INVENTION: Receptor/Immunoglobulin Polypeptides
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mr. George M. Gould, Esq.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/947,130
; FILING DATE: 19920916
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION DATA:
; FILING DATE: 18-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.

```

```

; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 4105/144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-235-6326
; TELEFAX: 201-235-3500
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: leukemia
; CELL TYPE: Promyelocytes
; CELL LINE: HL-60
; IMMEDIATE SOURCE:
; LIBRARY: human HL-60
; CLONE: lambda gt11-hil5ralpha12
; US-07-947-130-2

```

```

Query Match          74.0%; Score 37; DB 1; Length 335;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
Db 119 HAPGSPGT 127

```

```

RESULT 31
US-08-421-822-2
; Sequence 2, Application US/08421822
; Patent No. 5668256
; GENERAL INFORMATION:
; APPLICANT: Devos, Rene
; APPLICANT: Fiers, Walter
; APPLICANT: Tavernier, Jan
; TITLE OF INVENTION: Chimeric Interleukin-5
; TITLE OF INVENTION: Receptor/Immunoglobulin Polypeptides
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mr. George M. Gould, Esq.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/421,822
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/947,130
; FILING DATE: 16-SEP-1992
; APPLICATION NUMBER: EP 91810738.4
; FILING DATE: 18-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 4105/144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-235-6326
; TELEFAX: 201-235-3500

```

us-09-734-281-2.ra1

Wed May 22 11:04:36 2002

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: leukemia
CELL TYPE: promyelocytes
CELL LINE: HL-60
IMMEDIATE SOURCE:
LIBRARY: human HL-60
CLONE: lambda gt11-hL5ralpha12
US-08-421-823-2

Query Match 74.0%; Score 37; DB 1; Length 335;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 33
US-07-757-390-14
Sequence 14, Application US/07757390
Patent No. 5453491
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tomimaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07757,390
FILING DATE: 19910910
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-757-390-14

Query Match 74.0%; Score 37; DB 1; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: leukemia
CELL TYPE: promyelocytes
CELL LINE: HL-60
IMMEDIATE SOURCE:
LIBRARY: human HL-60
CLONE: lambda gt11-hL5ralpha12
US-08-421-823-2

Query Match 74.0%; Score 37; DB 1; Length 335;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 32
US-08-421-823-2
Sequence 2, Application US/08421823
Patent No. 5712121
GENERAL INFORMATION:
APPLICANT: Devos, Rene
APPLICANT: Fiers, Walter
APPLICANT: Tavernier, Jan
TITLE OF INVENTION: Chimeric Interleukin-5
TITLE OF INVENTION: Receptor/Immunoglobulin Polypeptides
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mr. George M. Gould, Esq.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: USA
ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,823
FILING DATE: 13-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,130
FILING DATE: 16-SEP-1992
APPLICATION NUMBER: EP 91810738.4
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 4105/144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-235-6326
TELEFAX: 201-235-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single


```
QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 34
US-08-442-282-14
; Sequence 14, Application US/08442282
; Patent No 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-442-281-14

Query Match 74.0%; Score 37; DB 1; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 36
US-08-939-727-14
; Sequence 14, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 35
US-08-442-281-14
; Sequence 14, Application US/08442281
; Patent No 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
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us-09-734-281-2.ra1

wed May 22 11:04:36 2002

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/757,390
 FILING DATE: 10-SEP-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7005-030
 TELEPHONE: 212 8698864/9741
 TELEFAX: 212 790-9090
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-939-727-14

Query Match 74.0%; Score 37; DB 2; Length 396;
 Best Local Similarity 66.7%; Pred No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0;

QY 1 YSSPGSPGT 9
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 Db 119 HAPPGSPGT 127

RESULT 37
 US-07-757-390-13
 ; Sequence 13, Application US/07757390
 ; Patent No. 5453491
 ; GENERAL INFORMATION:
 ; APPLICANT: Takatsu, Kiyoshi
 ; APPLICANT: Tominaga, Akira
 ; APPLICANT: Takagi, Satoshi
 ; APPLICANT: Murata, Yoshiyuki
 ; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/757,390
 ; FILING DATE: 19910910
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7005-030
 ; TELEPHONE: 212 8698864/9741
 ; TELEFAX: 212 790-9090
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 420 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-07-757-390-13

Query Match 74.0%; Score 37; DB 1; Length 420;
 Best Local Similarity 66.7%; Pred No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 :: |||||
 Db 119 HAPPGSPGT 127

RESULT 38
 US-08-442-282-13
 ; Sequence 13, Application US/08442282
 ; Patent No. 5760204
 ; GENERAL INFORMATION:
 ; APPLICANT: Takatsu, Kiyoshi
 ; APPLICANT: Tominaga, Akira
 ; APPLICANT: Takagi, Satoshi
 ; APPLICANT: Murata, Yoshiyuki
 ; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/442,282
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA: 07/757,390
 ; APPLICATION NUMBER:
 ; FILING DATE: 10-SEP-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7005-030
 ; TELEPHONE: 212 8698864/9741
 ; TELEFAX: 212 790-9090
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 420 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-442-282-13

Query Match 74.0%; Score 37; DB 1; Length 420;
 Best Local Similarity 66.7%; Pred No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
 :: |||||
 Db 119 HAPPGSPGT 127

RESULT 39
 US-08-442-281-13
 ; Sequence 13, Application US/08442281
 ; Patent No. 5807991
 ; GENERAL INFORMATION:

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; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS: 18
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-281-13

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Query Match          74.0%; Score 37; DB 1; Length 420;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

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RESULT 40
US-08-939-727-13
; Sequence 13, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-939-727-13

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Query Match          74.0%; Score 37; DB 2; Length 420;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

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Search completed: May 21, 2002, 11:18:36
Job time: 196 sec

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us-09-734-281-2.rai

Wed May 22 11:04:36 2002

INTERFERENCE
Wed May 22 11:04:23 2002

us-09-734-281-1.ra

Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: May 21, 2002, 11:15:20 ; Search time 21.42 Seconds
(without alignments)
10.263 Million cell updates/sec

Title: US-09-734-281-1
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/6C.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	9	4	US-08-617-987A-1
2	50	100.0	9	4	US-08-617-987A-2
3	50	100.0	27	2	US-08-244-951A-5
4	50	100.0	31	2	US-08-244-951A-4
5	50	100.0	34	2	US-08-602-264A-10
6	50	100.0	34	3	US-08-461-018A-10
7	50	100.0	34	4	US-09-216-958-10
8	50	100.0	67	2	US-08-244-951A-1
9	50	100.0	67	2	US-08-389-011-1
10	50	100.0	67	3	US-08-403-917A-1
11	50	100.0	67	4	US-09-348-952A-1
12	50	100.0	106	3	US-08-776-404B-1
13	50	100.0	112	3	US-08-666-360-1
14	50	100.0	351	1	US-08-159-969-2
15	50	100.0	352	2	US-08-726-306A-17
16	50	100.0	391	2	US-08-244-951A-10
17	50	100.0	391	2	US-08-389-011-23
18	50	100.0	391	3	US-08-403-917A-23
19	50	100.0	391	4	US-09-348-952A-23
20	50	100.0	441	4	US-08-244-603A-1
21	40	80.0	263	4	US-09-159-106-2
22	40	80.0	435	4	US-09-159-106-11
23	39	78.0	23	2	US-08-244-951A-3
24	39	78.0	33	2	US-08-244-951A-2
25	39	78.0	33	2	US-08-389-011-2
26	39	78.0	33	3	US-08-403-917A-2
27	39	78.0	33	4	US-09-348-952A-2

28 39 78.0 35 2 US-08-244-951A-6 Sequence 6, Appli
29 37 74.0 313 3 US-08-836-561-106 Sequence 106, App
30 37 74.0 335 1 US-07-947-130-2 Sequence 2, Appli
31 37 74.0 335 1 US-08-421-822-2 Sequence 2, Appli
32 37 74.0 335 1 US-08-421-823-2 Sequence 2, Appli
33 37 74.0 396 1 US-07-757-390-14 Sequence 14, Appl
34 37 74.0 396 1 US-08-442-282-14 Sequence 14, Appl
35 37 74.0 396 1 US-08-442-281-14 Sequence 14, Appl
36 37 74.0 396 2 US-08-939-727-14 Sequence 14, Appl
37 37 74.0 420 1 US-07-757-390-13 Sequence 13, Appl
38 37 74.0 420 1 US-08-442-282-13 Sequence 13, Appl
39 37 74.0 420 1 US-08-442-281-13 Sequence 13, Appl
40 37 74.0 420 2 US-08-939-727-13 Sequence 13, Appl
41 36 72.0 61 1 US-08-175-155-67 Sequence 67, Appl
42 36 72.0 61 1 US-08-477-509B-102 Sequence 102, App
43 36 72.0 61 2 US-08-707-237A-74 Sequence 74, Appl
44 36 72.0 61 3 US-08-482-085B-102 Sequence 102, App
45 36 72.0 61 4 US-09-444-791A-102 Sequence 102, App
46 36 72.0 62 1 US-08-642-255-100 Sequence 100, App
47 36 72.0 62 1 US-08-397-633A-43 Sequence 43, Appl
48 36 72.0 63 1 US-08-642-255-121 Sequence 121, App
49 36 72.0 63 1 US-08-397-633A-32 Sequence 32, Appl
50 36 72.0 65 1 US-08-642-255-125 Sequence 125, App
51 36 72.0 65 1 US-08-397-633A-46 Sequence 46, Appl
52 36 72.0 71 1 US-08-642-255-108 Sequence 108, App
53 36 72.0 71 1 US-08-642-255-115 Sequence 115, App
54 36 72.0 71 1 US-08-397-633A-21 Sequence 21, Appl
55 36 72.0 71 1 US-08-397-633A-27 Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-617-987A-1
; Sequence 1, Application US/08617987A
; Patent No. 6238892
; GENERAL INFORMATION:
; APPLICANT: MERCKEN, MARC
; APPLICANT: MANDELKOW, EVA-MARIA
; APPLICANT: VANDERMEEREN, MARC
; APPLICANT: VANNEHELEN, EUGEN
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED AGAINST THE
; FILE REFERENCE: 12546.4USF1
; CURRENT APPLICATION NUMBER: US/08/617,987A
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: 08/108,758
; PRIOR FILING DATE: 1993-09-02
; PRIOR APPLICATION NUMBER: 91402871.7
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: No. 6238892e = "S is phosphorylated"
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: No. 6238892e = "S is phosphorylated"
US-08-617-987A-1

Query Match 100.0%; Score 50; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 1 YSSPGSPGT 9

TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-244-951A-4

Query Match 100.0%; Score 50; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

RESULT 5
US-08-602-264A-10
; Sequence 10, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-602-264A-10

Query Match 100.0%; Score 50; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

RESULT 7
US-09-216-958-10
; Sequence 10, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-602-264A-10

Query Match 100.0%; Score 50; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

RESULT 6
US-08-461-018A-10
; Sequence 10, Application US/08461018A
; Patent No. 6071694
; GENERAL INFORMATION:
; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,018A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-461-018A-10

Query Match 100.0%; Score 50; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

RESULT 7
US-09-216-958-10
; Sequence 10, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,018A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-461-018A-10

Query Match 100.0%; Score 50; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

RESULT 7
US-09-216-958-10
; Sequence 10, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,018A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-461-018A-10

us-09-734-281-1.rai

Wed May 22 11:04:23 2002

MEDIUM TYPE: Diskette, 3.5 Inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA: US/09/216,958
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,018
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-216-958-10

Query Match 100.0%; Score 50; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 7 YSSPGSPGT 15

RESULT 8
US-09-244-951A-1
Sequence 1, Application US/08244951A
Patent No. 5843779
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERMEEREN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:

FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
FEATURE:
NAME/KEY: human tau protein 155-211
US-08-244-951A-1

Query Match 100.0%; Score 50; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 43 YSSPGSPGT 51

RESULT 9
US-08-389-011-1
Sequence 1, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERMEEREN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: linear
US-08-389-011-1

Query Match 100.0%; Score 50; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
Db 43 YSPGSPGT 51

RESULT 10
US-08-403-917A-1
Sequence 1, Application US/08403917A
Patent No. 6010913
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
PROTEIN TAU, HYBRIDOMAS SECRETING THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-403-917A-1

Query Match 100.0%; Score 50; DB 3; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
Db 43 YSPGSPGT 51

RESULT 11
US-09-348-952A-1
Sequence 1, Application US/09348952A
Patent No. 6232437
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
PROTEIN TAU, HYBRIDOMAS SECRETING THESE
ANTIBODIES, ANTIGEN RECOGNITION BY THESE
MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/348,952A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown

us-09-734-281-1.rai

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US-09-348-952A-1

Query Match 100.0%; Score 50; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
|||||
DB 43 YSSPGSPGT 51

RESULT 12

US-08-776-404B-1
; Sequence 1, Application US/08776404B
; Patent No. 6121003
; GENERAL INFORMATION:
; APPLICANT: VANNECHELEN, EUGEN
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR AN EPIOTOPE OF
; TITLE OF INVENTION: A PARTICULAR SUBCLASS OR FORM OF PHOSPHORYLATED TAU.
; TITLE OF INVENTION: HYBRIDOMAS SECRETING THEM, ANTIGEN RECOGNITION OF THESE
; TITLE OF INVENTION: ANTIBODIES AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776.404B
; FILING DATE: 27 Jan 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03032
; FILING DATE: 31 Jul 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870131.3
; FILING DATE: 29 Jul 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:003
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-776-404B-1

Query Match 100.0%; Score 50; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
|||||
DB 52 YSSPGSPGT 60

RESULT 13

US-08-666-360-1
; Sequence 1, Application US/08666360
; Patent No. 6008024
; GENERAL INFORMATION:

; APPLICANT: Monoclonal antibodies specific for PHF-tau,
; TITLE OF INVENTION: hybridomas secreting them, antigen recognition of these
; TITLE OF INVENTION: antibodies and their applications
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,360
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-666-360-1

Query Match 100.0%; Score 50; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 YSSPGSPGT 9
|||||
DB 55 YSSPGSPGT 63

RESULT 14

US-08-159-969-2
; Sequence 2, Application US/08159969
; Patent No. 5492812
; GENERAL INFORMATION:
; APPLICANT: Voorheis, Paul H.
; TITLE OF INVENTION: Diagnostic Method for Alzheimer's
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,969
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/738,778
; FILING DATE: 01-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 4697-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-159-969-2

Query Match 100.0%; Score 50; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 139 YSSPGSPGT 147

RESULT 15

US-08-726-306A-17
Sequence 17, Application US/08726306A
Patent No. 5958684

GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726.306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)

TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-726-306A-17

Query Match 100.0%; Score 50; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 139 YSSPGSPGT 147

RESULT 16

US-08-244-951A-10
Sequence 10, Application US/08244951A

Patent No. 5843779
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 391
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
FEATURE:
NAME/KEY: mTHMPH- τ fusion protein
US-08-244-951A-10

Query Match 100.0%; Score 50; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 178 YSSPGSPGT 186

RESULT 17

US-08-389-011-23
Sequence 23, Application US/08389011
Patent No. 5861257

GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

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us-09-734-281-1-rai

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; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,011
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,916
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 23:
; LENGTH: 391
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; US-08-389-011-23

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Query Match 100.0%; Score 50; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0

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Qy 1 YSSPGSPGT 9
Db 178 YSSPGSPGT 186

```

```

RESULT 18
US-08-403-917A-23
; Sequence 23, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VAN DER VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK

```

```

; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,917A
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 23:
; LENGTH: 391
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; US-08-403-917A-23

```

Query Match 100.0%; Score 50; DB 3; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0

```

Qy 1 YSSPGSPGT 9
Db 178 YSSPGSPGT 186

```

```

RESULT 19
US-09-348-952A-23
; Sequence 23, Application US/09348952A
; Patent No. 6232437
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VAN DER VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/348,952A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERTIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-09-348-952A-23

```

```

Query Match      100.0%; Score 50; DB 4; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
   |||||
Db 178 YSSPGSPGT 186

```

```

RESULT 20
US-08-244-603A-1
; Sequence 1, Application US/08244603A
; Patent No. 6200768
; GENERAL INFORMATION:
; APPLICANT: Mandelkow, Eva-Maria
; APPLICANT: Mandelkow, Eckhard
; APPLICANT: Lichtenberg-Kraag, Birgit
; APPLICANT: Biernat, Jacek
; APPLICANT: Drewes, Gerard
; APPLICANT: Steiner, Barbara
; TITLE OF INVENTION: No. 6200768el Tools For The Diagnosis And
; TITLE OF INVENTION: Treatment Of Alzheimer's Disease
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,603A
; FILING DATE:

```

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph A. Williams, Jr.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 28384/32778
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-484-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-244-603A-1

```

```

Query Match      100.0%; Score 50; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
   |||||
Db 197 YSSPGSPGT 205

```

```

RESULT 21
US-09-159-106-2
; Sequence 2, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Ferrer, Pau
; APPLICANT: Diers, Ivan
; APPLICANT: Halkier, Torben
; APPLICANT: Hedegaard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159,106
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-2

```

```

Query Match      80.0%; Score 40; DB 4; Length 263;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
   |||||
Db 244 SSPGSPGT 251

```

```

RESULT 22
US-09-159-106-11
; Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Ferrer, Pau
; APPLICANT: Diers, Ivan

```

APPLICANT: Halkier, Torben
APPLICANT: Hedegaard, Lisbeth
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
TITLE OF INVENTION: Activity
FILE REFERENCE: 4693-204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1997-04-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 435
TYPE: PRT
ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

Query Match 80.0%; Score 40; DB 4; Length 435;
Best Local Similarity 87.5%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPGSPGT 9
||||:||||
DB 297 SSPGNPGT 304

RESULT 23
US-08-244-951A-3
Sequence 3, Application US/08244951A
Patent No. 5843779
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
FEATURE:
NAME/KEY: human tau protein 199-221
US-08-244-951A-3

Query Match 78.0%; Score 39; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
|||||||
DB 1 SPGSPGT 7

RESULT 24
US-08-244-951A-2
Sequence 2, Application US/08244951A
Patent No. 5843779
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
FEATURE:
NAME/KEY: human tau protein 199-231
US-08-244-951A-2

Query Match 78.0%; Score 39; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
Db 1 SPGSPGT 7

RESULT 25
US-08-389-011-2
; Sequence 2, Application US/08389011
; Patent No. 5861257
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING BY THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,011
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,916
; FILING DATE: 19-JAN-1995
; APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1-CON
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-389-011-2

Query Match 78.0%; Score 39; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
Db 1 SPGSPGT 7

RESULT 26
US-08-403-917A-2
; Sequence 2, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING BY THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,917A
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-403-917A-2

Query Match 78.0%; Score 39; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPGT 9
Db 1 SPGSPGT 7

RESULT 27
US-09-348-952A-2

us-09-734-281-1.rai

Wed May 22 11:04:23 2002

```

; Sequence 2, Application US/09348952A
; Patent No. 6232437
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANNECHELEN, EUGEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09348,952A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; US-09-348-952A-2

Query Match 78.0%; Score 39; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPT 9
DB 1 SPGSPT 7

RESULT 28
US-08-244-951A-6
; Sequence 6, Application US/08244951A
; Patent No. 5843779
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANNECHELEN, EUGEN; VAN DE VOORDE, ANDRE

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,951A
; FILING DATE: 19-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; US-08-244-951A-6

Query Match 78.0%; Score 39; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPGSPT 9
DB 3 SPGSPT 9

RESULT 29
US-08-836-561-106
; Sequence 106, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; RECEPTOR ALPHA CHAIN
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY

```



```

; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-561-106

```

```

Query Match 74.0%; Score 37; DB 3; Length 313;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 99 HAPGSPGT 107

```

```

RESULT 30
US-07-947-130-2
; Sequence 2, Application US/07947130
; Patent No. 545337
; GENERAL INFORMATION:
; APPLICANT: Devos, Rene
; APPLICANT: Fliers, Walter
; APPLICANT: Tavernier, Jan
; TITLE OF INVENTION: Chimeric Interleukin-5
; TITLE OF INVENTION: Receptor/Immunoglobulin Polypeptides
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mr. George M. Gould, Esq.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/947,130
; FILING DATE: 19920916
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91810738.4
; FILING DATE: 18-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.

```

```

; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 4105/144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-235-6326
; TELEFAX: 201-235-3500
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: leukemia
; CELL TYPE: Promyelocytes
; CELL LINE: HL-60
; IMMEDIATE SOURCE:
; LIBRARY: human HL-60
; CLONE: lambda gt11-hIL5Ralphal2
; US-07-947-130-2

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Query Match 74.0%; Score 37; DB 1; Length 335;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 YSSPGSPGT 9
Db 119 HAPGSPGT 127

RESULT 31
US-08-421-822-2
; Sequence 2, Application US/08421822
; Patent No. 5668256
; GENERAL INFORMATION:
; APPLICANT: Devos, Rene
; APPLICANT: Fliers, Walter
; APPLICANT: Tavernier, Jan
; TITLE OF INVENTION: Chimeric Interleukin-5
; TITLE OF INVENTION: Receptor/Immunoglobulin Polypeptides
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mr. George M. Gould, Esq.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/421,822
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/947,130
; FILING DATE: 16-SEP-1992
; APPLICATION NUMBER: EP 91810738.4
; FILING DATE: 18-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 4105/144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-235-6326
; TELEFAX: 201-235-3500

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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: leukemia
CELL TYPE: Promyelocytes
CELL LINE: HL-60
IMMEDIATE SOURCE:
LIBRARY: human HL-60
CLONE: lambda gt11-hil5Ra1pha12
US-08-421-823-2

Query Match 74.0%; Score 37; DB 1; Length 335;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 119 HAPGSPGT 127

RESULT 32
US-08-421-823-2
Sequence 2, Application US/08421823
Patent No. 5712121
GENERAL INFORMATION:
APPLICANT: Devos, Rene
APPLICANT: Fiers, Walter
APPLICANT: Tavernier, Jan
TITLE OF INVENTION: Chimeric Interleukin-5
TITLE OF INVENTION: Receptor/Immunoglobulin Polypeptides
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mr. George M. Gould, Esq.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: USA
ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,823
FILING DATE: 13-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,130
FILING DATE: 16-SEP-1992
APPLICATION NUMBER: EP 91810738.4
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 4105/144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-235-6326
TELEFAX: 201-235-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: leukemia
CELL TYPE: Promyelocytes
CELL LINE: HL-60
IMMEDIATE SOURCE:
LIBRARY: human HL-60
CLONE: lambda gt11-hil5Ra1pha12
US-08-421-823-2

Query Match 74.0%; Score 37; DB 1; Length 335;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
Db 119 HAPGSPGT 127

RESULT 33
US-07-757-390-14
Sequence 14, Application US/07757390
Patent No. 5453491
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tomimaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-757-390-14

Query Match 74.0%; Score 37; DB 1; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 34
US-08-442-282-14
; Sequence 14, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-282-14

Query Match 74.0%; Score 37; DB 1; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 35
US-08-442-281-14
; Sequence 14, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-281-14

Query Match 74.0%; Score 37; DB 1; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 36
US-08-939-727-14
; Sequence 14, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/757,390
;; FILING DATE: 10-SEP-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 7005-030
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 790-9090
;; TELEFAX: 212 8698864/9741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 396 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-939-727-14

Query Match 74.0%; Score 37; DB 2; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 37
US-07-757-390-13
; Sequence 13, Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-757-390-13

Query Match 74.0%; Score 37; DB 1; Length 420;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 38
US-08-442-282-13
; Sequence 13, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-282-13

Query Match 74.0%; Score 37; DB 1; Length 420;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSPGSPGT 9
Db 119 HAPPGSPGT 127

RESULT 39
US-08-442-281-13
; Sequence 13, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:

APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,281
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-442-281-13

Query Match 74.0%; Score 37; DB 1; Length 420;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
:: |||||
Db 119 HAPPGSPGT 127

RESULT 40

US-08-939-727-13
Sequence 13, Application US/08939727
Patent No. 5916767

GENERAL INFORMATION:

APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,727
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-939-727-13

Query Match 74.0%; Score 37; DB 2; Length 420;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSPGSPGT 9
:: |||||
Db 119 HAPPGSPGT 127

Search completed: May 21, 2002, 11:18:35
Job time: 195 sec

09/734,281

SYSTEM:OS - DIALOG OneSearch
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 (c) 2002 BIOSIS
 File 6:NTIS 1964-2002/Jun W1
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 (c) 2002 Inst for Sci Info
 File 40:Enviroline(R) 1975-2002/May
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 (c) 2002 Cambridge Scientific Abstracts
 File 50:CAB Abstracts 1972-2002/Apr
 (c) 2002 CAB International
 *File 50: Truncating CC codes is recommended for full retrieval.
 See Help News50 for details.
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 (c) 2002 Elsevier Science B.V.
 *File 73: For information about Explode feature please see Help News73.
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 File 77:Conference Papers Index 1973-2002/Mar
 (c) 2002 Cambridge Sci Abs
 File 94:JICST-EPlus 1985-2002/Mar W5
 (c)2002 Japan Science and Tech Corp(JST)
 *File 94: There is no data missing. UDs have been adjusted to reflect the current months data. See Help News94 for details.
 File 98:General Sci Abs/Full-Text 1984-2002/Apr
 (c) 2002 The HW Wilson Co.
 File 103:Energy SciTec 1974-2002/Apr B2
 (c) 2002 Contains copyrighted material
 *File 103: For access restrictions see Help Restrict.
 File 143:Biol. & Agric. Index 1983-2002/Apr
 (c) 2002 The HW Wilson Co
 File 144:Pascal 1973-2002/May W3
 (c) 2002 INIST/CNRS
 File 155:MEDLINE(R) 1966-2002/May W2
 *File 155: This file has been reloaded. Accession numbers have changed.
 File 156:ToxFile 1966-2002/Feb W4
 (c) 2002
 File 162:CAB HEALTH 1983-2002/Apr
 (c) 2002 CAB INTERNATIONAL
 *File 162: Truncating CC codes is recommended for full retrieval.
 See Help News162 for details.
 File 172:EMBASE Alert 2002/May W3
 (c) 2002 Elsevier Science B.V.
 File 305:Analytical Abstracts 1980-2002/Apr W4
 (c) 2002 Royal Soc Chemistry
 *File 305: Frequency of updates and Alerts changing to weekly.
 See HELP NEWS 305.
 File 369:New Scientist 1994-2002/May W2
 (c) 2002 Reed Business Information Ltd.
 File 370:Science 1996-1999/Jul W3
 (c) 1999 AAAS
 *File 370: This file is closed (no updates). Use File 47 for more current information.
 File 399:CA SEARCH(R) 1967-2002/UD=13621
 (c) 2002 AMERICAN CHEMICAL SOCIETY
 *File 399: Use is subject to the terms of your user/customer agreement.
 RANK charge added: see HELP RATES 399.
 File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
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 774614 PHOSPHORYL?
 959154 MONOCLONAL

131828 MAB
 S1 1305 TAU AND PHOSPHORYL? AND (MONOCLONAL OR MAB)
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 ? s s2 and PY<1996
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 Processed 10 of 26 files ...
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 >>> or undefined in one or more files.
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 Processed 20 of 26 files ...
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 Completed processing all files
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 S3 304 S2 AND PY<1996
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 Processing
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 >>> or undefined in one or more files.
 Processing
 Processed 20 of 26 files ...
 Completed processing all files
 304 S3
 67358859 PY<1993
 S4 111 S3 AND PY<1993
 ? t s4/7/all
 >>>Format 7 is not valid in file 143
 4/7/1 (Item 1 from file: 5)
 DIALOG(R)File 5:BIOSIS Previews(R)
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08798405 BIOSIS NO.: 199395087756
 The antineoplastic agent estramustine and the derivative estramustine phosphate inhibit secretion of interleukin-3 in leukemic cells: Possible roles of MAPs.
 AUTHOR: Martinez Jorge(a); Santibanez Juan Francisco; Vial Clarisa; Maccioni Ricardo B
 AUTHOR ADDRESS: (a)Inst. Nutricion y Tecnol. de Alimentos, Univ. de Chile, Casilla 138-11, Santiago**Chile
 JOURNAL: Molecular and Cellular Biochemistry 117 (2):p165-173
 %%%1992%%%

ISSN: 0300-8177
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The antineoplastic drug estramustine is an adduct of estradiol and nor-nitrogen mustard. It has been shown that this drug interferes with microtubule assembly, an effect mediated by estramustine interaction with microtubule-associated proteins (MAPs). In the present report we demonstrate that estramustine and the %%%phosphorylated%%% derivative of the drug, estramustine-phosphate, inhibit the secretion of interleukin-3 by WEHI-3B cells. These studies also show that the estramustine derivative specifically interacts with a MAPs component found in these cells, which exhibited characteristics resembling those of %%%tau%%% protein isoforms. Western blots using a unique %%%monoclonal%%% antibody MTB6.22 that recognizes microtubule-binding domains on MAPs, indicated that this WEHI protein factor contained the antigenic determinant that are functionally significant for microtubule assembly. ELISA assays using this antibody, also showed a decrease in the levels of the immunoreactive protein in WEHI cells after treatment with EMP. Interestingly, it has been recently described that the action of estramustine-phosphate is mediated by a direct interaction with MAP-binding sites on the microtubule surface, which are recognized by the site-specific %%%monoclonal%%% antibody. These findings together with immuno-precipitation experiments using anti-interleukin-3 antibodies and the inhibitory effect of the estramustine derivative on WEHI secretion process suggest that this anti-mitotic agent may block IL-3 secretion by a mechanism involving its interaction with a '%%tau%%-like' MAPs component present in these cells.

4/7/2 (Item 2 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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08787925 BIOSIS NO.: 199395077276
%%Phosphorylation%%% sites on %%%tau%%% by %%%tau%%% protein kinase I, a bovine derived kinase generating an epitope of paired helical filaments.
AUTHOR: Ishiguro Koichi(a); Omori Akira; Takamatsu Masako; Sato Kazuki; Arioka Manabu; Uchida Tsuneko; Imahori Kazutomo
AUTHOR ADDRESS: (a)Mitsubishi Kasei Inst. Life Sci., 11 Minamiooya, Machida-shi, Tokyo, 194**Japan
JOURNAL: Neuroscience Letters 148 (1-2):p202-206 %%%1992%%
ISSN: 0304-3940
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Tau%%% protein kinase I (TPKI) isolated from bovine brain has been determined to %%%phosphorylate%%% %%%tau%%% at four distinct sites by detecting modified Ser and Thr residues with protein sequencer. Ser199, Thr231, Ser396 and Ser413 were all found to have been %%%phosphorylated%%% by TPKI (numbering of amino acids was done in relation to the longest human %%%tau%%% (Neuron, 3 (1989) 519-526)). These phosphorylations generate an epitope of PHF (paired helical filaments) and eliminate the recognition of %%%tau%%% by the %%%monoclonal%%% antibody, %%%tau%%-1. These results suggested that TPKI might be responsible for at least some of the %%%phosphorylation%%% of %%%tau%%% to induce PHF formation

4/7/3 (Item 3 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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08775405 BIOSIS NO.: 199395064756
Glycogen synthase kinase-3 induces Alzheimer's disease-like %%%phosphorylation%%% of %%%tau%%: Generation of paired helical filament

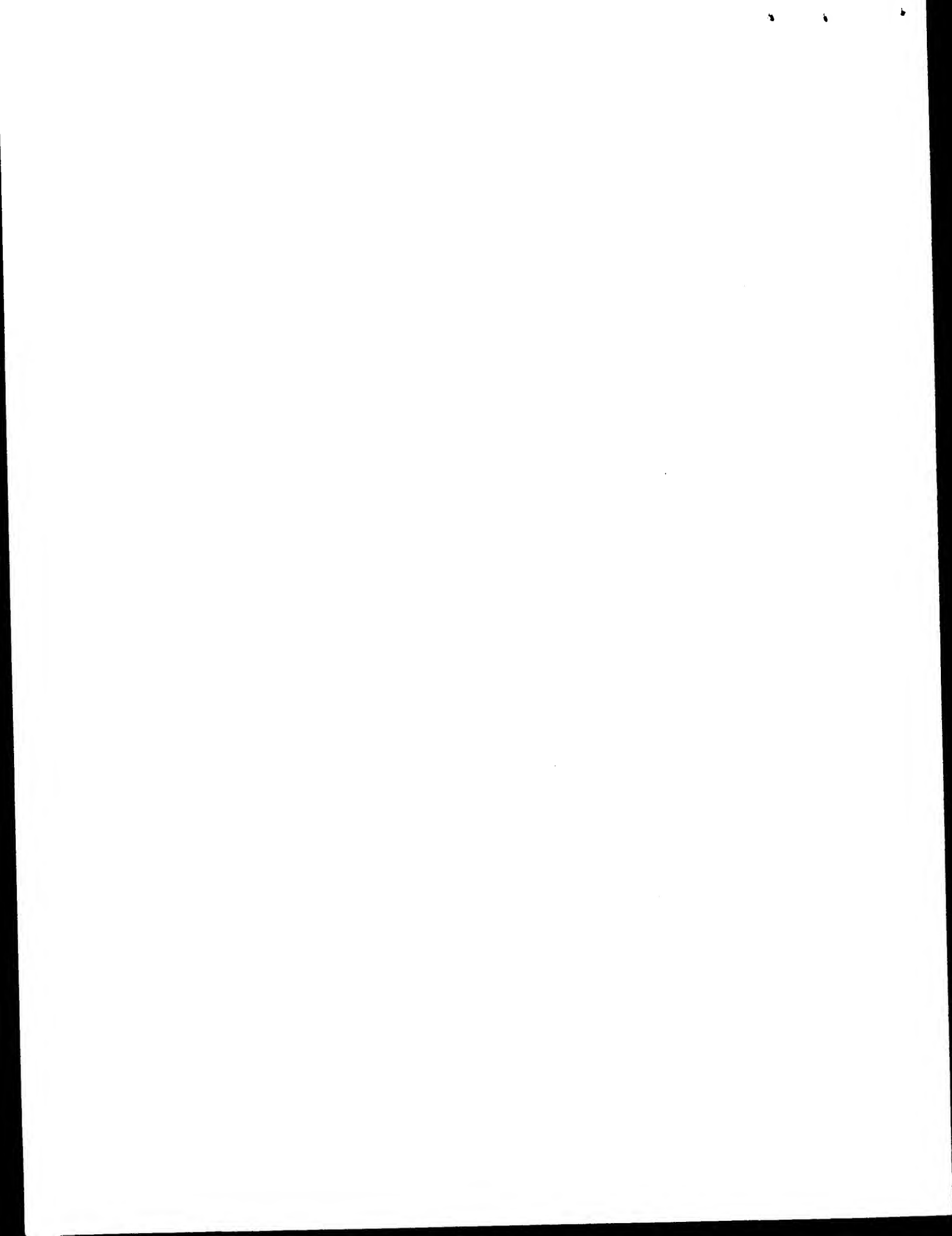
epitopes and neuronal localisation of the kinase.
AUTHOR: Hanger Diane P(a); Hughes Kenneth; Woodgett James R; Brion Jean-Pierre; Anderton Brian H
AUTHOR ADDRESS: (a)Dep. Neurosci., Inst. Psychiatry, De Crespigny Park, Denmark Hill, London SE5 8AF**UK
JOURNAL: Neuroscience Letters 147 (1):p58-62 %%%1992%%
ISSN: 0304-3940
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Glycogen synthase kinase-3 (GSK-3) reduced the mobility of human %%%tau%%% on SDS-PAGE, prevented binding of the %%%monoclonal%%% antibody (%%%mAb%%%), %%%Tau%%-1, and induced binding of the %%%mAb%%% 8D8. Recombinant %%%tau%%% %%%phosphorylated%%% by GSK-3 aligned on SDS-PAGE with the abnormally %%%phosphorylated%%% %%%tau%%% (PHF-%%tau%%%) associated with the paired helical filaments in Alzheimer's disease brain. %%%Phosphorylated%%% serine-396 (numbering of the largest human brain %%%tau%%% isoform) was identified as a binding site on %%%tau%%% for %%%mAb%%% 8D8. The localisation of GSK-3 within granular structures in pyramidal cells indicates that GSK-3-alpha and GSK-3-beta may have a role in the production of PHF-%%tau%%% in Alzheimer's disease.

4/7/4 (Item 4 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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08740909 BIOSIS NO.: 199395030260
Proline-directed %%%phosphorylation%%% of human %%%tau%%% protein.
AUTHOR: Vulliet Richard(a); Halloran S Mitchell; Braun Ruedi K; Smith Alan J; Lee Gloria
AUTHOR ADDRESS: (a)Dep. Vet. Pharmacol. Toxicol., Univ. Calif., Davis, Calif. 95616**ussia
JOURNAL: Journal of Biological Chemistry 267 (31):p22570-22574 %%%1992%%
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The primary sequence of the microtubule-associated proetin %%%tau%%% contains multiple repeats of the sequence -X-Ser-/Thr-Pro-X-, the consensus sequence for the proline-directed protein kinase (p34-cdc2/p58-cyclin A). When %%%phosphorylated%%% by proline-directed protein kinase in vitro, %%%tau%%% was found to incorporate up to 4.4 mol of phosphate/mol of protein. Isoelectric focusing of the tryptic phosphopeptides demonstrated the presence of five distinct peptides with pI values of approximately 6.9, 6.5, 5.6-5.9, 4.7, and 3.6. Mapping of the tryptic phosphopeptides by high performance liquid chromatography techniques demonstrated three distinct peaks. Data from gas phase sequencing, amino acid analysis, and phosphoamino acid analysis suggest that proline-directed protein kinase %%%phosphorylates%%% %%%tau%%% at four sites. Each site demonstrates the presence of a proline residue on the carboxyl-terminal side of the %%%phosphorylated%%% residue. Two %%%phosphorylation%%% sites are located adjacent to the three-repeat microtubule-binding domain that has been found to be required for the in vivo co-localization of %%%tau%%% protein to microtubules. Two other putative %%%phosphorylation%%% sites are located within the identified epitope of the %%%monoclonal%%% antibody %%%Tau%%-1. %%%Phosphorylation%%% of these sites altered the immunoreactivity of %%%tau%%% to %%%Tau%%-1 antibody. Since the neuronal microtubule-associated protein %%%tau%%% is multiply %%%phosphorylated%%%



in Alzheimer's disease, and %%%Tau%%-1 immunoreactivity is similarly reduced in neurofibrillary tangles and enhanced after dephosphorylation, phosphorylation at one or more of three sites may correlate with abnormally %%%phosphorylated%% sites in %%%tau%% protein in Alzheimer's disease.

4/7/5 (Item 5 from file: 5)
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08729888 BIOSIS NO.: 199395019239

A serine fwdarw proline change in the Alzheimer's disease-associated epitope %%%Tau%%-2 results in altered secondary structure, but %%%phosphorylation%% overcomes the conformational gap.

AUTHOR: Lang Emma; Otvos Laszlo Jr(a)
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JOURNAL: Biochemical and Biophysical Research Communications 188 (1):p
162-169 %%%1992%%
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Monoclonal%% antibody %%%Tau%% 2 was raised against bovine %%%tau%% protein, was reported to recognize a conformational epitope, and stained %%%tau%% was found in neurofibrillary tangles of Alzheimer's disease, but not normal human %%%tau%%. We synthesized tetradeca peptides corresponding to the original bovine sequence, its serine fwdarw proline substituted analog, the genuine human sequence of this region, and the bovine epitope %%%phosphorylated%% on the crucial serine. The secondary structure of the peptides was determined by circular dichroism. It was found that only the original bovine epitope showed a tendency to form the beta-pleated sheets characteristic of the neurofibrillary tangles. The spectra of the human peptide, its analog, and the %%%phosphorylated%% bovine sequence were very similar, featuring a weak, helical beta-turn character. Eventual %%%phosphorylation%% of epitopes of this otherwise heavily %%%phosphorylated%% protein may overcome inter-species conformational gaps.

4/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08717649 BIOSIS NO.: 199395007000

Immunological and conformational characterization of a %%%phosphorylated%% immunodominant epitope on the paired helical filaments found in Alzheimer's disease.

AUTHOR: Lang Emma; Szendrei Gyorgyi I; Lee Virginia M-Y; Otvos Laszlo Jr(a)
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JOURNAL: Biochemical and Biophysical Research Communications 187 (2):p
783-790 %%%1992%%
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The immunological recognition pattern of one of the most commonly used %%%monoclonal%% antibodies, PHF-1, which detects the paired helical filaments of Alzheimer's disease, exhibits a high degree of similarity with the recognition of a polyclonal antibody, anti-T3P, raised against a synthetic phosphopeptide, GAETVYKS(Phospho)PVVS6D, corresponding to

amino acids 389-402 of the microtubule-associated protein %%%tau%%. A panel of 16 synthetic non-%%phosphorylated%% and %%%phosphorylated%% peptides, excised from different regions of %%%tau%% and peptide analogs thereof, were used to show that PHF-1 is indeed directed against the T3 fragment. Circular dichroism spectroscopy shows that the %%%phosphorylated%% peptide exhibits a limited propensity to form intramolecular beta-pleated sheets, and alteration is found in the reverse-turn structure that dominates the middle section of the molecule. The shift in the turn-forming amino acids may also allow a stacking procedure, may interfere with microtubule assembly, and, consequently, may be accountable for deposit formation.

4/7/7 (Item 7 from file: 5)
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08427296 BIOSIS NO.: 000094134500

%%MONOCLONAL%% ANTIBODIES WITH SELECTIVE SPECIFICITY FOR ALZHEIMER %%%TAU%% ARE DIRECTED AGAINST PHOSPHATASE-SENSITIVE EPITOPES

AUTHOR: MERCKEN M; VANDERMEEREN M; LUEBKE U; SIX J; BOONS J; VAN DE VOORDE
A: MARTIN J-J; GHEUENS J
AUTHOR ADDRESS: LABORATORY MOLECULAR NEUROSCIENCE AGING RESEARCH, MAILMAN RESEARCH CENTER, MCLEAN HOSPITAL, BELMONT, MASS. 02178, USA.
JOURNAL: ACTA NEUROPATHOL 84 (3). 1992. 265-272. %%%1992%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

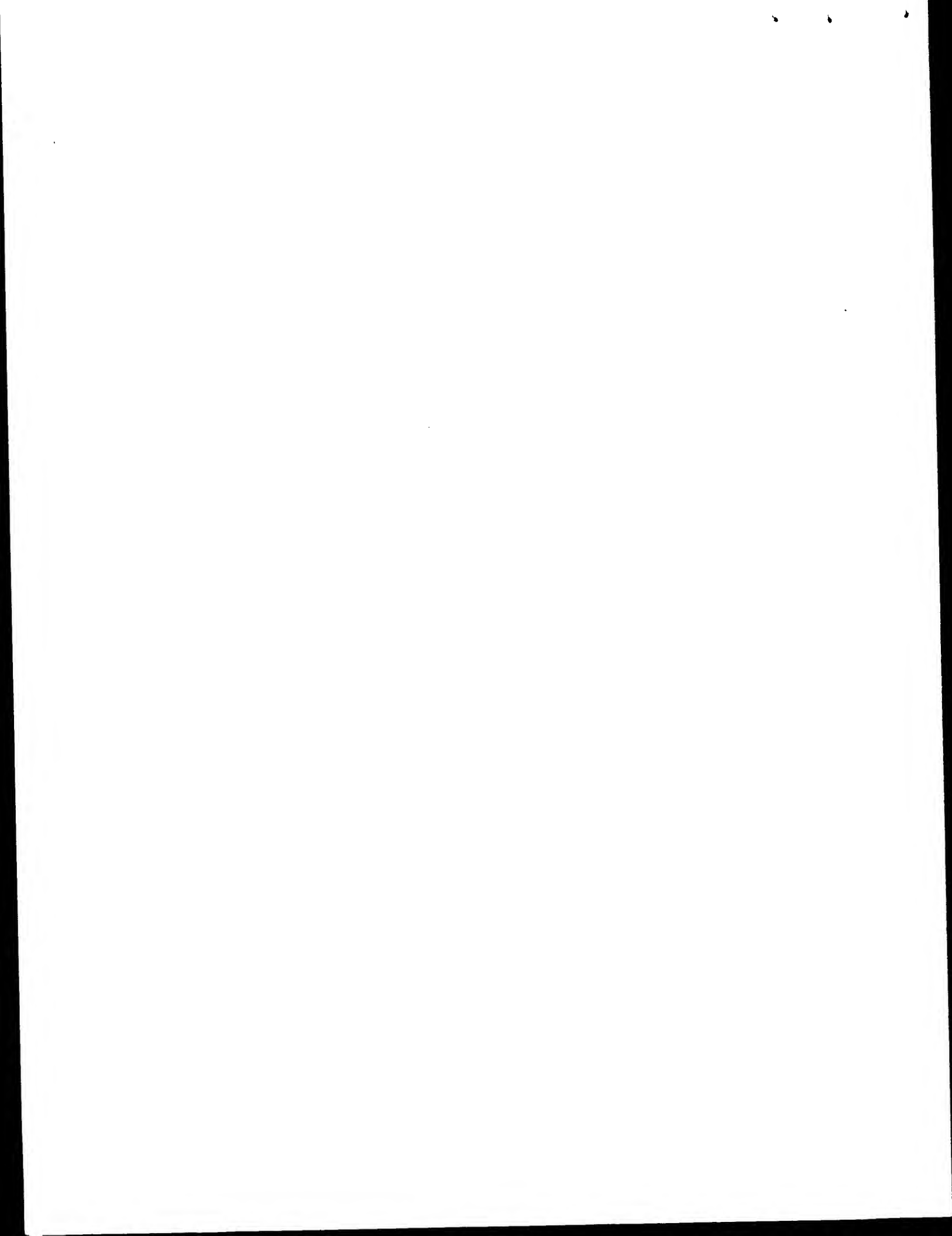
ABSTRACT: A modified form of the microtubule-associated protein %%%Tau%% is the major component of the paired helical filaments (PHF) found in Alzheimer's disease. The characterization of these posttranslational %%%Tau%% modifications is hindered by the lack of sufficient PHF-%%Tau%%-specific markers. Here we describe several %%%monoclonal%% antibodies, prepared by immunization with PHF, two of which showed a selective specificity for PHF-%%Tau%% without cross-reactivity with normal %%%Tau%%. Epitope recognition by these two monoclonals was sensitive to alkaline phosphatase treatment. In Western blotting these %%%monoclonal%% antibodies reacted specifically with the abnormally %%%phosphorylated%% epitopes on Alzheimer's disease-associated PHF-%%Tau%%. One of the new antibodies can be used for the construction of a sandwich enzyme-linked immunosorbent assay for the specific detection of PHF-%%Tau%% without cross-reactivity to normal %%%Tau%% proteins.

4/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08405595 BIOSIS NO.: 000094123249

%%TAU%% AND UBIQUITIN IN THE HUMAN HYPOTHALAMUS IN AGING AND ALZHEIMER'S DISEASE

AUTHOR: SWAAB D F; GRUNDKE-IQBAL I; IQBAL K; KREMER H P H; RAVID R; VAN DE NES J A P
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JOURNAL: BRAIN RES 590 (1-2). 1992. 239-249. %%%1992%%
FULL JOURNAL NAME: Brain Research
CODEN: BRREAA



RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Immunocytochemical staining of hypothalamic cell groups with four antibodies to Alzheimer paired helical filaments (PHF) (i.e., anti-PHF serum 60e and %%%monoclonal%% antibody (%%mAb%%) Alz-50, both directed against normal and abnormally %%%phosphorylated%% %%%tau%%. %%%mAb%%-1, which recognizes %%%tau%%; and %%%mAb%% 3-39 to PHF, which recognizes the carboxy terminal domain of ubiquitin) revealed a clear distinction between 12 Alzheimer's disease (AD) patients and seven controls in the hypothalamus. Dystrophic neurites, which appeared to be the most specific components in AD, were most conspicuous after Alz-50 staining. Alz-50 also stained neuronal cytoplasm and normal, thin, beaded neurites in the paraventricular nucleus (PVN) of controls, even of young cases. This staining was clearly distinct from the staining of cytoplasm and dystrophic neurites in the PVN of Alzheimer patients. The abundant staining of dystrophic neurites and cell bodies in the nucleus tuberalis lateralis (NTL) in AD, in which no neuronal loss is observed, suggests that alterations in cytoskeletal markers do not necessarily indicate impending cell death. Moreover, the cytoskeletal changes in the NTL, sexually dimorphic and suprachiasmatic nuclei in AD indicate that this condition is not restricted to cortical areas of nuclei projecting to the cortex. Consequently, the pathophysiological implications of cytoskeletal staining in AD are at present far from clear. The human hypothalamus may not only provide a better insight into the pathogenesis of Alzheimer's disease, but could also be of help in the neuropathological diagnosis of this condition.

4/7/9 (Item 9 from file: 5)
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08380441 BIOSIS NO.: 000094110945
IMPLICATION OF BRAIN CDC2 AND MAP2 KINASES IN THE
%%PHOSPHORYLATION%% OF
%%TAU%% PROTEIN IN ALZHEIMER'S DISEASE
AUTHOR: LEDESMA M D; CORREAS I; AVILA J; DIAZ-NIDO J
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MADRID, SPAIN.
JOURNAL: FEBS (FED EUR BIOCHEM SOC) LETT 308 (2). 1992. 218-224.
%%1992%%
FULL JOURNAL NAME: FEBS (Federation of European Biochemical
Societies)
Letters
CODEN: FEBLA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Brain %%%tau%% protein is %%%phosphorylated%% in vitro by cdc2 and MAP2 kinases, obtained through immunoaffinity purification from rat brain extracts. The %%%phosphorylation%% sites are located on the %%%tau%% molecule both upstream and downstream of the tubulin-binding motifs. A synthetic peptide comprising residues 194-213 of the %%%tau%% sequence, which contains the epitope recognized by the %%%monoclonal%% antibody %%%tau%%-1, is also efficiently %%%phosphorylated%% in vitro by cdc2 and MAP2 kinases. %%%Phosphorylation%% of this peptide markedly reduces its interaction with the antibody %%%tau%%-1, as it has been described for %%%tau%% protein in Alzheimer's disease. Both cdc2 and MAP2 kinases are present in brain extracts obtained from Alzheimer's disease patients. Interestingly, the level of cdc2 kinase may be increased in patient brains as compared with non-demented controls. These results suggest a role for cdc2 and MAP2 kinases in %%%phosphorylating%% %%%tau%% protein at the %%%tau%%-1 epitope in Alzheimer's disease.

4/7/10 (Item 10 from file: 5)
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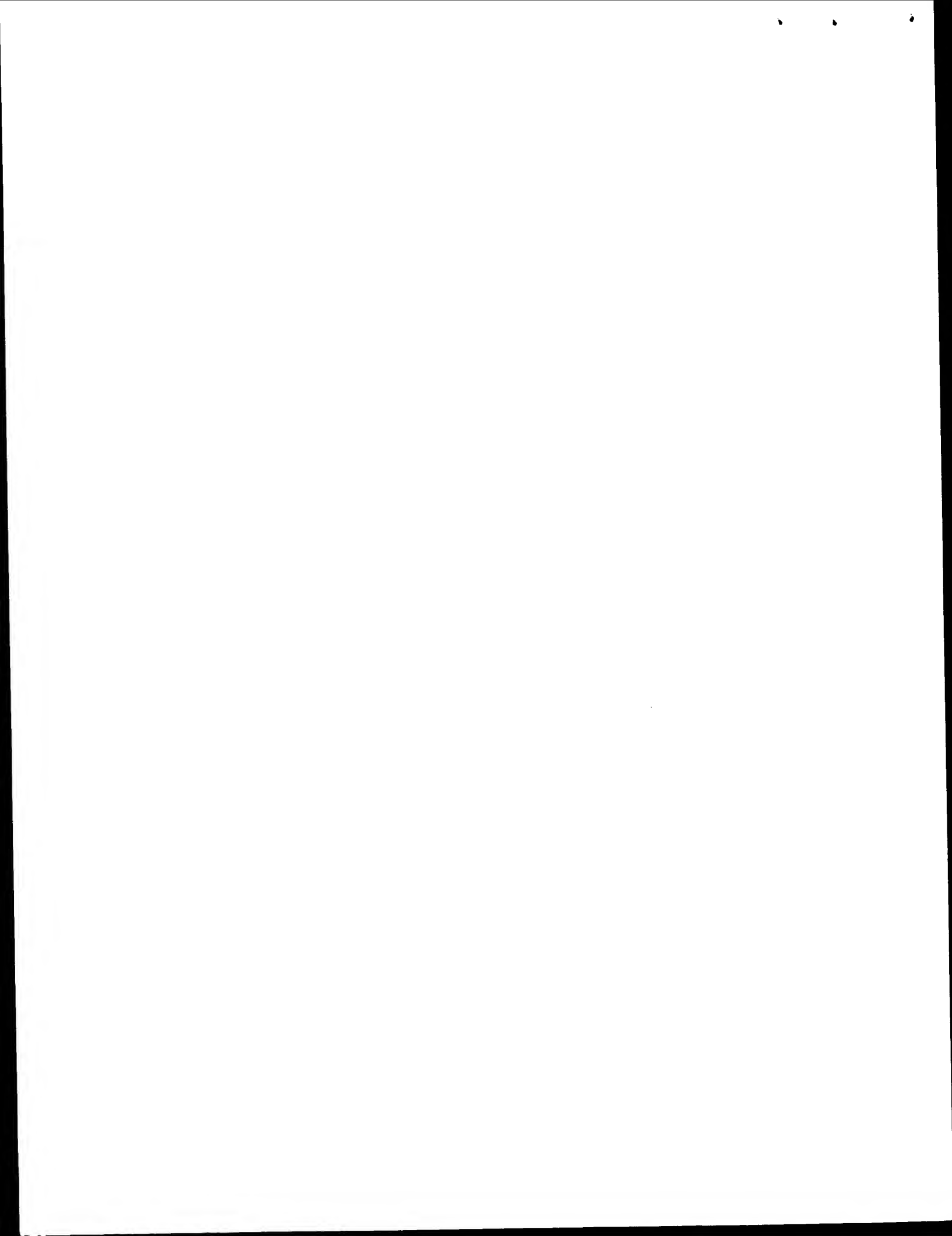
08336193 BIOSIS NO.: 000094087441
BRAIN LEVELS OF MICROTUBULE-ASSOCIATED PROTEIN
%%TAU%% ARE ELEVATED IN
ALZHEIMER'S DISEASE A RADIOIMMUNO-SLOT-BLOT ASSAY FOR
NANOGRAMS OF THE
PROTEIN
AUTHOR: KHATOON S; GRUNDKE IQBAL I; IQBAL K
AUTHOR ADDRESS: NEW YORK STATE INST. BASIC RES.
DEVELOPMENTAL DISABILITIES,
1050 FOREST HILL ROAD, STATEN ISLAND N.Y. 10314.
JOURNAL: J NEUROCHEM 59 (2). 1992. 750-753. %%1992%%
FULL JOURNAL NAME: Journal of Neurochemistry
CODEN: JONRA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The microtubule-associated protein %%%tau%%, which stimulates the assembly of .alpha.-beta. tubulin heterodimers into microtubules, is abnormally %%%phosphorylated%% in Alzheimer's disease (AD) brain and is the major component of paired helical filaments. In the present study, the levels of %%%tau%%, and abnormally %%%phosphorylated%% %%%tau%%, were determined in brain homogenates of AD and age-matched control cases. A radioimmuno-slot-blot assay was developed, using a primary %%%monoclonal%% antibody, %%%Tau%%-1, and a secondary antibody, anti-mouse 125I-immunoglobulin G. To assay the abnormally %%%phosphorylated%% %%%tau%%, the blots were treated with alkaline phosphatase before immunolabeling. The levels of total %%%tau%% were about eightfold higher in AD (7.3 +/- 2.7 ng/mu.g of protein) than in control cases (0.9 +/- 0.2 ng/mu.g), and this increase was in the form of the abnormally %%%phosphorylated%% protein. These studies indicate that the abnormal %%%phosphorylation%% - not a decrease in the level of %%%tau%% - is a likely cause of neurofibrillary degeneration in AD.

4/7/11 (Item 11 from file: 5)
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08293779 BIOSIS NO.: 000094065077
%%PHOSPHORYLATION%%-DEPENDENT EPITOPES OF
NEUROFILAMENT ANTIBODIES ON
%%TAU%% PROTEIN AND RELATIONSHIP WITH ALZHEIMER
%%TAU%%
AUTHOR: LICHTENBERG-KRAAG B; MANDELKOW E-M; BIERNAT J;
STEINER B; SCHROETER
C; GUSTKE N; MEYER H E; MANDELKOW E
AUTHOR ADDRESS: MAX-PLANK-UNIT FOR STRUCTURAL MOLECULAR
BIOL., C/O DESY,
NOTKESTRASSE 85, D-2000 HAMBURG 52, WEST GERMANY.
JOURNAL: PROC NATL ACAD SCI U S A 89 (12). 1992. 5384-5388.
%%1992%%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences
of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have studied the %%%phosphorylation%% of %%%tau%% protein from Alzheimer paired helical filaments, of %%%tau%% from normal human brain, and of recombinant %%%tau%% isoforms. As a tool we used %%%monoclonal%% antibodies against neurofilament protein that



crossreact

with %%%tau%%% in a %%%phosphorylation%%%dependent manner. This allowed

us to deduce the state of %%%phosphorylation%%% in normal and pathological %%%tau%%%, as well as antibody epitopes. The epitope of antibody SMI33 is at the first Lys-Ser-Pro sequence motif (residues 234-236) and requires an unphosphorylated Ser-235. Antibody SMI31 binds

between Ser-396 (in the second Lys-Ser-Pro motif) and Ser-404, both of which must be %%%phosphorylated%%%. SMI34 has a conformational epitope

that depends on the interaction between regions on either side of the microtubule-binding region; it also requires %%%phosphorylation%%%. The %%%phosphorylatable%%% serines detected by the SMI antibodies are part of

Ser-Pro motifs and can be %%%phosphorylated%%% by a protein kinase activity that can be used to induce a paired helical filament-like state in human brain %%%tau%%% in vitro. The phosphates are incorporated in several stages that can be identified by antibody reactivity and gel shift. This suggests a role for the %%%phosphorylation%%% sites in Alzheimer disease, as well as the involvement of a Ser-Pro-directed protein kinase.

4/7/12 (Item 12 from file: 5)

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08183925 BIOSIS NO.: 000094007698

THE SWITCH OF %%%TAU%%% PROTEIN TO AN ALZHEIMER-LIKE STATE INCLUDES THE

%%%PHOSPHORYLATION%%% OF TWO SERINE PROLINE MOTIFS UPSTREAM OF THE

MICROTUBULE BINDING REGION

AUTHOR: BIERNAT J; MANDELKOW E-M; SCHROETER C;

LICHTENBERG-KRAAG B; STEINER

B; BERLING B; MEYER H; MERCKEN M; VANDERMEEREN A; GOEDERT M; MANDELKOW E

AUTHOR ADDRESS: MAX-PLANCK-UNIT STRUCTURAL MOL. BIOL., C/O DESY,

NOTKESTRASSE 85, D-2000 HAMBURG 52, GER.

JOURNAL: EMBO (EUR MOL BIOL ORGAN) J 11 (4). 1992. 1593-1597.

%%%1992%%%

FULL JOURNAL NAME: EMBO (European Molecular Biology Organization) Journal

CODEN: EMJOD

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: The paired helical filaments (PHFs) of Alzheimer's disease consist mainly of the microtubule-associated protein %%%tau%%%. PHF %%%tau%%% differs from normal human brain %%%tau%%% in that it has a

higher Mr and a special state of %%%phosphorylation%%%. However, the protein kinase(s) involved, the %%%phosphorylation%%% sites on %%%tau%%%

and the resulting conformational changes are only poorly understood. Here we show that a new %%%monoclonal%%% antibody, AT8, records the PHF-like

state of %%%tau%%% in vitro, and we describe a kinase activity that turns normal %%%tau%%% into a PHF-like state. The epitope of AT8 is around residue 200, outside the region of internal repeats and requires the %%%phosphorylation%%% of serines 199 and/or 202. Both of these are followed by a proline, suggesting that the kinase activity belongs to the family of proline-directed kinases. The epitope of AT8 is nearly coincident with that of another %%%phosphorylation%%%dependent antibody,

TAU1 [Binder, L.I., Frankfurter, A. and Rebhun, L. (1985) J. Cell Biol., 101, 1371-1378], but the two are complementary since TAU1 requires a dephosphorylated epitope.

4/7/13 (Item 13 from file: 5)

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07889611 BIOSIS NO.: 000092138901

EFFECTS OF INJECTED ALZHEIMER BETA AMYLOID CORES IN RAT BRAIN

AUTHOR: FRAUTSCHY S A; BAIRD A; COLE G M

AUTHOR ADDRESS: DEP. MOL. CELLULAR GROWTH BIOL., WHITTIER INST. DIABETICS

ENDOCRINOL., 9894 GENESEE, LA JOLLA, CALIF. 92037.

JOURNAL: PROC NATL ACAD SCI U S A 88 (19). 1991. 8362-8366.

%%%1991%%%

FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the

United States of America

CODEN: PNASA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Although amyloid deposits have long been known to accumulate in

Alzheimer disease (AD) brain, their origin and significance remain speculative. Because of the lack of an in vivo model where amyloid deposits can be induced, the relationship of the extracellular beta-amyloid deposits to another AD pathology has never been directly investigated. Therefore, we injected SDS-isolated amyloid cores into rat cortex and hippocampus. Similarly isolated lipofuscin fractions from control human brains were injected on the contralateral side. Rats were perfused and brains were examined immunohistochemically at 2 days, 7 days, and 1 month after injection. Alz-50, a %%%monoclonal%%% antibody against abnormally %%%phosphorylated%%% %%%tau%%% proteins, stained

neurons along the cortical needle track at 2 but not 7 days after injection of either amyloid or lipofuscin. At 1 month, however, ubiquitin, Alz-50 antigen, and silver-positive structures were observed only in response to amyloid. In 7 of 10 animals, there was considerable neuronal loss in the hippocampal layers. In each instance, these effects were in the immediate vicinity of beta-protein immunoreactive material. Marked neuronal loss was never observed at any time after lipofuscin injection. These results indicate a neuronal response to amyloid. When preparations of mature plaque amyloid isolated from the AD brain are injected into the rat brain, they exert neurotoxic effects and induce antigen found in the AD brain.

4/7/14 (Item 14 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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07867990 BIOSIS NO.: 000092127356

MOLECULAR MILESTONES THAT SIGNAL AXONAL MATURATION AND THE COMMITMENT OF

HUMAN SPINAL CORD PRECURSOR CELLS TO THE NEURONAL OR GLIAL PHENOTYPE IN

DEVELOPMENT

AUTHOR: TOHYAMA T; LEE V M-Y; RORKE L B; TROJANOWSKI J Q

AUTHOR ADDRESS: DEP. PATHOLOGY, CHILDREN'S HOSP.

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PHILADELPHIA, PA. 19104.

JOURNAL: J COMP NEUROL 310 (3). 1991. 285-299. %%%1991%%%

FULL JOURNAL NAME: Journal of Comparative Neurology

CODEN: JCNEA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Insights into the programmatic induction of neuronal and glial genes during human embryogenesis have depended largely on extrapolations of data derived from experimental mammals. However, the assumptions upon

which these extrapolations are based have not been rigorously tested. Indeed, practically no information is available even on the human counterparts if the relatively small subset of well-characterized, developmentally regulated neuron and glial specific genes of the mammalian CNS. Thus, the developmental programs upon which human neural

embryogenesis are based remain largely undeciphered. We have addressed this problem in immunohistochemical studies conducted on 22 human fetal spinal cords with gestational ages (GAs) that ranged from 6 to 40 weeks by using %%%monoclonal%%% antibodies to several classes of neuron or

glial specific polypeptides. These polypeptides included: representatives of four different types (Types I-IV) of intermediate filament proteins, i.e., vimentin filament protein (VFP), glial fibrillary acidic protein (GFAP), different phospho-isoforms of the high (NF-H), middle (NF-M), and

low (NF-L) molecular weight (Mr) neurofilament (NF) subunits, both acidic and basic cytokeratin (CK) proteins; three different microtubule associated proteins (MAPs), i.e., MAP2, MAP5, and τ ; two different synaptic or coated vesicle proteins, i.e., synaptophysin (SYP) and clathrin light chain B (LCb); an oligodendroglial specific protein, i.e., myelin basic protein (MBP); and a receptor for a CNS trophic factor, i.e., the nerve growth factor receptor (NGFR). The major findings derived from these studies may be summarized as follows: 1) the most primitive neuroepithelial cells only expressed VFP and MAP5; 2) postmitotic, postmigratory neurons transiently expressed NGFR in the earliest development stages, while NF-H, NF-M, NF-L, MAP2, MAP5, clathrin

LCb, and SYP were expressed throughout development although the time of initial onset of each of these proteins differed; for example, NF-M isoforms generally appeared before NF-L and NF-H isoforms, and the most highly phosphorylated NF-H variants emerged much later than NF-M;

moreover, the induction of SYP in anterior horn cells followed the induction of proteins that are thought to determine neuronal polarity (e.g., NF-L, NF-M, NF-H, MAP2, τ); 3) GFAP positive astrocytes

became evident after the appearance of many neuron specific proteins although radial glia transiently expressed VFP earlier in development; 4) MBP appeared in the cell bodies of glial cells contemporaneously with GFAP, and in the myelin sheaths of white matter well before axons acquired a fully mature complement of cytoskeletal proteins; and 5) although programmed neuron death undoubtedly occurred during the GAS examined here, this process was not associated with presence of debris containing any of the developmentally regulated polypeptides examined in this study. We concluded that human neurogenesis and gliogenesis in the developing spinal cord is a highly orchestrated process in which neuron specific and glial specific genes are induced in a manner quite similar to that described in previous studies of other experimental animals. However, unlike some reports on neurogenesis in rodents and birds, the acquisition of the molecular, neuronal phenotypes in the human spinal cord was exclusively a postmitotic, postmigratory series of events. Nevertheless, as in these other species, the induction of neuron specific gene products in human spinal cord neurons occurred in a step-wise, asynchronous manner. Finally, the absence of cellular debris containing any of the developmentally regulated antigens we studied here, at a time during which massive neuron death is likely to be in progress, suggests that the induction of these neuron specific genes may identify subsets of neurons destined to survive into maturity.

4/7/15 (Item 15 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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07710219 BIOSIS NO.: 000092046000
ALTERED τ PHOSPHORYLATION OF τ PROTEIN IN
HEAT-SHOCKED RATS AND
PATIENTS WITH ALZHEIMER DISEASE
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TEX. 77030.
JOURNAL: PROC NATL ACAD SCI U S A 88 (10). 1991. 4543-4547.
 τ 1991
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences
of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Six hours after heat shocking 2- to 3-month-old male and female

Sprague-Dawley rats at 42 degree. C for 15 min, we analyzed τ protein immunoreactivity in SDS extracts of cerebrums and peripheral

nerves by using immunoblot analysis and immunohistochemistry with the anti- τ monoclonal antibody τ -1, which recognizes

a phosphate-dependent non-phosphorylated epitope, and with 125I-labeled protein A. In the cerebral extracts, we found altered phosphorylation of τ in heat-shocked females, characterized by a marked reduction in the amount of nonphosphorylated τ , a doubling of the ratio of total phosphorylated plus

nonphosphorylated τ to nonphosphorylated τ , and the appearance of the slowest moving phosphorylated τ polypeptide (68 kDa). Similar, but milder, changes were observed in male rats. These changes progressively increased in females from 3 to 6 h after heat shocking. In contrast, both phosphorylated τ and nonphosphorylated τ were reduced in peripheral nerves after

heat shocking. In immunoblots of SDS extracts from Alzheimer disease-affected brain, the two slowest moving phosphorylated τ polypeptides (62 kDa and 66 kDa, respectively) were detected by τ -1 after dephosphorylation and by τ -2 (an anti-

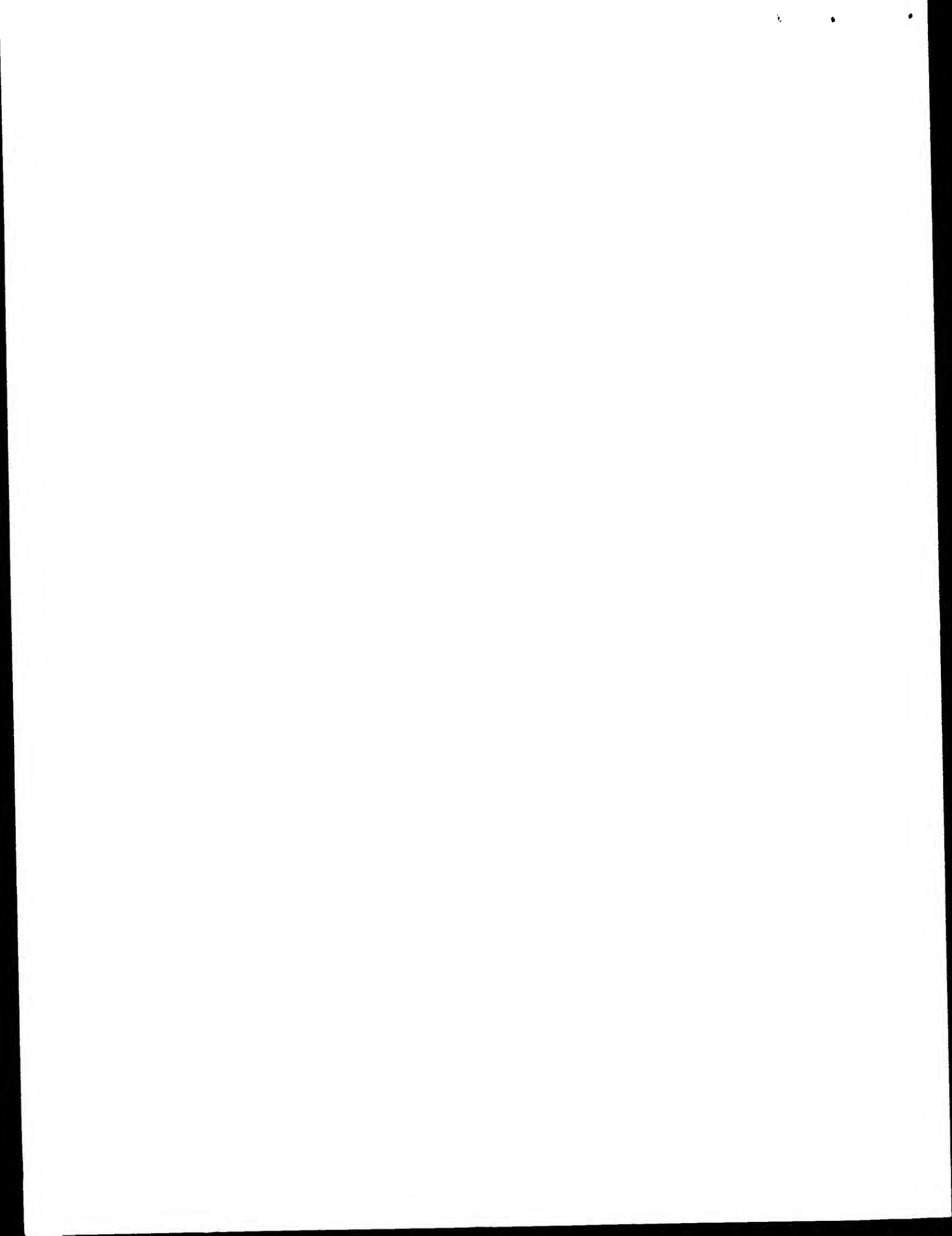
τ monoclonal antibody that recognizes a phosphate-independent epitope) without prior dephosphorylation only in regions that contained τ immunoreactivity in histologic preparations. In addition, quantitative immunoblot analysis of cortex and the underlying white matter with τ -1 and 125I-labeled protein A

showed that the amount of phosphorylated τ progressively increased in the Alzheimer disease-affected cerebral cortex, while concurrently a proportionally lesser amount of τ entered the white matter axons. The similar findings for the rat heat-shock model and Alzheimer disease suggest that life stressors may play a role in the etiopathogenesis of Alzheimer disease.

4/7/16 (Item 16 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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07615129 BIOSIS NO.: 000091133013
 τ IN ALZHEIMER'S DISEASE AND DOWN'S SYNDROME
IS INSOLUBLE AND
ABNORMALLY PHOSPHORYLATED
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JOURNAL: BIOCHEM J 275 (1). 1991. 99-104. τ 1991
FULL JOURNAL NAME: Biochemical Journal
CODEN: BJOA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Some investigators have described the presence in Alzheimer's disease brain extracts of several abnormal forms of the microtubule-associated protein τ , based on their unusual mobility in SDS-PAGE. It has been proposed that these abnormal forms of τ may be the result of aberrant τ phosphorylation. In this study we show that τ in extracts of Alzheimer's disease brain can be separated into two fractions based upon its solubility (100,000 g times 1 h supernatant) in non-denaturing conditions (100 mM-Mes, pH 6.5, 0.5 M-MgCl2, 1 mM-EGTA and 1 M-NaCl). The τ isoforms with decreased mobility in SDS/PAGE are predominantly in an insoluble fraction, whereas the soluble τ is indistinguishable by its mobility in SDS/PAGE from τ in soluble extracts of control



brain.

Insoluble τ displaying abnormal mobility on SDS/PAGE was only found in Alzheimer and adult Down's syndrome brains and was absent from the brains of age-matched controls and from fetal and infant Down's syndrome brains. There was a good correlation between the presence of insoluble τ in brain extracts and the abundance of neurofibrillary tangles and senile neuritic plaques. The monoclonal antibody τ 1 stained insoluble τ on Western blots only after treatment of the nitrocellulose transfers with alkaline phosphatase, implying that this insoluble τ is in a particular state of phosphorylation. We conclude that, in Alzheimer's disease, a fraction of τ has a modified phosphorylation state and a decreased solubility; these modifications may precede formation of the neurofibrillary tangles characteristic of Alzheimer's disease and Down's syndrome in adults.

4/7/17 (Item 17 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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07526493 BIOSIS NO.: 000091089622
ABNORMAL PHOSPHORYLATION OF τ
UBIQUITINATION IN
NEUROFIBRILLARY PATHOLOGY OF ALZHEIMER DISEASE
AUTHOR: BANCHER C; GRUNDKE IQBAL I; IQBAL K; FRIED V A; SMITH H T;
WISNIEWSKI H M
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JOURNAL: BRAIN RES 539 (1). 1991. 11-18. 1991
FULL JOURNAL NAME: Brain Research
CODEN: BRREA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: On tissue sections of Alzheimer brain, 4 antibodies to τ immunolabel not only neurofibrillary tangles, neuritic plaques and neuropil threads but also the tangle-free cytoplasm of a subset of hippocampal and cortical neurons we believe to be at a stage of alteration preceding the formation of paired helical filaments (PHF). Pretreatment of tissue sections with alkaline phosphatase leads to an increase in staining intensity and in number of immunoreactive lesions with antibodies directed to an amino terminal and to a mid-region of the τ molecule. The diffuse neuronal staining could not be observed with any of 7 monoclonal antibodies recognizing ubiquitin. We conclude (1) that abnormal phosphorylation of τ occurs prior to its incorporation into PHF and leads to its accumulation in the nerve cell body and (2) that ubiquitin is seen associated only when a neurofibrillary tangle is already formed.

4/7/18 (Item 18 from file: 5)
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07430728 BIOSIS NO.: 000091036717
CYCLIC AMP AGONISTS INDUCE THE PHOSPHORYLATION OF
PHOSPHOLIPASE C-
 τ AND OF A 76-KDA PROTEIN CO-PRECIPITATED BY
ANTI-PHOSPHOLIPASE
C- τ MONOCLONAL ANTIBODIES IN
BALB-C-3T3 CELLS RELATIONSHIP
TO INOSITOL PHOSPHATE FORMATION
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JOURNAL: BIOCHEM J 272 (2). 1990. 297-304. 1990

FULL JOURNAL NAME: Biochemical Journal
CODEN: BIJOA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Previous studies have demonstrated enhanced phosphorylation of phospholipase C- τ (PLC- τ), a key regulatory enzyme in phosphoinositide metabolism, in cells treated with platelet-derived growth factor (PDGF) and epidermal growth factor, both of which act via specific receptor tyrosine kinases. Our studies on BALB/c-3T3 cells show that agents that promote cellular cyclic AMP accumulation also increase the phosphorylation, specifically the serine phosphorylation, of this enzyme. Increased phosphorylation of PLC- τ (2-3-fold) was evident within 5-10 min of addition of isobutylmethylxanthine (IBMX) and either cholera toxin or forskolin to cells, and persisted for at least 3 h. Treatment of cells with cyclic AMP agonists also enhanced, with similar kinetics, the phosphorylation of a 76 kDa protein co-precipitated by anti-PLC- τ monoclonal antibodies. Brief exposure of cells to cholera toxin/IBMX or forskolin/IBMX decreased inositol phosphate formation induced by the GTP-binding protein (G-protein) activator aluminium fluoride by approx. 50%, but was without effect on PDGF-stimulated inositol phosphate formation. These findings suggest that PLC- τ and perhaps the 76 kDa co-precipitated protein, are substrates of cyclic AMP-dependent protein kinase in BALB/c-3T3 cells; however, the lack of effect of cyclic AMP elevation on PDGF-stimulated inositol phosphate formation indicates that the intrinsic activity of PLC- τ is unaltered by cyclic AMP-mediated phosphorylation.

4/7/19 (Item 19 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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07358870 BIOSIS NO.: 000090137781
ALZ-50 RECOGNIZES A PHOSPHORYLATED EPITOPE OF
 τ PROTEIN
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JOURNAL: J NEUROSCI 10 (10). 1990. 3295-3304. 1990
FULL JOURNAL NAME: Journal of Neuroscience
CODEN: JNRSO
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Alz-50 is a monoclonal antibody that detects antigens enriched in the brain tissue of Alzheimer's disease (AD) patients. Although Alz-50 recognizes τ , an identified integral constituent of the AD paired helical filament (PHF), the exact nature of the antigenic site is unknown. An immunoblot analysis demonstrated that the antigenic sites to Alz-50 are diminished by acid phosphatase treatment. Consistent with this finding, Alz-50 antigens were more concentrated in brain homogenates prepared with phosphatase inhibitors. The epitope in τ with which Alz-50 reacts is located in the carboxy terminus within a 14-amino acid region from just beyond the microtubule-binding repeats to the carboxy terminus. An isolated carboxy-terminal chymotryptic peptide from bovine brain τ reactive with Alz-50 was analyzed by fast-atom-bombardment mass spectroscopy (FAB-MS) and was found to be present as both a monophosphopeptide and a nonphosphorylated peptide. The immunohistological analysis has demonstrated that Alz-50 staining of neurofibrillary tangles (NFTs) is sensitive to acid phosphatase but not to alkaline phosphatase. Furthermore, Alz-50 staining of NFTs was effectively adsorbed by a high concentration of phosphoserine but not by serine or phosphothreonine. These results strongly suggest that Alz-50 recognizes a phosphorylated epitope in the carboxy terminus of τ , which has not been previously detected by using alkaline

phosphatase. The strong Alz-50 staining in AD samples may represent another association between a %%%phosphorylation%% state and neurofibrillary lesions. As a marker of the inchoate tangle-bearing neuron, the characterization of the Alz-50 epitope in %%%tau%% offers a partial molecular basis for the modifications that contribute to the assembly of PHFs.

4/7/20 (Item 20 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07298210 BIOSIS NO.: 000090078097
PATHOLOGICAL PROTEINS %%%TAU%% 64 AND 69 ARE SPECIFICALLY EXPRESSED IN THE SOMATODENDRITIC DOMAIN OF THE DEGENERATING CORTICAL NEURONS DURING ALZHEIMER'S DISEASE DEMONSTRATION WITH A PANEL OF ANTIBODIES AGAINST %%%TAU%% PROTEINS
AUTHOR: DELACOURTE A; FLAMENT S; DIBE E M; HUBLAU P; SABLONNIERE B; HEMON B; SHERRER V; DEFOSSEZ A
AUTHOR ADDRESS: A.D.E.R.M.A., UNITE INSERM 156, FAC. MED. LILLE, F-59045
LILLE CEDEX, FR.
JOURNAL: ACTA NEUROPATHOL 80 (2). 1990. 111-117. %%%1990%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Bundles of paired helical filaments (PHF) accumulate in the pyramidal neurons that degenerate during Alzheimer's disease. This neurofibrillary degeneration is highly correlated with clinical signs of dementia. During this degeneration process, %%%Tau%% proteins, which are the major antigenic components of PHF, are abnormally %%%phosphorylated%% and two pathological isoforms named %%%Tau%% 64 and 69 are expressed. We have studied their immunoblot distribution in the cortical gray and white matter from different regions of normal and Alzheimer brains, to determine if the degenerating process preferentially affects the somatodendritic or the axonal domain. Two categories of antibodies were used. The first category consisted of anti-human native %%%Tau%%, anti-%%Tau%% proteins from different vertebrates, anti-PHF, %%%monoclonal%% antibody Alz-50 and an anti-C terminal repeated region of %%%Tau%%. In control brains, these antibodies strongly detected normal %%%Tau%% proteins in the gray matter while %%%Tau%% immunodetection was weak in the white matter. In Alzheimer brain cortices, each antibody detected %%%Tau%% 64 and 69 in gray matter extracts but not at all in white matter extracts. The second category of anti-%%Tau%% consisted of the anti-PHF saturated with normal brain protein extracts. This antiserum only probed the abnormally %%%phosphorylated%% %%%Tau%% proteins. It detected %%%Tau%% 64 and 69 exclusively in the cortical gray matter of Alzheimer brains. Moreover, a 55-kDa %%%Tau%% protein was also immunolabelled, which might be an intermediary form between normal %%%Tau%% and %%%Tau%% 64 and 69. Our results demonstrate that %%%Tau%% proteins are normal and major components of the somatodendritic domain and that %%%Tau%% pathology, reflected by the presence of %%%Tau%% 64 and 69, affects preferentially this domain during Alzheimer's disease.

4/7/21 (Item 21 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07226418 BIOSIS NO.: 000090006280

IMMUNOCYTOCHEMICAL AND ULTRASTRUCTURAL STUDIES OF PICK'S DISEASE

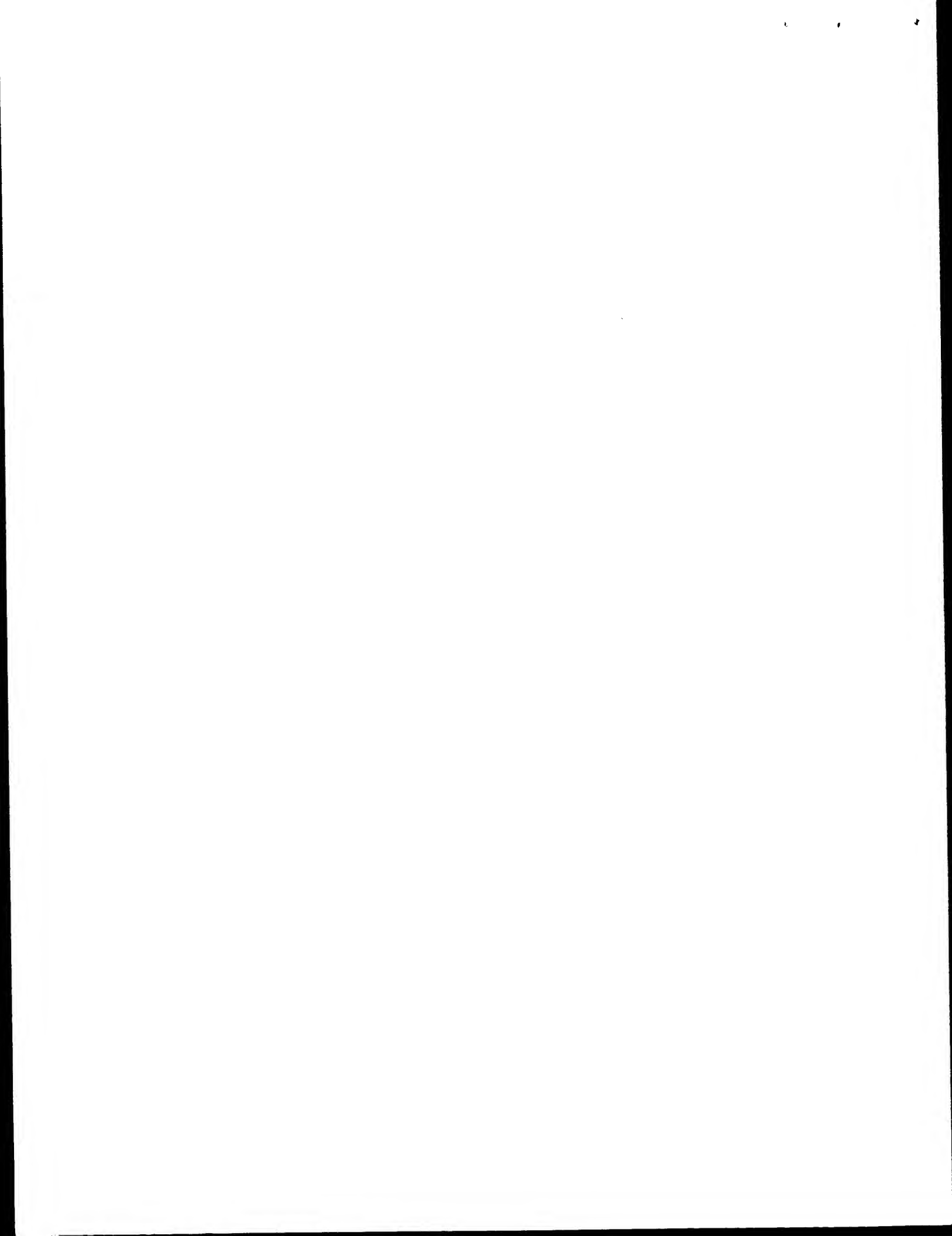
AUTHOR: MURAYAMA S; MORI H; IHARA Y; TOMONAGA M
AUTHOR ADDRESS: DIV. NEUROPATHOL., DEP. PATHOL. CB NO. 7525, BRINKHOUS-BULLITT BUILDING NO. 409, UNIV. N.C. 27599-7525.
JOURNAL: ANN NEUROL 27 (4). 1990. 394-405. %%%1990%%
FULL JOURNAL NAME: Annals of Neurology
CODEN: ANND
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cerebral cortical changes in 10 cases with Pick's disease were studied immunocytochemically and ultrastructurally. All cases contained Pick's argentophilic bodies and ballooned neurons. The antibodies against %%%phosphorylated%% %%%tau%% proteins that intensely stained all Pick bodies recognized numerous neuronal processes around Pick body-bearing cells and focal portions in the perikarya of ballooned neurons. %%%Monoclonal%% and polyclonal anti-ubiquitin antibodies stained not only some Pick bodies consisted of accumulation of randomly oriented, approximately 15-nm straight filaments and paired twisted profiles with a minimal diameter of 13 nm, maximal diameter of 26 nm, and twist periodicity of 120 nm. These Pick body-type filaments were also observed in the perikarya of ballooned neurons and neuronal processes around Pick body-bearing cells. Our studies demonstrate, for the first time, the characteristic pathological feature of neuropil in Pick's disease. Pick body-bearing cells and ballooned neurons show unique immunocytochemical and ultrastructural properties that may be a clue to the pathogenesis of Pick's disease.

4/7/22 (Item 22 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07038474 BIOSIS NO.: 000089120029
ALZHEIMER DISEASE PROTEINS A68 SHARE EPITOPES WITH %%%TAU%% BUT SHOW DISTINCT BIOCHEMICAL PROPERTIES
AUTHOR: KSIEZAK-REDING H; BINDER L I; YEN S-H
AUTHOR ADDRESS: DEP. PATHOL., ALBERT EINSTEIN COLL. MED., 1300 MORRIS PARK AVE., BRONX, N.Y. 10461.
JOURNAL: J NEUROSCI RES 25 (3). 1990. 420-430. %%%1990%%
FULL JOURNAL NAME: Journal of Neuroscience Research
CODEN: JNRED
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Alz 50, a %%%monoclonal%% antibody raised against Alzheimer brain homogenate, reacts with neurofibrillary tangles, microtubule-associated proteins %%%tau%%, and Alzheimer brain proteins of molecular weight 70-60 kDa (A68). To study the relationship between A68 and normal human %%%tau%% we compared the biochemical properties of these proteins and tested the reactivity of A68 with eight antibodies (Alz 50, %%%Tau%% 60, %%%Tau%%-2, %%%Tau%% 14, %%%Tau%%-1, Ab 636.7, NP14, %%%Tau%% 46) that bind to various regions of %%%tau%% molecule. On Western blots, all %%%tau%%-reactive antibodies, except %%%Tau%%-1, recognized A68. Pretreatment with alkaline phosphatase was required for the %%%Tau%%-1 binding to A68. A68 consisted of three polypeptides of 68, 64, and 60 kDa, while %%%tau%% contained 4-6 polypeptides of 50-65 kDa. A68 was less heterogenous than %%%tau%% in the number of pI variants on two-dimensional gels. All A68 variants were more acidic (pI 5.5-6.5) than human %%%tau%% (pI 6.5-8.5). Phosphatase treatment had only a minor effect on the pI and mobility of A68. Limited proteolysis of A68 with trypsin or chymotrypsin generated large fragments of 56-66 kDa (chymotrypsin) and 40-45 kDa (trypsin). While none of the fragments was recognized by Alz 50, the chymotryptic fragments were reactive with all



the other τ antibodies, and the tryptic fragments were positive with five of the antibodies (τ 14, τ -1, Ab 636.7, NP14, and τ 46). The peptide maps of A68 differed from that of τ in the number and the size of the peptide fragments. The differences in biochemical properties of these proteins and the sharing multiple epitopes suggest that A68 is a modified form of τ . The modification in part may be due to phosphorylation, although other changes rendering different isoelectrical properties and susceptibility to proteases need to be considered. The removal of the Alz 50 epitope by a cleavage of a 2-3 kDa fragment which does not contain the most C-terminal epitope (τ 46) indicates that the Alz 50 epitope is located at the N-terminal periphery of the A68 molecule.

4/7/23 (Item 23 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06994695 BIOSIS NO.: 000089095959
IMMUNOCYTOCHEMICAL AND ULTRASTRUCTURAL STUDIES OF LOWER MOTOR NEURONS IN AMYOTROPHIC LATERAL SCLEROSIS
AUTHOR: MURAYAMA S; MORI H; IHARA Y; BOULDIN T W; SUZUKI K; TOMONAGA M
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JOURNAL: ANN NEUROL 27 (2). 1990. 137-148. τ 1990
FULL JOURNAL NAME: Annals of Neurology
CODEN: ANNE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Neuronal inclusions in lower motor neurons in 23 cases of adult-onset sporadic amyotrophic lateral sclerosis were studied immunocytochemically and ultrastructurally. Monoclonal and polyclonal antiubiquitin antibodies recognized four structures in the neuronal perikarya: (1) all Lewy body-like inclusions in 6 cases with a relatively short clinical course, (2) a small percentage of Bunina bodies in 4 cases with abundant Bunina bodies, (3) ill-defined structures closely associated with Bunina bodies (Bunina body-related structures) in 15 cases, and (4) a focally aggregated meshwork of fine filamentous structures not associated with Bunina bodies in all cases. These four structures were not recognized by the antibodies raised against cytoskeletal proteins (neurofilament, tubulin, microtubule-associated protein 2, and phosphorylated τ). Electron microscopy revealed Lewy body-like inclusions to be accumulations of randomly oriented filaments, approximately 15 nm in diameter, covered by fine granules. Bundles of coated filaments 12 nm in diameter that sometimes formed Bunina body-like structures were also observed in the perikarya. Immunoelectron microscopy showed the reaction product with antiubiquitin to be on the filaments, 15 nm in diameter, of Lewy body-like inclusions. Our study revealed the existence of two types of filaments in lower motor neurons of patients with amyotrophic lateral sclerosis: (1) ubiquitin-positive, granule-associated filaments, approximately 15 nm in diameter, that form Lewy body-like inclusions; and (2) 12 nm coated filaments that may be a candidate for another ubiquitin-positive structure and possibly a precursor or Bunina bodies. These two types of filaments may represent early pathological changes of lower motor neurons in amyotrophic lateral sclerosis.

4/7/24 (Item 24 from file: 5)
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06951929 BIOSIS NO.: 000089073934
INCREASED MICROTUBULE ASSEMBLY IN BOVINE BRAIN TUBULIN LACKING THE TYPE III ISOTYPE OF BETA TUBULIN
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JOURNAL: J BIOL CHEM 265 (3). 1990. 1794-1799. τ 1990
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Tubulin, the major constituent protein of microtubules, is a heterodimer of α and β subunits. Both α and β exist in multiple isotypic forms. It is not clear if different isotypes perform different functions. In order to approach this question, we have made a monoclonal antibody specific for the β III isotype of tubulin. This particular isotype is neuron-specific and appears to be phosphorylated near the C terminus. We have used immunoaffinity depletion chromatography to prepare tubulin lacking the β III subunit. We find that removal of the β III isotype results in a tubulin mixture able to assemble much more rapidly than is unfractionated tubulin when reconstituted with either of the two microtubule-associated proteins (MAPs), τ or MAP 2. Our results suggest that the different isotypes of tubulin differ from each other in their ability to polymerize into microtubules. We have also found that the anti- β III antibody can stimulate microtubule assembly when reconstituted with tubulin and either τ or MAP 2. When reconstituted with tubulin lacking the β III isotype, the antibody causes the tubulin to polymerize into a polymer that is a microtubule in the presence of MAP 2 and a ribbon in the presence of τ .

4/7/25 (Item 25 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06927455 BIOSIS NO.: 000089060848
MOLECULAR MARKERS OF PRIMITIVE NEUROECTODERMAL TUMORS AND OTHER PEDIATRIC CENTRAL NERVOUS SYSTEM TUMORS MONOCLONAL ANTIBODIES TO NEURONAL AND GLIAL ANTIGENS DISTINGUISH SUBSETS OF PRIMITIVE NEUROECTODERMAL TUMORS
AUTHOR: MOLENAAR W M; JANSSEN D S; GOULD V E; RORKE L B; FRANKE W W; LEE V
M-Y; PACKER R J; TROJANOWSKI J Q
AUTHOR ADDRESS: DEP. PATHOL. LAB. MED., MED. PATHOL. SECT., DIV. ANATOMIC PATHOL., UNIV. PA. HOSP., BASEMENT MALONEY A009, 34TH AND SPRUCE ST., PHILADELPHIA, PA. 19104-4283.
JOURNAL: LAB INVEST 61 (6). 1989. 635-643. τ 1989
FULL JOURNAL NAME: Laboratory Investigation
CODEN: LAI
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Seventy-one tumors of the central nervous system in children were studied immunohistologically. Thirty-seven were classified histologically as PNETs, of which 35 were located in the cerebellum (medulloblastomas), one in the cerebrum, and one in the spinal cord. The 34 non-PNETs included five ependymomas, seven gangliogliomas, 15 astrocytomas, and seven tumors of other histology. We used monoclonal antibodies specific for neurofilament (NF) triplet proteins, for microtubule associated protein 2 and τ , protein and for glial fibrillary acidic protein (GFAP) and myelin basic protein. In addition, a monoclonal antibody to epithelial membrane antigen was applied. The presence or absence of these antigens defined four major groups of PNETs: 1) PNETs not otherwise specified (10 cases), 2) PNETs with neuronal differentiation (eight cases), 3) PNETs with astrocytic differentiation (six cases), and 4) PNETs with both neuronal and astrocytic differentiation (12 cases). One case showed ependymal differentiation. The pattern of expression of NF isoforms in PNETs was reminiscent of that seen during normal mammalian development, such that phosphorylated NF-H was only present in combination with NF-N

and

NF-L. Among the other central nervous system tumors, all astrocytomas and

gangliogliomas were positive for GFAP, and the gangliogliomas also expressed all NF isoforms. Three atypical teratoid tumors and two rhabdoid tumors showed strong positivity for epithelial membrane antigen and also for GFAP. We conclude that the differentiation antigens described here serve to distinguish PNETs from other pediatric central nervous system tumors and to identify subsets of PNETs. Accordingly, PNETs represent a heterogeneous group of pediatric brain tumors capable of neuronal and glial differentiation.

4/7/26 (Item 26 from file: 5)

DIALOG(R)File 5:BIOSIS Previews(R)

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06885544 BIOSIS NO.: 000089039472

AN IMMUNOHISTOCHEMICAL STUDY OF NEUROPEPTIDES AND NEURONAL CYTOSKELETAL

PROTEINS IN THE NEUROEPITHELIAL COMPONENT OF A SPONTANEOUS MURINE OVARIAN

TERATOMA PRIMITIVE NEUROEPITHELIUM DISPLAYS

IMMUNOREACTIVITY FOR NEUROPEPTIDES AND NEURON-ASSOCIATED BETA TUBULIN

ISOTYPE

AUTHOR: CACCAMO D V; HERMAN M M; FRANKFURTER A; KATSETOS C S; COLLINS V P;

RUBINSTEIN L J

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CHARLOTTESVILLE, VA. 22908.

JOURNAL: AM J PATHOL 135 (5). 1989. 801-814. %%%1989%%%

FULL JOURNAL NAME: American Journal of Pathology

CODEN: ATPAA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Approximately one third of the female mice of the LTXBO strain

develop spontaneous ovarian teratomas. These tumors contain a large neuroepithelial component, which includes primitive neural structures resembling embryonic neural tubes (medulloepithelial rosettes), ependymoblastic and ependymal rosettes, neuroblasts, mature ganglionic neurons, myelinated neurites, and astrocytes. The purpose of this study was to characterize these tumors according to the immunohistochemical location of some well-characterized trophic and regulatory neuropeptides and neurotransmitters, several neuronal-associated cytoskeletal proteins, and other proteins indicative of neuronal and glial differentiation. Medulloepithelial rosettes showed focal serotonin-like opioid peptide-like and gamma-amino butyric acid-like immunoreactivity, and displayed immunostaining for the neuron-associated class III .beta.-tubulin isotype. The mature ganglion cells were also immunoreactive for these markers, and, in addition, for somatostatin, cholecystokinin, bombesin, glucagon, vasoactive intestinal peptide, and neuropeptide Y. Mature ganglion cells were also immunoreactive for proteins associated with the neuronal cytoskeleton (including microtubule-associated proteins, MAP2 and %%%tau%%%, and higher molecular weight %%%phosphorylated%%% and non-%%%phosphorylated%%% neurofilament

subunits), neuron-specific enolase, and synaptophysin. Undifferentiated stem cells, ependymoblastic and ependymal rosettes, and astroglia all stained with a %%%monoclonal%%% antibody that recognizes all mammalian .beta.-tubulin isotypes, but did not react with antibodies to neuronal-associated cytoskeletal proteins or neuropeptides. Neuropeptide-like immunoreactivity and demonstration of the class III .beta.-tubulin isotype indicate early neuronal commitment in neoplastic primitive neuroepithelium. These patterns of immunoreactivity closely follow those encountered in the normal neurocytogenesis of the mammalian and avian forebrain, and increase the precision with which the early stages of progressive neuroepithelial differentiation can be analyzed in human embryonal tumors of the CNS.

4/7/27 (Item 27 from file: 5)

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06867202 BIOSIS NO.: 000089016793

ABNORMAL PROCESSING OF MULTIPLE PROTEINS IN ALZHEIMER DISEASE

AUTHOR: ZHANG H; STERNBERGER N H; RUBINSTEIN L J; HERMAN M M; BINDER L I;

STERNBERGER L A

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21201.

JOURNAL: PROC NATL ACAD SCI U S A 86 (20). 1989. 8045-8049. %%%1989%%%

FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the

United States of America

CODEN: PNASA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Cerebrovascular amyloid is the main constituent of the perivascular and neuritic plaques typical of Alzheimer disease, whereas neurofilaments and microtubule-associated %%%tau%%% protein have been considered primary contributors to the formation of the characteristic Alzheimer tangles. Plaques and tangles and their constituents have at times been ascribed a role in pathogenesis of the disease. Normally, neurofilaments become %%%phosphorylated%%% only upon axonal entry. In many neurologic disorders, neurofilament %%%phosphorylation%%%, as detected by any of the available %%%monoclonal%%% antibodies (mAbs) to neurofilament %%%phosphorylated%%% epitopes is shifted from an axonal

to a cell-body location. An exception is provided by Alzheimer disease, where tangles (which are neuronal cell-body-derived structures) exhibit only one %%%phosphorylated%%% epitope. However, the very presence of neurofilaments in tangles and plaques has been questioned because of a reported cross-reaction of mAbs to %%%phosphorylated%%% neurofilaments

with %%%tau%%% protein. On reinvestigating this cross-reactivity we found

that four of five mAbs to %%%phosphorylated%%% neurofilaments and four of

five mAbs to nonphosphorylated neurofilaments failed to react with %%%tau%%% protein. A fifth %%%mAb%%% (07-5) to %%%phosphorylated%%%

neurofilament cross-reacted with partially denatured %%%tau%%% protein at

an affinity 1/1700th of that for denatured neurofilaments; nondenatured %%%tau%%% protein in tissue sections did not cross-react. A fifth %%%mAb%%% (02-40) to nonphosphorylated neurofilament also cross-reacted

weakly. In Alzheimer disease normal-appearing axons were revealed with all the mAbs to %%%phosphorylated%%% neurofilaments, but tangles were revealed with only one of them (%%%mAb%%% 07-5). %%%mAb%%% to %%%tau%%%

protein did not stain or did so indistinctly. Four of five mAbs to nonphosphorylated neurofilaments failed to reveal axons. Upon dephosphorylation of tissue, staining by mAbs to %%%phosphorylated%%% neurofilaments disappeared, and axons were revealed with the %%%mAb%%% to

%%%tau%%% protein and all mAbs to the nonphosphorylated neurofilaments.

Tangles became stained with %%%tau%%% %%%mAb%%% and one %%%mAb%%% to the

nonphosphorylated neurofilaments (%%%mAb%%% 10-1). Quantitative evaluation of immunocytochemical staining intensities and immunoblot cross-reactivity showed that neurofilaments are, indeed, constituents of tangles apparently exceeding the concentration of %%%tau%%% protein 17-fold. Contribution of both conformation and primary structure to IgG specificity may explain the lack of any cross-reaction of mAbs to neurofilaments with %%%tau%%% protein in intact tissue and the appearance

of cross-reaction in immunoblots where conformation specificity may be largely lost. The present data extend earlier findings of abnormal processing of neurofilaments and %%%tau%%% protein in Alzheimer disease

and, together with reported abnormal processing of cerebrovascular amyloid .beta.-protein, suggest that inhibition of the processing of multiple proteins is basic to the pathogenesis of Alzheimer disease, whereas formation of plaques and tangles could be merely the most striking histologic results.

4/7/28 (Item 28 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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06778057 BIOSIS NO.: 000088087494
IDENTIFICATION AND LOCALIZATION OF A TAU PEPTIDE
TO PAIRED HELICAL
FILAMENTS OF ALZHEIMER DISEASE
AUTHOR: IQBAL K; GRUNDKE-IQBAL I; SMITH A J; GEORGE L; TUNG
Y-C; ZAIDI T
AUTHOR ADDRESS: NEW YORK STATE INST. BASIC RES.
DEVELOPMENTAL DISABILITIES,
1050 FOREST HILL RD., STATEN ISLAND, N.Y. 10314.
JOURNAL: PROC NATL ACAD SCI U S A 86 (14). 1989. 5646-5650.
1989
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences
of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Amino acid sequencing of a CNBr digest of the tau protein isolated from bovine brain revealed an amino acid sequence of 17 residues, Pro-Gly-Leu-Lys-Glu-Ser-Pro-Leu-Gln-Ile-Gly-Ala-Ala-Pro-Gly-Leu-Lys, which we call peptide I, with heterogeneity at position 11 of glycine (peptide Ia) and proline (peptide Ib); peptide I showed no homology with the previously reported cDNA-derived mouse and human tau sequences. Antisera raised to synthetic peptides corresponding to peptides Ia and Ib labeled all the bovine tau polypeptides recognized by other monoclonal and polyclonal antibodies to bovine tau. Antisera to peptide Ib did not label any mouse tau polypeptides; however, an anti-Ia antiserum labeled two of the four mouse tau polypeptides. Antisera to both peptides labeled paired helical filaments (PHF) as neurofibrillary tangles, plaque neurites, and neuropil threads in Alzheimer disease brain and PHF polypeptides on immunoblots. Immunostaining with anti-Ia antisera of PHF in tissue sections and PHF polypeptides, but not bovine tau, on immunoblots was markedly increased when pretreated with alkaline phosphatase. These studies suggest that (i) the amino acid sequences of some isoforms of tau peptide might be different from that predicted from cDNAs, (ii) a tau peptide that is absent in the predicted sequences is present in PHF in Alzheimer disease, and (iii) tau in PHF is abnormally phosphorylated.

4/7/29 (Item 29 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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06743025 BIOSIS NO.: 000088052455
BIOCHEMISTRY OF PAIRED HELICAL FILAMENTS PHF
AUTHOR: IHARA Y
AUTHOR ADDRESS: TOKYO METROPOLITAN INST. GERONTOL., JPN.
JOURNAL: JPN J GERIATR 25 (4). 1988. 364-367. 1988
FULL JOURNAL NAME: Japanese Journal of Geriatrics
CODEN: NIRZA
RECORD TYPE: Abstract
LANGUAGE: JAPANESE

ABSTRACT: Since 1980, the nature of PHF has been heavily focused in several laboratories. The most unexpected observation was that PHF are insoluble

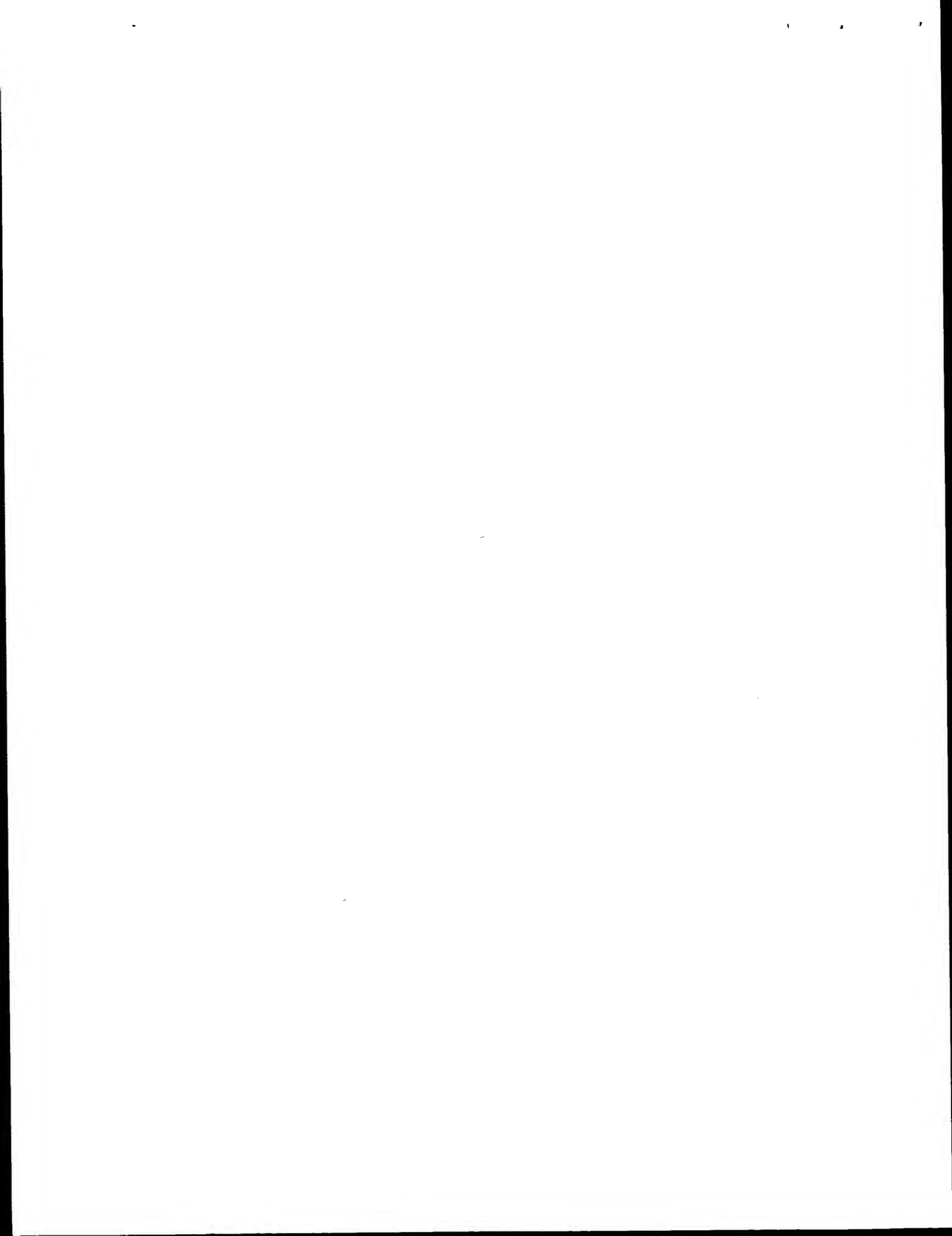
in harsh denaturants or detergents including SDS, urea and guanidine HCl. This unusual insolubility of PHF made possible high grade purification of PHF, but prevented the application of analytical biochemical methods to the identification of the PHF components. Therefore, we took an immunochemical approach using specific antibodies to PHF, which were prepared by immunization of purified PHF. Our strategy was to search for soluble polypeptides reactive with antiPHF, instead of analyzing PHF directly. Polyclonal antibodies to PHF were found to label tau, a neuron-specific microtubule-associated phosphoprotein. The analysis of PHF antisera showed that there are two populations of tau antibodies: one is reactive with both phosphorylated and nonphosphorylated forms of tau, the other is specific for phosphorylated tau. In addition, antibodies specific for nonphosphorylated tau could not be detected in the PHF antisera.

From these observations, one of the antigenic determinants of PHF has been considered as phosphorylated tau. A hybridoma producing a monoclonal antibody to PHF (DF2) was obtained by the fusion of mouse myeloma cells and rat spleen cells immunized with PHF. DF2 was confirmed to specifically bind to PHF. In the blot of the soluble fraction of brain homogenates, DF2 labeled a small polypeptide Mr. approx. 5 kD, which was identified as ubiquitin by its purification and subsequent protein sequencing. Moreover, five ubiquitin fragments were identified in the PHF digest. Thus ubiquitin is a component of PHF. Two components, tau and ubiquitin, have been identified in PHF immunochemically and protein chemically, respectively. Two lines of evidence suggest that PHF contain the components other than tau or ubiquitin: first, ghost tangles (extracellular tangles) are not stained with antiPHF or tau antibodies, although they appear to be made of PHF. Second, the staining activity of antiPHF cannot be absorbed out with excess amount of tau. These strongly suggest that PHF contain as-yet-unidentified components.

4/7/30 (Item 30 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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06675461 BIOSIS NO.: 000087117638
SENILE PLAQUE NEURITES FAIL TO DEMONSTRATE ANTI-PAIRED
HELICAL FILAMENT AND
ANTI-MICROTUBULE-ASSOCIATED PROTEIN-TAU
IMMUNOREACTIVE PROTEINS IN
THE ABSENCE OF NEUROFIBRILLARY TANGLES IN THE NEOCORTEX
AUTHOR: PROBST A; ANDERTON B H; BRION J-P; ULRICH J
AUTHOR ADDRESS: DEP. PATHOL., DIV. NEUROPATHOL., UNIV. BASEL,
SWITZERLAND.
JOURNAL: ACTA NEUROPATHOL 77 (4). 1989. 430-436. 1989
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Although much work has been directed recently towards unravelling the protein chemistry of neurofibrillary tangle (NFT) and senile plaque (SP) components in Alzheimer's disease, the pathogenesis of these lesions remains largely unknown and the problem of their relationship is unresolved. In particular, although paired helical filaments (PHF) have long been documented in SP neurites, we do not know if they are of pathogenetic relevance for the formation of the SP. To investigate the relationship between NFT and SP, we examined antigenic properties of proteins in SP neurites in neocortical tissues of patients with senile dementia of Alzheimer type, in the presence or absence of NFT in the same cortical area. We used two polyclonal antibodies directed against PHF and microtubule-associated protein (MAP)-tau and three monoclonal antibodies (MAbs) (RT97, BF10, 147) to phosphorylated epitopes of human neurofilament polypeptides, as well as the Gallyas silver impregnation method which specifically stains PHF in NFT and neurites.



The main finding of our investigations consists in a differential pattern of immunoreactivity of SP neurites depending on the presence or absence of NFT in the neocortex. In the presence of NFT, there were numerous neuropil threads and SP neurites containing Gallyas-positive, as well as anti-PHF- and anti- τ -labelled material. In the absence of NFT

in the neocortex there was a striking absence of any Gallyas-positive or PHF- and τ -immunoreactive structure in the cortical neuropil and

in SP neurites, irrespective of the maturation stage of the SP. In contrast with these results, the number of neurites labelled by MAb RT97, BF10 and 147 in SP and in the neuropil was apparently unaffected by the presence or absence of NFT. Amyloid in SP, remained consistently unstained by all antibodies of the panel as well as by the Gallyas stain. Our findings indicate that PHF and τ polypeptides are

facultative components of SP neurites and suggest that the development of SP may occur independently of PHF pathology in neocortical neurons.

4/7/31 (Item 31 from file: 5)
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06664050 BIOSIS NO.: 000087106227
IMMUNOCYTOCHEMICAL CHARACTERIZATION OF NEUROFIBRILLARY TANGLES IN

AMYOTROPIC LATERAL SCLEROSIS AND PARKINSONISM-DEMENTIA OF GUAM WEST PACIFIC OCEAN

AUTHOR: SHANKAR S K; YANAGIHARA R; GARRUTO R M; GRUNDKE-IQBAL I; KOSIK K S;

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JOURNAL: ANN NEUROL 25 (2). 1989. 146-151. %1989%

FULL JOURNAL NAME: Annals of Neurology

CODEN: ANNE

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Cryostat-cut sections of formalin-fixed and unfixed hippocampus

from 23 Guamanian Chamorros with clinically and neuropathologically verified amyotrophic lateral sclerosis (ALS) (8 cases) and parkinsonism-dementia (PD) (15 cases) and from 12 neurologically normal Guamanians (5 with and 7 without neurofibrillary degeneration) were evaluated by the immunoperoxidase technique, using τ monoclonal antibodies against τ phosphorylated neurofilament, human fetal microtubule-associated protein τ , and paired helical filaments. On immunostaining, all three antibodies showed intracellular tangles in the hippocampal neurons of patients with ALS, patients with PD, and in neurologically normal Guamanians with neurofibrillary pathology, but the correlation of immunostaining between these antibodies was not absolute. Extracellular or ghost tangles were immunostained only with the antibody against paired helical filaments. Our immunocytochemical data indicate that the antigenic composition of neurofibrillary tangles in Guamanian ALS and PD is similar to that of Alzheimer's disease, suggesting a common pathogenetic pathway for neurofibrillary tangle formation in these neurodegenerative disorders.

4/7/32 (Item 32 from file: 5)
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06644905 BIOSIS NO.: 000087087082
ACCUMULATION OF ABNORMALLY τ PHOSPHORYLATED τ PRECEDES THE FORMATION OF NEUROFIBRILLARY TANGLES IN ALZHEIMER'S DISEASE

AUTHOR: BANCHER C; BRUNNER C; LASSMANN H; BUDKA H; JELLINGER K; WICHE G;

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JOURNAL: BRAIN RES 477 (1-2). 1989. 90-99. %1989%

FULL JOURNAL NAME: Brain Research

CODEN: BRREA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: The intraneuronal accumulation of paired helical filaments in the

form of neurofibrillary tangles is one hallmark of the brain pathology in Alzheimer's disease. At certain predilection sites, a small number of similar lesions are also present in the brains of the majority of aged non-demented individuals. As suggested by several studies before, these abnormal cytoskeletal structures contain determinants of microtubule-associated protein τ and ubiquitin. The present study uses a morphological classification of neurofibrillary tangles into different stages of maturation, as suggested by Alzheimer in 1911, and shows by quantitative immunocytochemistry that early stages of neurofibrillary degeneration contain abnormally τ phosphorylated τ . Immunoreactivity for the altered τ is seen not only

in tangles but also in the cytoplasm of some nerve cells lacking neurons without tangles are present in age-matched non-demented individuals as in Alzheimer cases, but are absent in young controls. In contrast, incorporation of an epitope, recognized by a τ monoclonal antibody (3-39) raised to paired helical filaments, which is directed against a determinant residing in the 50-65 amino acid residue region of ubiquitin occurs late in the process of tangle maturation and is most pronounced in extracellular 'ghost tangles'. It is suggested that the accumulation of abnormally τ phosphorylated τ is one of the earliest cytoskeletal changes in the process of tangle formation. Exposure of certain ubiquitin epitopes in the pathological fibers may reflect an unsuccessful attempt of proteolytic degradation.

4/7/33 (Item 33 from file: 5)
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06631242 BIOSIS NO.: 000087073404
PROGRESSIVE SUPRANUCLEAR PALSY EXTENSIVE NEUROFIL THREADS IN ADDITION TO

NEUROFIBRILLARY TANGLES VERY SIMILAR ANTIGENICITY OF SUBCORTICAL NEURONAL

PATHOLOGY IN PROGRESSIVE SUPRANUCLEAR PALSY AND ALZHEIMER'S DISEASE

AUTHOR: PROBST A; LANGUI D; LAUTENSCHLAGER C; ULRICH J; BRION J P; ANDERTON

B H

AUTHOR ADDRESS: DEP NEUROPATHOL., INST. PATHOL., UNIV. BASEL, SCHOEBEINSTRASSE 40, CH-4003 BASEL, SWITZ.

JOURNAL: ACTA NEUROPATHOL 77 (1). 1988. 61-68. %1988%

FULL JOURNAL NAME: Acta Neuropathologica

CODEN: ANPTA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Light microscopic immunohistochemical investigations were performed on neurofibrillary tangles (NFT) in four histologically confirmed cases of Alzheimer's disease (AD) and in five patients with a progressive supranuclear palsy (PSP). The antibody panel included antisera to the neuronal microtubule-associated protein, τ , and to

isolated paired helical filaments (PHF), as well as mouse τ monoclonal antibodies (MAbs) to τ phosphorylated τ epitopes on high and medium molecular weight neurofilament subunits (RT97 and BF10, respectively). Paraffin sections were also impregnated with the Gallyas silver method, which specifically stains tangles and cortical neuropil threads in AD, but does not stain normal neurofilaments. All tangles in PSP and AD showed consistent immunostaining with antibodies to τ

protein and isolated PHF, regardless of their localization. MAbs RT97 and BF10, however, did not stain or only weakly stained, subcortical tangles in PSP and AD, whereas most cortical NFT in AD were intensely

immunostained. All tangles in PSP were as heavily impregnated with Gallyas as they were in AD. Furthermore there were extensive networks of Gallyas-positive, τ - and PHF-immunoreactive neurites in subcortical gray areas containing NFT, and bundles of positive axons in white matter tracts interconnecting subcortical nuclei of PSP. Our studies indicate a much more extensive disruption of fibrillar proteins in PSP subcortical neurons than previously reported. They furthermore indicate a very similar antigenic profile of NFT in PSP and AD, as far as subcortical neurons are concerned.

4/7/34 (Item 34 from file: 5)
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06619784 BIOSIS NO.: 000087061946
AN ANTIGENIC PROFILE OF LEWY BODIES IMMUNOCYTOCHEMICAL INDICATION FOR
PROTEIN τ - AND UBIQUITINATION
AUTHOR: BANCHER C; LASSMANN H; BUDKA H; JELLINGER K; GRUNDKE-IQBAL I; IQBAL
K; WICHE G; SEITELBERGER F; WISNIEWSKI H M
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JOURNAL: J NEUROPATHOL EXP NEUROL 48 (1). 1989. 81-93.
 τ -epitopes
FULL JOURNAL NAME: Journal of Neuropathology & Experimental Neurology
CODEN: JNENA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: An antigenic profile of subcortical and cortical Lewy bodies was determined in the presence or absence of neurofibrillary tangles in the same brain using antisera and τ -antibodies to various cytoskeletal elements as well as to determinants not present in the normal cytoskeleton. The cores of many Lewy bodies were strongly reactive with a τ -antibody to paired helical filaments which has been shown to recognize ubiquitin. This antibody also stained Marinesco bodies in the same tissue sections. Two τ -antibodies to τ -epitopes of neurofilament proteins (SM I 31, SM

I 34) stained the peripheries of about 40% of all discernable Lewy bodies on untreated paraffin sections. Reactivity with a τ -antibody to neurofilaments (SM I 33) appeared only after pretreatment of the sections with phosphatase. Lewy bodies did not bind antibodies to τ -protein. Our results show that, as previously shown for neurofibrillary tangles, Lewy bodies also contain ubiquitin. The uncovering of neurofilament epitopes by treatment with phosphatase indicates that abnormal τ -phosphorylation of cytoskeletal elements may play a role in the pathogenesis of the Lewy body.

4/7/35 (Item 35 from file: 5)
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06565581 BIOSIS NO.: 000087007742
ALZHEIMER DISEASE TANGLES SHARE IMMUNOLOGICAL SIMILARITIES WITH
MULTIPHOSPHORYLATION REPEATS IN THE TWO LARGE NEUROFILAMENT PROTEINS
AUTHOR: LEE V M-Y; OTVOS L JR; SCHMIDT M L; TROJANOWSKI J Q
AUTHOR ADDRESS: DEP. PATHOL., LAB. MED., UNIV. PENNSYLVANIA SCH. MED., PHILADELPHIA, PA. 19104.
JOURNAL: PROC NATL ACAD SCI U S A 85 (19). 1988. 7384-7388.
 τ -epitopes
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the United States of America
CODEN: PNAS A
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Immunological and structural analyses of neurofilament (NF) proteins with > 500 anti-NF τ -antibodies (mAbs) enumerated epitopes shared by NF proteins and Alzheimer neurofibrillary tangles. We identified the multiphosphorylation domain of the rat heaviest NF subunit-tandem repeats of Lys-Ser-Pro-Xaa (where Xaa is a small unchanged amino acid and serine is τ -phosphorylated)-as the determinant recognized by 15 of the 16 mAbs from this collection of > 500 mAbs that detected neurofibrillary tangles. Most (11) of these 16 mAbs also recognized the previously characterized multiphosphorylation repeat in the human middle sized NF subunit. However, although these mAbs shared the ability to recognize NFTs, the antigen-binding domains of these 16 mAbs represented 13 separate classes based on their differential recognition of 12 synthetic peptides derived from the rat heaviest NF subunit and the human middle-sized NF subunit multiphosphorylation sites, NF subunits of 10 diverse species, and normal human τ -protein.

We conclude that NFTs share highly specific immunological and structural properties with specific rat heaviest NF subunit and human middle-sized NF subunit multiphosphorylation repeats.

4/7/36 (Item 36 from file: 5)
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06244054 BIOSIS NO.: 000086078236
MORPHOLOGICAL DIFFERENTIATION OF EMBRYONIC RAT SYMPATHETIC NEURONS IN
TISSUE CULTURE I. CONDITIONS UNDER WHICH NEURONS FORM AXONS BUT NOT DENDRITES
AUTHOR: BRUCKENSTEIN D A; HIGGINS D
AUTHOR ADDRESS: DEP. PHARMACOL. THER., FARBER 127, SCH. MED., STATE UNIV. NEW YORK, BUFFALO, N.Y. 14214.
JOURNAL: DEV BIOL 128 (2). 1988. 324-336. τ -epitopes
FULL JOURNAL NAME: Developmental Biology
CODEN: DEBIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have examined the morphology of fetal rat sympathetic neurons grown in serum-free medium in the absence of nonneuronal cells. Because cell density can affect phenotypic expression in vitro, the morphological analysis was subdivided into the study of isolated neurons (neurons whose somata were at least 150 μ m from their nearest neighbor) and of more highly aggregated neurons. When isolated neurons were injected with intracellular markers, it was found that most (79%) had a single process emanating from their somata and that this unipolar state persisted for at least 8 weeks in vitro. The processes of unipolar sympathetic neurons had the appearance of axons in that they were thin and long, had a constant diameter, and were relatively unbranched. Cytochemical methods revealed that such processes had other axonal characteristics: (1) they were more reactive with a τ -antibody against τ -phosphorylated forms of the M and H neurofilament subunits than with an antibody to nonphosphorylated forms of these proteins; (2) they also reacted with antibodies to the τ -microtubule-associated protein and to the τ -phosphorylated forms of the H neurofilament subunit; and (3) they contained only small amounts of RNA as determined by [³H]uridine autoradiography. These data indicate that neurons which normally form dendrites in vivo need not express this capacity in vitro and that axonal and dendritic growth can be dissociated under some conditions in culture. While most isolated neurons were unipolar, neurons in regions of high neuronal cell density were usually multipolar. In addition to axons, multipolar neurons had processes with some of the characteristics expected of rudimentary dendrites: they ended locally (usually within 100 μ m), were often highly branched, and reacted with an antibody to nonphosphorylated forms of the M and H neurofilament subunits. The effects of density were most prominent when neurons were within aggregates in which the somata were in close apposition. Density-dependent changes in morphology were less frequently observed

when neuronal somata were separated by greater distances (30-100 μ m). These data indicate that the morphology of sympathetic neurons is subject to environmental regulation and that neuron-neuron interactions can promote the extension of rudimentary dendrites in vitro.

4/7/37 (Item 37 from file: 5)
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06151013 BIOSIS NO.: 000085114165
IDENTIFICATION OF THE MAJOR MULTIPHOSPHORYLATION SITE IN MAMMALIAN NEUROFILAMENTS
AUTHOR: LEE V M-Y; OTVOS L JR; CARDEN M J; HOLLOSI M; DIETZSCHOLD B; LAZZARINI R A
AUTHOR ADDRESS: DIV. NEUROPATHOL., DEP. PATHOL. LAB. MED., UNIV. PA. SCH. MED., PHILADELPHIA, PA. 19104.
JOURNAL: PROC NATL ACAD SCI U S A 85 (6). 1988. 1998-2002. %1988%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the United States of America
CODEN: PNAS
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The sequence Lys-Ser-Pro-Val-Pro-Lys-Ser-Pro-Val-Glu-Glu-Lys-Gly repeats six times serially in the human mid-sized neurofilament (NF) protein (NF-M). To establish whether Lys-Ser-Pro-Val(Ala) is the major site for in vivo NF %phosphorylation%, peptides based on the NF-M repeat were synthesized and chemically %phosphorylated%. These synthetic peptides were probed with 515 %monoclonal% antibodies (mAbs) that were raised to, and distinguished, several differentially %phosphorylated% forms of NF proteins. Studies with 95 of those mAbs that recognized the peptides before and after chemical %phosphorylation% demonstrated that a highly immunogenic epitope shared by the peptides is present in NFs from all species tested, including invertebrates. This suggests the phylogenetic conservation of a major NF %phosphorylation% site. Lastly, a cross-reactive antigenic determinant shared by the peptides and the major NF %phosphorylation% site was shown to exist in neurofibrillary tangles of patients with Alzheimer disease as well as in two neuron-specific microtubule-associated proteins (MAPs), i.e., MAP2 and %tau%.

4/7/38 (Item 38 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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06097134 BIOSIS NO.: 000085060283
ACCUMULATION OF %PHOSPHORYLATED% NEUROFILAMENTS IN ANTERIOR HORN MOTONEURONS OF AMYOTROPHIC LATERAL SCLEROSIS PATIENTS
AUTHOR: MUNOZ D G; GREENE C; PERL D P; SELKOE D J
AUTHOR ADDRESS: DEP. PATHOL., COLL. MED., UNIV. SASKATCHEWAN, SASKATOON, SASKATCHEWAN S7N 0W0, CANADA.
JOURNAL: J NEUROPATHOL EXP NEUROL 47 (1). 1988. 9-18. %1988%
FULL JOURNAL NAME: Journal of Neuropathology & Experimental Neurology
CODEN: JNENA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Perikaryal collections of intermediate filaments have been described in the anterior horn motoneurons of patients with amyotrophic lateral sclerosis (ALS), but these inclusions have generally been considered rare and mainly associated with the familial form of ALS.

Using the %monoclonal% antibody NF2F11, which recognizes %phosphorylated% neurofilament epitopes, we showed that focal collections of neurofilaments in anterior horn motoneurons were a characteristic finding in sporadic as well as in familial ALS; they were present in seven of nine ALS patients, but in none of nine control spinal cords. These neurofilamentous collections are not cross-reactive with antibodies directed against paired helical filaments and the microtubule associated protein %tau%. In addition, diffuse staining for %phosphorylated% neurofilament epitopes in chromatolytic anterior horn perikarya was significantly more frequent in ALS patients than in controls.

4/7/39 (Item 39 from file: 5)
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06086926 BIOSIS NO.: 000085050075
%PHOSPHORYLATION% DETERMINES TWO DISTINCT SPECIES OF %TAU% IN THE CENTRAL NERVOUS SYSTEM
AUTHOR: PAPASOZOMENOS S C; BINDER L I
AUTHOR ADDRESS: DEP. PATHOL., LAB. MED., UNIV. TEX. MED. SCH., PO BOX 20708, HOUSTON, TEX. 77225, USA.
JOURNAL: CELL MOTIL CYTOSKELETON 8 (3). 1987. 210-226. %1987%
FULL JOURNAL NAME: Cell Motility and the Cytoskeleton
CODEN: CMCYE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The %monoclonal% antibody, %Tau%-1, which had previously been used to localize %tau% to the axonal compartment in brain has been reutilized for light and electron microscopic immunohistochemistry following phosphatase treatment of tissue. We report here that a significant quantity of %tau% in the central nervous system is %phosphorylated% in situ at or near the %Tau%-1 epitope, preventing the binding of the %Tau%-1 antibody. Upon removal of this/these phosphate group(s), however, %Tau%-1 was observed in the somatodendritic compartment of neurons as well as in axons. Furthermore, intense staining was also observed in astrocytes and in perineuronal glial cells. This immunoreactivity was present along the lengths of microtubules and on ribosomes (polysomes). Treatment of immunoblots of extracts of whole cerebral cortex with phosphatase confirmed the immunohistochemical results in that a 50-65% increase in %Tau%-1 binding to the %tau% region of the blot was noted. Moreover, a novel %monoclonal% antibody, %Tau%-2, was also used in these experiments. This antibody binds only to %tau% and localizes along microtubules in axons, somata, dendrites, and astrocytes and on ribosomes (polysomes) without phosphatase pretreatment.

4/7/40 (Item 40 from file: 5)
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06076967 BIOSIS NO.: 000085040116
PHOSPHATASE AND CARBOCYANINE DYE BINDING DEFINE DIFFERENT TYPES OF PHOSPHATE GROUPS IN MAMMALIAN NEUROFILAMENTS
AUTHOR: KSIEZAK-REDING H; YEN S-H
AUTHOR ADDRESS: DEP. PATHOL., ALBERT EINSTEIN COLL. MED., 1300 MORRIS PARK AVE., BRONX, N.Y. 10461.
JOURNAL: J NEUROSCI 7 (11). 1987. 3554-3560. %1987%
FULL JOURNAL NAME: Journal of Neuroscience
CODEN: JNRSD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The %phosphorylation% state of human and bovine spinal cord

neurofilaments (NF) was studied by direct phosphate analysis and carbocyanine dye ("Stains-all") binding to NF polypeptides resolved on SDS-polyacrylamide gels. Electrophoretically purified NF-H (200 kDa), NF-M (160 kDa), and NF-L (68 kDa) of human origin contained 24, 18, and 4 mol phosphate/mol protein, whereas bovine NF contained 53, 23, and 5 mol phosphate/mol protein, respectively. Incubation of NF preparations with E. coli alkaline phosphatase removed about 55% of the phosphate from NF-H, about 30% of the phosphate from both human and bovine NF-M, but did

not change the phosphate content of NF-L. This treatment also inhibited or substantially reduced the binding of electroblotted NF-H and NF-M to 2 anti-NF %%%monoclonal%%% antibodies known to recognize %%%phosphorylated%%% sites on projection side arms. "Stainsall" was found

to be a very sensitive probe for detection of %%%phosphorylated%%% cytoskeletal proteins. Without the phosphatase treatment, NF and other phosphoproteins, MAP1, MAP2, tubulin, and %%%tau%%%, all bound the carbocyanine dye on SDS gels, forming blue dye-protein complexes. Measured densitometrically at 615 nm, the staining intensity (relative units/mol protein) was 9, 9, and 3 for human and 10, 13, and 6 for bovine NF-H, NF-M, and NF-L, respectively. NF-H bound the dye less efficiently than was expected from its phosphate content. After phosphatase treatment, NF-H, with half of its phosphate residues remaining, no longer formed blue complex with "Stains-all", the staining intensity of NF-M decreased by 20-40%, and the staining of NF-L was not changed. The results of dye binding, phosphate analysis, and immunostaining showed that there are at least 2 sets of phosphate groups in mammalian NF, which react differently with the phosphatase.

4/7/41 (Item 41 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05810170 BIOSIS NO.: 000034033319
%%PHOSPHORYLATION%% OF MICROTUBULE-ASSOCIATED
PROTEINS MAP2 AND %%%TAU%%
BY NEURAL PP60C-S-R-C IN-VITRO
AUTHOR: KIM H
AUTHOR ADDRESS: DEP. CELL BIOL. ANAT., UNIV. ALA., BIRMINGHAM,
ALA. 35294,
USA.
JOURNAL: TWENTY-SEVENTH ANNUAL MEETING OF THE AMERICAN
SOCIETY FOR CELL
BIOLOGY, ST. LOUIS, MISSOURI, USA, NOVEMBER 16-20, 1987. J CELL
BIOL 105 (4
PART 2). 1987. 108A. %%%1987%%
CODEN: JCLBA
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH

4/7/42 (Item 42 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05733122 BIOSIS NO.: 000084081528
NEUROFIBRILLARY TANGLES IN ALZHEIMER'S DISEASE AND
PROGRESSIVE SUPRANUCLEAR
PALS ANTIGENIC SIMILARITIES AND DIFFERENCES
MICROTUBULE-ASSOCIATED
PROTEIN %%%TAU%% ANTIGENICITY IS PROMINENT IN ALL
TYPES OF TANGLES
AUTHOR: BANCHER C; LASSMANN H; BUDKA H; GRUNDKE-IQBAL I;
IQBAL K; WICHE G;
SEITELBERGER F; WISNIEWSKI H M
AUTHOR ADDRESS: NEUROL. INST., UNIV. VIENNA,
SCHWARZSPANIERSTRASSE 17,
A-1090 WIEN, AUSTRIA.
JOURNAL: ACTA NEUROPATHOL 74 (1). 1987. 39-46. %%%1987%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The antigenic profile of neurofibrillary tangles (NFT) in Alzheimer's disease (AD), senile dementia of Alzheimer type (SDAT), progressive supranuclear palsy (PSP) and in non-demented aged humans was investigated by light and electron microscopic immunocytochemistry using antisera and %%%monoclonal%%% antibodies to tubulin, microtubule-associated proteins (MAP1, MAP2 and %%%tau%%%), neurofilament proteins and determinants unique to Alzheimer paired helical filaments (PHF). Antibodies to %%%tau%%% proteins labeled NFT in all cases investigated (AD, SDAT, PSP and non-demented aged humans). However, one %%%monoclonal%%% antibody to PHF recognized numerous tangles in AD/SDAT, but only a small minority of the PSP tangles. Antibodies to tubulin, MAP1, MAP2 and neurofilament proteins did not selectively stain NFT. Whereas pretreatment of sections with phosphatase was required for the detection of tangles with %%%Tau%%-1 %%%monoclonal%%% antibody, digestion of sections with either phosphatase or pronase had no significant effect on the staining pattern obtained with the other antibodies. Our studies show that, as previously described for AD/SDAT, %%%phosphorylated%%% %%%tau%%% polypeptides are also a major antigenic determinant of tangles in PSP, indicating that tangle formation may follow a common pathogenetic pathway in neurofibrillary degenerations. There is, however at least one epitope in AD/SDAT tangles which seems to be absent on, or at least inaccessible in the 15-nm straight fibrils of PSP.

4/7/43 (Item 43 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05702307 BIOSIS NO.: 000084050712
A %%%MONOCLONAL%%% ANTIBODY THAT RECOGNIZES A
%%PHOSPHORYLATED%%% EPIOTOPE
IN ALZHEIMER NEUROFIBRILLARY TANGLES NEUROFILAMENTS AND
%%TAU%%
PROTEINS IMMUNOSTAINS GRANULOVACUOLAR DEGENERATION
AUTHOR: DICKSON D W; KSIEZAK-REDING H; DAVIES P; YEN S-H
AUTHOR ADDRESS: DEP. PATHOL., ALBERT EINSTEIN COLL. MED., 1300
MORRIS PARK
AVE., K-438, BRONX, NY 10461, USA.
JOURNAL: ACTA NEUROPATHOL 73 (3). 1987. 254-258. %%%1987%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A %%%monoclonal%%% antibody, raised against extracts from Alzheimer brain, that recognizes a %%%phosphorylated%%% epitope in high molecular weight neurofilament proteins and %%%tau%%% proteins also immunostains Alzheimer neurofibrillary tangles, neurites in senile plaques and granulovacuolar degeneration. This result suggests that granulovacuolar degeneration may contain %%%phosphorylated%%% proteins, possibly due to autophagy of %%%phosphorylated%%% perikaryal proteins that appear to be increased in Alzheimer's disease.

4/7/44 (Item 44 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05700178 BIOSIS NO.: 000084048583
RECOGNITION OF ALZHEIMER PAIRED HELICAL FILAMENTS BY
%%MONOCLONAL%%
NEUROFILAMENT ANTIBODIES IS DUE TO CROSSREACTION WITH
%%TAU%%% PROTEIN
AUTHOR: NUKINA N; KOSIK K S; SELKOE D J
AUTHOR ADDRESS: HARVARD MED. SCH., CENT. NEUROL. DISEASES,
DEP. MED., 75
FRANCIS ST., BOSTON, MASS. 02115.
JOURNAL: PROC NATL ACAD SCI U S A 84 (10). 1987. 3415-3419.
%%1987%%

FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Neurofibrillary tangles and senile plaques are the principal pathological features of Alzheimer disease. Neurofibrillary tangles and the neurites of senile plaques contain paired helical filaments (PHF) that consist of two 10-nm filaments twisted into a double helix. The precursor proteins of PHF are not fully known. To identify these precursors, numerous immunochemical studies have been carried out during the past decade. Two apparently conflicting results have been reported. (i) Some, but not all, %%%monoclonal%%% antibodies to neurofilaments stained neurofibrillary tangle. (ii) Polyclonal antibodies prepared to PHF purified in NaDodSO₄ because of their unusual insolubility did not recognize normal proteins, including neurofilaments, on electrophoretic transfer blots of human brain homogenates. These results have been confirmed in several laboratories, including by the use of electron microscopic labeling. Recently, we reported that polyclonal PHF antibodies include antibodies to %%%tau%%% proteins, a family of heat-stable microtubule-associated phosphoproteins, and that antibodies to %%%tau%%% stain Alzheimer neurofibrillary tangles. Those %%%monoclonal%%% neurofilament antibodies that recognize tangles are reported to be directed against %%%phosphorylated%%% epitopes. These facts prompted us to reexamine certain neurofilament %%%monoclonal%%% antibodies that stain neurofibrillary tangles. All %%%monoclonal%%% neurofilament antibodies that stain tangles that we examined, including those initially reported, reacted with %%%tau%%% proteins. Our results suggest that these antibodies react with %%%phosphorylated%%% proteins in PHF, not neurofilament proteins, highlighting the problem of using antibodies to %%%phosphorylated%%% protein epitopes in immunochemical studies. Independent evidence for the presence of neurofilament proteins in human paired helical filaments is now required.

4/7/45 (Item 45 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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05604691 BIOSIS NO.: 000083077831
TWO %%%MONOCLONAL%%% ANTIBODIES RECOGNIZE ALZHEIMER'S NEUROFIBRILLARY TANGLES NEUROFILAMENT AND MICROTUBULE-ASSOCIATED PROTEINS
AUTHOR: KSIEZAK-REDING H; YEN S-H
AUTHOR ADDRESS: DEP. OF PATHOL. FORCH. 538 , ALBERT EINSTEIN COLL. OF MED., 1300 MORRIS PARK AVE., BRONX, NY 10461, USA.
JOURNAL: J NEUROCHEM 48 (2). 1987. 455-462. %%%1987%%
FULL JOURNAL NAME: Journal of Neurochemistry
CODEN: JONRA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Two %%%monoclonal%%% antibodies that recognize Alzheimer's neurofibrillary tangles (ANTs), AD10 and AB18, have been characterized by immunoblotting against human and calf spinal cord neurofilament (NF) and calf brain microtubule preparations. Both antibodies bind to the 200-kilodalton (kd) (NF-H) and 160-kd (NF-M) but not to the 68-kd (NF-L) NF triplet proteins. They also bind to high-molecular-weight microtubule-associated proteins (MAPs) and %%%tau%%%AD10 immunostains MAP2 and MAP1 families, whereas AB18 stains mainly MAP1 bands. Preincubation of intact filament preparation or nitrocellulose strips containing electroblotted NF proteins with *Escherichia coli* alkaline phosphatase completely blocks AD10 binding and partially blocks binding of AB18. These results suggest that the determinants recognized by these antibodies are %%%phosphorylated%%%. Immunoblotting of peptide fragments generated by limited proteolysis of NF proteins with .alpha.-chymotrypsin

and *Staphylococcus aureus* V8 protease shows that the localization of the antigenic determinants to AD10 and AB18 in NF-H is .apprx. 100 and 60 kd, respectively, away from the carboxy terminal, a region previously shown to form the NF projection side arm. In NF-M, the antigenic determinants to both antibodies are located also in the projection side arm, in a 60-kd polypeptide adjacent to the .alpha.-helical filament core. The results show that ANTs contain at least two %%%phosphorylated%%% antigenic sites that are present in NF and MAPs, a finding suggesting that ANTs may be composed of proteins or their fragments with epitopes shared by cytoskeletal proteins.

4/7/46 (Item 46 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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05553214 BIOSIS NO.: 000083026354
MICROHETEROGENEITY OF MICROTUBULE-ASSOCIATED %%%TAU%%% PROTEINS IS DUE TO DIFFERENCES IN %%%PHOSPHORYLATION%%%
AUTHOR: BUTLER M; SHELANSKI M L
AUTHOR ADDRESS: DEP. PHARMACOLOGY, NEW YORK UNIV. SCH. MED., NEW YORK, NY 10016.
JOURNAL: J NEUROCHEM 47 (5). 1986. 1517-1522. %%%1986%%
FULL JOURNAL NAME: Journal of Neurochemistry
CODEN: JONRA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have studied the heterogeneity of the microtubule-associated . %%%tau%%% proteins using . %%%tau%%% -specific antibodies and two-dimensional electrophoresis. Both %%%monoclonal%%% and polyclonal antibodies to . %%%tau%%% proteins recognize five bands in cow brain microtubule proteins run on sodium dodecyl sulfate (SDS)-polyacrylamide gels, with apparent molecular weights between 56,000 and 66,000. Immunoblots of cow brain microtubules separated on two-dimensional gels, using nonequilibrium pH gradient electrophoresis in the first dimension and SDS-gel electrophoresis in the second, reveal that > 30 isoforms of . %%%tau%%% exist. The . %%%tau%%% proteins vary in pI from 6.5 to 8.5, with the higher-molecular weight forms being more acidic. The microheterogeneity of . %%%tau%%% is not induced by cycling of microtubules, because two-dimensional immunoblots of . %%%tau%%% from total brain are almost identical to those of . %%%tau%%% from cyclized tubules. Adult rat brain . %%%tau%%%, which appears as three doublet bands on SDS gels, also exhibits considerable isoelectric heterogeneity, as does . %%%tau%%% from 7-day-old rats, which appears as only one band on SDS gels. After dephosphorylation of cow brain . %%%tau%%% with alkaline phosphatase, the highest-molecular-weight band disappears on SDS gels. On two-dimensional gels, the number of . %%%tau%%% variants decreases by more than half after dephosphorylation, and the more basic species increase greatly in intensity. Preliminary experiments with . %%%tau%%% labeled in vivo with 32PO₄ also indicate that the more acidic . %%%tau%%% proteins are the more highly %%%phosphorylated%%% forms. Thus, isoelectric heterogeneity of . %%%tau%%% proteins exists at all ages and is due, at least in part, to differences in the state of %%%phosphorylation%%% of . %%%tau%%% isoforms.

4/7/47 (Item 47 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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05484350 BIOSIS NO.: 000033085203
MICROTUBULE ASSOCIATED PROTEIN %%%TAU%%% IN ALZHEIMER PAIRED HELICAL FILAMENTS PHF
AUTHOR: IQBAL K; GRUNDKE-IQBAL I; WISNIEWSKI H M
AUTHOR ADDRESS: INST. BASIC RES. DEV. DISABILITIES, STATEN ISLAND, N.Y. 10314, USA.
JOURNAL: ELEVENTH MEETING OF THE INTERNATIONAL SOCIETY

FOR NEUROCHEMISTRY
AND THE EIGHTEENTH MEETING OF THE AMERICAN SOCIETY FOR
NEUROCHEMISTRY, LA
GUAIRA, VENEZUELA, MAY 31-JUNE 5, 1987. J NEUROCHEM 48
(SUPPL.). 1987.
S157. %1987%
CODEN: JONRA
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH

4/7/48 (Item 48 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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05263909 BIOSIS NO.: 000082104534
DEFECTIVE BRAIN MICROTUBULE ASSEMBLY IN ALZHEIMER'S
DISEASE
AUTHOR: IQBAL K; GRUNDKE-IQBAL I; ZAIDI T; MERZ P A; WEN G Y;
SHAIKH S S;
WISNIEWSKI H M; ALAFUZOFF I; WINBLAD B
AUTHOR ADDRESS: NYS INST. BASIC RES. DEV. DISABILITIES, 1050
FOREST HILL
ROAD, STATEN ISLAND, NEW YORK 10314, USA.
JOURNAL: LANCET 2 (8504). 1986. 421-426. %1986%
FULL JOURNAL NAME: Lancet
CODEN: LANCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Brains obtained within 2-4 hours post mortem and
histopathologically confirmed for Alzheimer's disease and non-Alzheimer
brains from age-matched controls were examined for in-vitro assembly of
microtubules and neurofilaments. Microtubule assembly was observed only
in control but not in Alzheimer brains, and neurofilaments were obtained
from both types of brain. The microtubule-associated protein
%tau%,
which stimulates assembly for microtubules from tubulin, was abnormally
%phosphorylated% in Alzheimer but not in control brain microtubule
preparations. Alzheimer brains did not show the presence of any inhibitor
of microtubule assembly or any abnormality of tubulin. DEAE-dextran, a
polycation which mimics %tau% in stimulating microtubule assembly,
induced the assembly of microtubules in Alzheimer brain. Tubulin from
both normal and Alzheimer brains was labelled on western blots by a
%monoclonal% antibody to the tyrosinylated carboxy-terminal
epitope
of alpha. tubulin. These studies suggest that in Alzheimer's disease
tubulin can be assembled into brain microtubules, but the process is
defective, probably because of abnormal %phosphorylation% of
%tau%. This post-translational alteration of %tau% might be
the
cause of the neurofibrillary abnormality in Alzheimer's disease.

4/7/49 (Item 49 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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05234674 BIOSIS NO.: 000082075296
ABNORMAL %PHOSPHORYLATION% OF THE
MICROTUBULE-ASSOCIATED PROTEIN
%TAU% IN ALZHEIMER CYTOSKELETAL PATHOLOGY
AUTHOR: GRUNDKE-IQBAL I; IQBAL K; TUNG Y-C; QUINLAN M;
WISNIEWSKI H M;
BINDER L I
AUTHOR ADDRESS: N.Y. STATE UNIV. BASIC RES. DEV. DISABILITIES,
1050 FOREST
HILL ROAD, STATEN ISLAND, N.Y. 10314.
JOURNAL: PROC NATL ACAD SCI U S A 83 (13). 1986. 4913-4917.
%1986%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences
of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract

LANGUAGE: ENGLISH

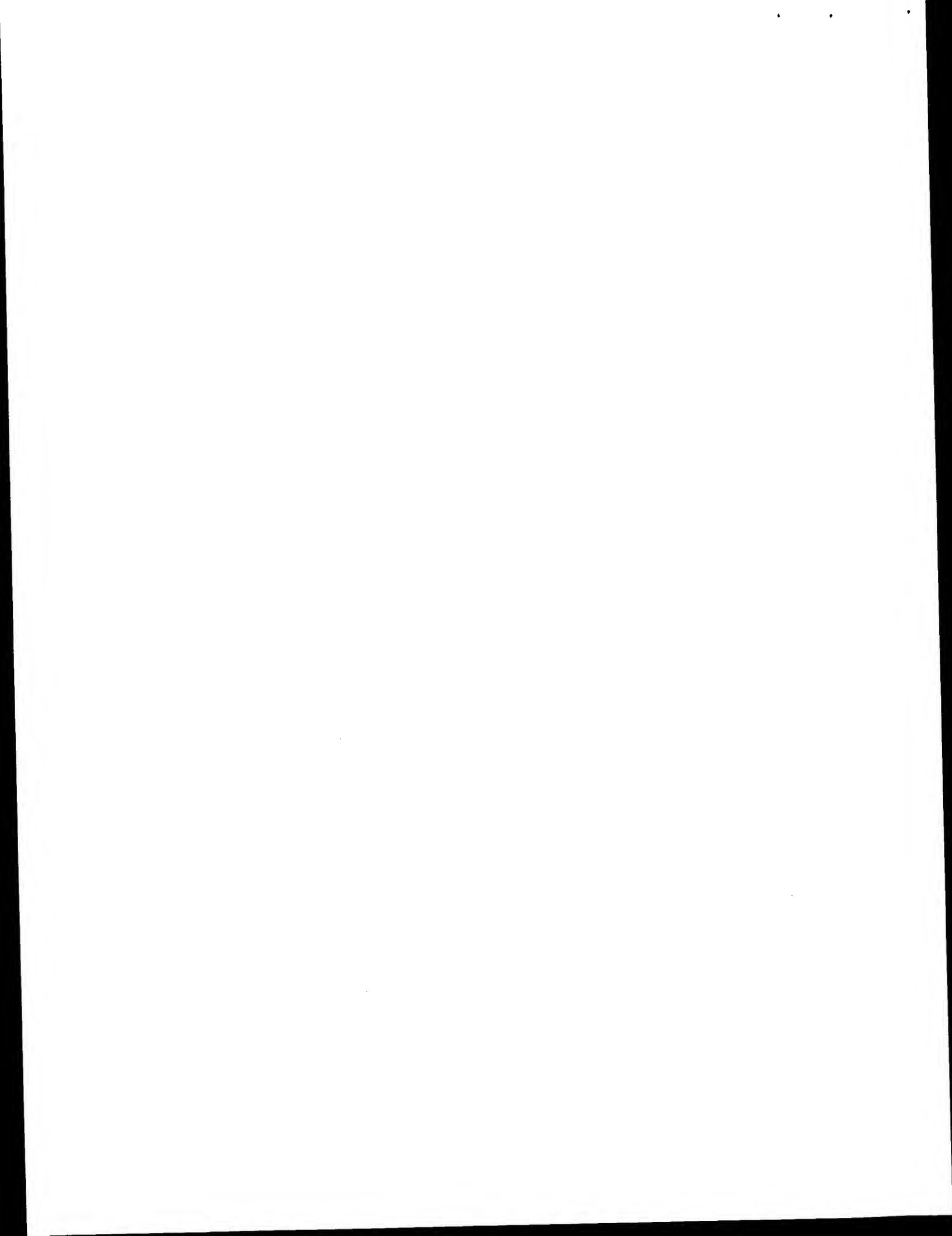
ABSTRACT: A %monoclonal% antibody to the microtubule-associated
protein
%tau% (%tau%) labeled some neurofibrillary tangles and
plaque
neurites, the two major locations of paired-helical filaments (PHF), in
Alzheimer disease brain. The antibody also labeled isolated PHF that had
been repeatedly washed with NaDodSO4. Dephosphorylation of the tissue
sections with alkaline phosphatase prior to immunolabeling dramatically
increased the number of tangles and plaques recognized by the antibody.
The plaque core amyloid was not stained in either dephosphorylated or
nondephosphorylated tissue sections. On immunoblots PHF polypeptides
were
labeled readily only when dephosphorylated. In contrast, a commercially
available %monoclonal% antibody to a %phosphorylated%
epitope of
neurofilaments that labeled the tangles and the plaque neurites in tissue
did not label any PHF polypeptides on immunoblots. The PHF polypeptides,
labeled with the %monoclonal% antibody to %tau%,
electrophoresed with those polypeptides recognized by antibodies to
isolated PHF. The antibody to %tau%-labeled microtubules from
normal human brains assembled in vitro but identically treated Alzheimer
brain preparations had to be dephosphorylated to be completely recognized
by this antibody. These findings suggest that %tau% in Alzheimer
brain is an abnormally %phosphorylated% protein component of PHF.

4/7/50 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

02130742 Genuine Article#: KD144 Number of References: 42
Title: COMPARISON OF METHODS FOR THE INVITRO ASSEMBLY OF
POSTMORTEM HUMAN
BRAIN MICROTUBULES THAT RETAIN THE
MICROTUBULE-ASSOCIATED PROTEIN
%TAU%
Author(s): SPARKMAN DR
Corporate Source: UNIV TEXAS, SW MED CTR, DEPT PATHOL, 5323 HARRY
HINES
BLVD/DALLAS/TX/75235
Journal: JOURNAL OF NEUROSCIENCE METHODS, %1992%, V45,
N1-2 (OCT-NOV)
, P41-53
ISSN: 0165-0270

Language: ENGLISH Document Type: ARTICLE
Abstract: Several methods for the in vitro assembly of microtubules from
postmortem human brain were compared for the purpose of obtaining
microtubule preparations that best retained their
microtubule-associated proteins. The polymerized microtubules from the
preparations were examined by negative staining and electron microscopy
and shown to consist of well-formed microtubules with varying amounts
of abnormal assembly products that differed between methods. The
microtubule protein was analyzed by SDS-polyacrylamide gel
electrophoresis, quantitative densitometry, as well as trans-blotted
onto membranes which were reacted with %monoclonal% antibodies
to
tubulin subunits and microtubule-associated proteins. All the
preparations were found to contain both the alpha- and beta-tubulin
subunits with quantitative differences, but they varied most, both
quantitatively and qualitatively, in their content of
microtubule-associated proteins. The optimal method for the assembly of
soluble tubulin from postmortem human brain cytosol into intact
microtubules which specifically retained most of their MAPs, especially
%tau%, employed 4 M glycerol assembly buffer in the presence of
10
muM taxol and 1 mM GTP. The isolation methods were used to compare
young and aged brains, and there were fewer microtubule-associated
proteins, especially %tau%, associated with the microtubules in
advanced age, in all preparations.

4/7/51 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02066136 Genuine Article#: JY197 Number of References: 51
Title: IMMUNOCYTOCHEMISTRY OF NEUROFIBRILLARY TANGLES
WITH ANTIBODIES TO
SUBREGIONS OF %%%TAU%%%PROTEIN - IDENTIFICATION OF
HIDDEN AND CLEAVED
%%TAU%% EPITOPES AND A NEW %%%PHOSPHORYLATION%%
SITE

Author(s): DICKSON DW; KSIEZAKREDING H; LIU WK; DAVIES P;
CROWE A; YEN SHC
Corporate Source: YESHIVA UNIV ALBERT EINSTEIN COLL MED, DEPT
PATHOL
NEUROPATHOL, 1300 MORRIS PK AVE/BRONX//NY/10461; YESHIVA
UNIV ALBERT
EINSTEIN COLL MED, ROSE F KENNEDY CTR RES MENTAL RETARDAT
& HUMAN
DEV/BRONX//NY/10461

Journal: ACTA NEUROPATHOLOGICA, %%%1992%%, V84, N6 (NOV),
P596-605

ISSN: 0001-6322

Language: ENGLISH Document Type: ARTICLE

Abstract: Antibodies to multiple epitopes spanning the length of the
%%tau%% molecule were used to study Alzheimer neurofibrillary
tangles
(NFT) using immunocytochemical methods and several different methods
of

fixation and tissue processing, including staining of vibratome
sections, hydrated autoclaving of paraffin sections and
immunofluorescence of NFT isolated from fresh brain tissue. Smears and
sections were pretreated with trypsin and/or phosphatase to further
characterize antibody binding. In tissue fixed briefly in
periodate-lysine-paraformaldehyde, %%%tau%% immunoreactivity was
detected in astrocytes, but only a few %%%tau%% epitopes were
detected

in NFT with this fixation method. In contrast, all %%%tau%% epitopes
were detected in NFT in tissue fixed in formaldehyde for prolonged
periods of time. In the hippocampus, the number of NFT detected in the
dentate fascia was in proportion to the duration of dementia, as we
previously noted. Dentate fascia NFT were intracellular (i-NFT) and
were reactive with antibodies recognizing epitopes in both the carboxy-
and amino-terminal regions of %%%tau%%, but not the
microtubule-binding domain of %%%tau%%, suggesting that
microtubule-binding domain epitopes are hidden in i-NFT. In contrast,
NFT in the subiculum and layer II of the parahippocampal cortex were
mostly extracellular (e-NFT), especially in severe cases of long
duration. e-NFT were immunoreactive with antibodies to the
microtubule-binding domain, but only weakly reactive with antibodies to
carboxy- or amino-terminal epitopes, suggesting that e-NFT may contain
fragments of %%%tau%%. In both isolated NFT and NFT in sections,
amino-terminal epitopes, including the Alz-50 epitope, were sensitive
to trypsin proteolysis, which suggests that the lack of staining of
e-NFT by antibodies to the amino-terminal regions of %%%tau%% is due
to proteolysis. Antibodies reactive with amino-terminal epitopes also
stained fewer NFT following hydrated autoclaving, while those reacting
with the carboxy half of %%%tau%% stained more NFT after hydrated
autoclaving. Thus, although carboxy-terminal regions are not detected
in e-NFT, they are probably masked, rather than proteolytically
cleaved, since they can be revealed by hydrated autoclaving. Finally,
phosphatase treatment of isolated NFT revealed enhanced immunostaining
not only with %%%Tau%%-1, as in previous studies demonstrating
abnormal %%%phosphorylation%% of %%%tau%% proteins in NFT, but
also

with an antibody to exon 2, which reveals yet another
%%phosphorylation%% site in %%%tau%% of NFT.

4/7/52 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01955811 Genuine Article#: JP530 Number of References: 40
Title: IMMUNOHISTOCHEMICAL STUDIES ON THE NEW TYPE OF
ASTROCYTIC INCLUSIONS
IDENTIFIED IN A PATIENT WITH BRAIN MALFORMATION
Author(s): KATO S; HIRANO A; UMAHARA T; HERZ F; SHIODA K;
MINAGAWA M
Corporate Source: MONTEFIORE MED CTR, DIV NEUROPATHOL, 111 E

210TH

ST/BRONX//NY/10467; MONTEFIORE MED CTR, DIV
NEUROPATHOL, 111 E 210TH
ST/BRONX//NY/10467; MONTEFIORE MED CTR, DEPT
PATHOL/BRONX//NY/10467;
SAITAMA MED SCH, DEPT PATHOL/MOROYAMA/SAITAMA
35004/JAPAN/; SAITAMA MED
SCH, DEPT NEUROPSYCHIAT/MOROYAMA/SAITAMA 35004/JAPAN/
Journal: ACTA NEUROPATHOLOGICA, %%%1992%%, V84, N4 (SEP),
P449-452
ISSN: 0001-6322

Language: ENGLISH Document Type: NOTE

Abstract: Immunohistochemical studies were carried out on the new type of
cerebral cortical astrocytic inclusions recently discovered in a
20-year-old patient with maldeveloped brain and micropolygyria. The
inclusions appeared as eosinophilic structures (hematoxylin and eosin
stain) and did not exhibit argyrophilia (modified Bielschowsky method).
The inclusions were strongly stained by the antibody against S-100
protein (S 100) and to a lesser extent by the antibody to
microtubule-associated protein 18 (MAP 18). In contrast to Rosenthal
fibers, the astrocytic inclusions did not react with antibodies to
alpha-B-crystallin, glial fibrillary acidic protein and ubiquitin. No
positive reactions were obtained with antibodies against heat-shock
protein 27 (HSP 27), HSP 72, actin, vimentin, desmin, cytokeratin,
myelin basic protein, beta-tubulin, MAP 2, %%%tau%% protein, paired
helical filament, %%%phosphorylated%% neurofilament protein (NFP),
nonphosphorylated NFP, synaptophysin, cathepsin D,
alpha-1-antichymotrypsin, alpha-1-antitrypsin and basic fibroblast
growth factor. By immunoelectron microscopy, the products of the
reaction with the anti-S 100 antibody appeared as heterogeneous
granular deposits and with the antibody to MAP 18 they were randomly
scattered throughout the astrocytic inclusions. Our results demonstrate
that the immunohistochemical profile of the recently described
inclusions differs from that of Rosenthal fibers. Whether the novel
inclusions are involved in congenital astrocyte dysfunction and
cerebral malformation remains to be established.

4/7/53 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01952677 Genuine Article#: JN807 Number of References: 74
Title: APPROPRIATE TARGET INTERACTIONS PREVENT ABNORMAL
CYTOSKELETAL
CHANGES IN NEURONS - A STUDY WITH INTRASCATIC GRAFTS
OF THE SEPTUM AND
THE HIPPOCAMPUS
Author(s): DOERING LC
Corporate Source: MCMASTER UNIV, DIV ANAT, HSC 1R1, 1200 MAIN ST
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L8N 3Z5/ONTARIO/CANADA/

Journal: JOURNAL OF NEUROSCIENCE, %%%1992%%, V12, N9 (SEP),
P3399-3413

ISSN: 0270-6474

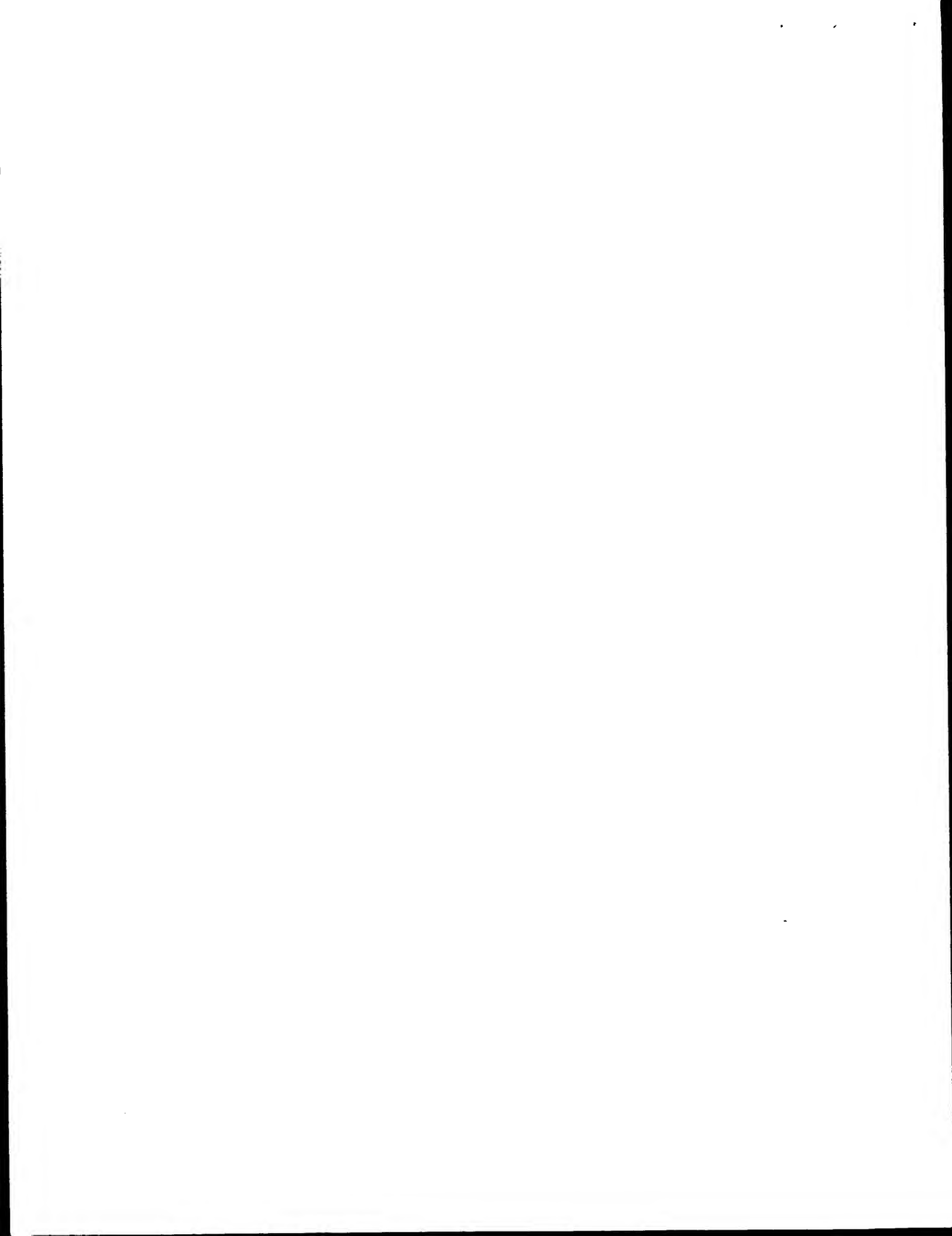
Language: ENGLISH Document Type: ARTICLE

Abstract: Transplantation of embryonic CNS regions into the PNS provides
an

opportunity to study temporal and spatial changes in the cytoskeleton
that are associated with aging and neurodegenerative diseases. In this
study, the fetal septum was transplanted alone or with the hippocampus
into the sciatic nerves of young adult rats to determine whether the
proper central neural target could prevent the expression of abnormal
cytoskeletal changes. The substantia nigra, a nontarget area of the
septum, served as control co-grafts. After 1, 3, 6, 12, and 18 months
of survival, the grafts were examined by immunocytochemistry with
antibodies to %%%phosphorylated%% and nonphosphorylated
neurofilaments, microtubule-associated proteins (MAPs), and glial
fibrillary acidic protein (GFAP).

Subpopulations of neurons in the septal transplants expressed CAT
and the NGF receptor (192-IgG). Long-term (12-18 months) expression of
these two markers was only observed when the septum was combined with
the hippocampus.

Although isolated single grafts of septum survived within the PNS



substratum, significant neuronal loss, extensive graft shrinkage, and aberrant cytoskeletal immunoreactivity were prominent in the long-term group. Changes that reflected an aging process included the ectopic expression of τ -phosphorylated neurofilaments in neuronal perikarya, swollen axons, and a loss of MAP2 immunoreactivity that paralleled dendrite regression. In addition, abnormal "curly" fibers in the neuropil were also immunolabeled with an antibody directed against τ (5E2). Introduction of hippocampal co-grafts increased the final size of the septal transplants and prevented the cytoskeletal changes that accompanied the degeneration in the single septal grafts. The degree of GFAP immunostaining in the septum corresponded with advancing graft age and was minimized when grafted with the hippocampal formation. When the septum was combined with the substantia nigra, the grafts also underwent shrinkage and no protective influence from aberrant cytoskeletal staining was observed.

These experiments exemplify the importance of an appropriate CNS neural target on the maintenance of long-term cholinergic neuron survival and normal morphology at the cytoskeletal level and illustrate the usefulness of these CNS-PNS constructs to examine conditions that influence the cytoskeleton.

4/7/54 (Item 5 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01939271 Genuine Article#: JMB12 Number of References: 37
Title: PATHOLOGICAL-CHANGES IN OLFACTORY NEURONS IN ALZHEIMERS-DISEASE
Author(s): TALAMO BR; FENG WH; PEREZCRUET M; ADELMAN L; KOSIK K; LEE VMY;
CORK LC; KAUER JS
Corporate Source: TUFTS UNIV,SCH MED,DIV NEUROSCI/BOSTON//MA/02111; NEW ENGLAND MED CTR/BOSTON//MA/02111; HARVARD UNIV,SCH MED/BOSTON//MA/02115 ; UNIV PENN,SCH MED/PHILADELPHIA//PA/19104; JOHNS HOPKINS UNIV,SCH MED/BALTIMORE//MD/21205
Journal: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, 1991, V640, DEC (DEC 3), P1-7
ISSN: 0077-8923
Language: ENGLISH Document Type: ARTICLE

4/7/55 (Item 6 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01873790 Genuine Article#: JH625 Number of References: 57
Title: IMMUNE ELECTRON-MICROSCOPIC CHARACTERIZATION OF MONOCLONAL ANTIBODIES TO ALZHEIMER NEUROFIBRILLARY TANGLES
Author(s): WRZOLEK MA; MERZ PA; KASCSAK R; GRUNDKEIQBAL I; IQBAL K;
RUBENSTEIN R; TONNADEMASI M; GOLLER NL; MEHTA P; WISNIEWSKI HM
Corporate Source: NEW YORK STATE INST BASIC RES DEV DISABILITIES,1050 FOREST HILL RD/STATEN ISL//NY/10301; NEW YORK STATE INST BASIC RES DEV DISABILITIES,1050 FOREST HILL RD/STATEN ISL//NY/10301
Journal: AMERICAN JOURNAL OF PATHOLOGY, 1992, V141, N2 (AUG), P 343-355
Language: ENGLISH Document Type: ARTICLE
Abstract: Characterization of eleven monoclonal antibodies raised to isolated sodium dodecyl sulfate (SDS)-treated Alzheimer's neurofibrillary tangles (ANT), has revealed the presence of at least two different epitopes. MAb's were tested for reactivity to ubiquitin and paired helical filaments (PHF) isolated by three different procedures. The effect of protease and/or alkaline phosphatase pretreatment on the reactivity of the MAb's with isolated PHF was also

examined All MAb's that had reacted strongly in the ELISA with sonicated

SDS-treated ANT also immune decorated isolated PHF to varying degrees.

Two MAb's exhibited a high reactivity to PHF: 3-39 and 5-25. τ -MAB's

3-39 was found to recognize a protease sensitive epitope. In contrast τ -MAB's 5-25 was found to consistently decorate isolated PHF in all

preparations and exhibited a strong reactivity to ubiquitin, and the epitope in isolated PHF was not protease sensitive. Thus structural PHF after protease treatment and detergent treatment contain an antigenic site that is present in ubiquitin.

4/7/56 (Item 7 from file: 34)

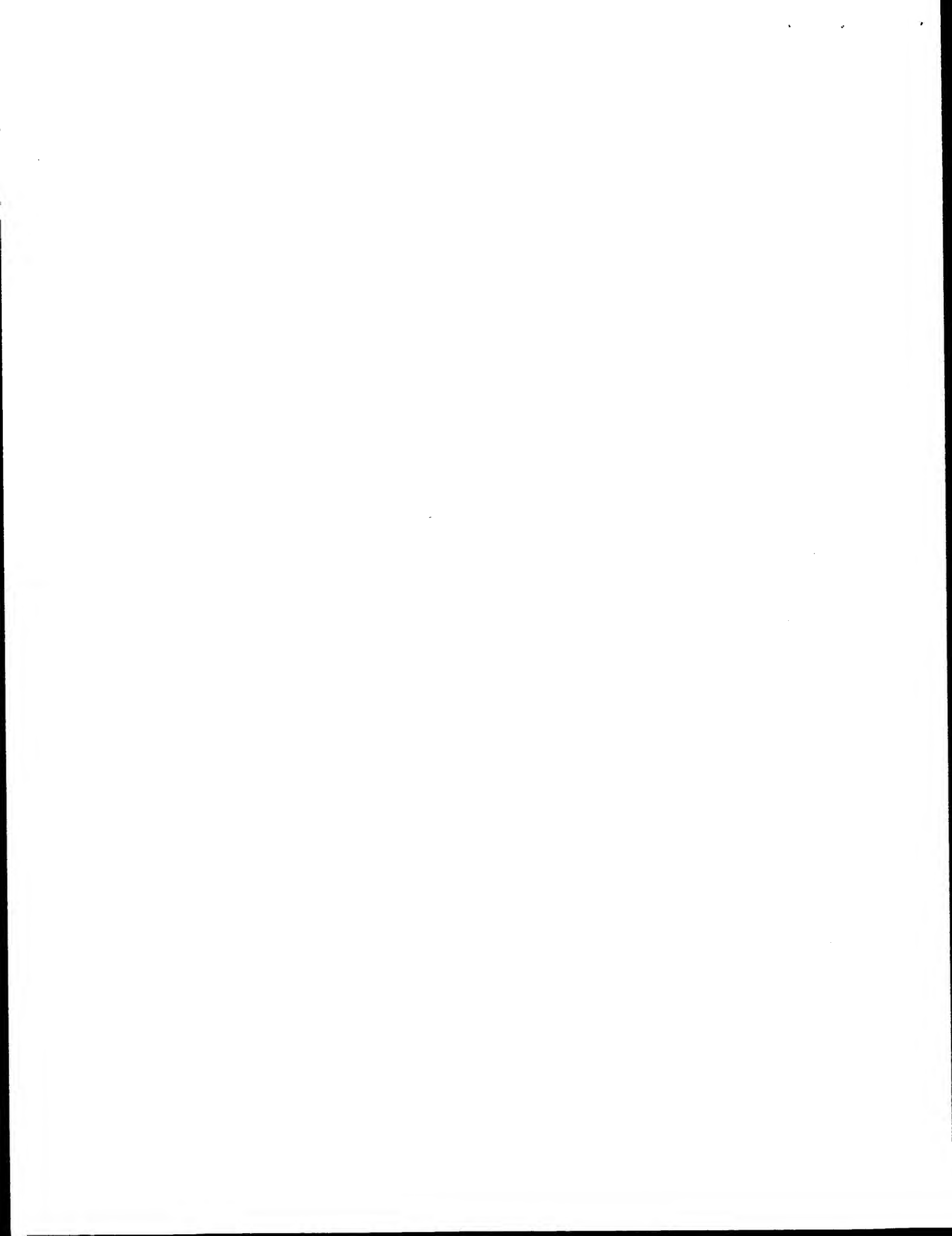
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

01717048 Genuine Article#: HV352 Number of References: 87
Title: UBIQUITINATION AND ABNORMAL PHOSPHORYLATION OF PAIRED HELICAL FILAMENTS IN ALZHEIMERS-DISEASE
Author(s): IQBAL K; GRUNDKEIQBAL I
Corporate Source: NEW YORK STATE INST BASIC RES DEV DISABILITIES,1050 FOREST HILL RD/STATEN ISL//NY/10314
Journal: MOLECULAR NEUROBIOLOGY, 1991, V5, N2-4, P399-410
Language: ENGLISH Document Type: ARTICLE
Abstract: The most characteristic cellular change in Alzheimer's disease is the accumulation of aberrant filaments, the paired helical filaments (PHF), in the affected neurons. There is growing evidence from a number of laboratories that dementia correlates better with the accumulation of PHF than of the extracellular amyloid, the second major lesion of Alzheimer's disease. PHF are both morphologically and biochemically unlike any of the normal neurofibrils. The major polypeptides in isolated PHF are microtubule-associated protein τ . τ in PHF is phosphorylated differently from τ in microtubules. This abnormal phosphorylation of τ in PHF occurs at several sites. The accumulation of abnormally phosphorylated τ in the affected neurons in Alzheimer's disease brain precedes both the formation and the ubiquitination of the neurofibrillary tangles. In Alzheimer's disease brain, tubulin is assembly competent, but the in vitro assembly of microtubules is not observed. In vitro, the phosphate groups in PHF are less accessible than those of τ to alkaline phosphatase. The in vitro dephosphorylated PHF polypeptides stimulate microtubule assembly from bovine tubulin. It is hypothesized that a defect in the protein phosphorylation/dephosphorylation system is one of the earliest events in the cytoskeletal pathology in Alzheimer's disease. Production of nonfunctional τ by its phosphorylation and its polymerization into PHF most probably contributes to a microtubule assembly defect, and consequently, to a compromise in both axoplasmic flow and neuronal function.

4/7/57 (Item 8 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

01712492 Genuine Article#: HV090 Number of References: 40
Title: THE JUVENILE MICROTUBULE-ASSOCIATED PROTEIN MAP2C IS A ROD-LIKE MOLECULE THAT FORMS ANTIPARALLEL DIMERS
Author(s): WILLE H; MANDELKOW EM; MANDELKOW E
Corporate Source: DESY,MAX PLANCK UNIT STRUCT MOLEC BIOL,NOTKESTR85/W-2000 HAMBURG 52//GERMANY//; DESY,MAX PLANCK UNIT STRUCT MOLEC BIOL,NOTKESTR85/W-2000 HAMBURG 52//GERMANY//
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1992, V267, N15 (MAY 25), P



10737-10742

Language: ENGLISH Document Type: ARTICLE

Abstract: We have developed a procedure to isolate the microtubule-associated protein 2c (MAP2c), a juvenile form of MAP2 occurring in mammalian brain. The shape, size, self-association, and antibody interactions of MAP2c were studied. Monomeric MAP2c is an elongated molecule with a length approximately 48 nm, considerably shorter than the higher molecular weight forms MAP2a or b of adult brain. Two %%%monoclonal%%% antibodies whose epitopes are near the N

or

C terminus, respectively, are located close to the opposite ends of the MAP2c rods. This places constraints on the types of internal folding of the molecule.

MAP2c self-associates into dimers and fibrous aggregates. The dimers are predominantly antiparallel and nearly in register, as judged by antibody labeling.

4/7/58 (Item 9 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

(c) 2002 Inst for Sci Info. All rts. reserv.

01634193 Genuine Article#: HN274 Number of References: 20

Title: DETERGENT-INSOLUBLE CORTICAL LEWY BODY FIBRILS SHARE EPITOPES WITH

NEUROFILAMENT AND %%%TAU%%%

Author(s): POLLANEN MS; BERGERON C; WEYER L

Corporate Source: UNIV TORONTO,CTR RES NEURODEGENERAT DIS,TANZ NEUROSCI

BLDG,ROOM 121/TORONTO M5S 1A8/ONTARIO/CANADA/; UNIV TORONTO,CTR RES

NEURODEGENERAT DIS,TANZ NEUROSCI BLDG,ROOM 121/TORONTO M5S

1A8/ONTARIO/CANADA/; TORONTO HOSP,TORONTO GEN DIV/TORONTO/ONTARIO/CANADA/

Journal: JOURNAL OF NEUROCHEMISTRY, %%%1992%%%, V58, N5 (MAY), P1953-1956

Language: ENGLISH Document Type: NOTE

Abstract: Lewy bodies are cytoskeletal inclusions associated with neuronal injury and death in idiopathic Parkinson's disease and other neurodegenerative disorders. The chemical composition of the 8-10-nm fibrils of the Lewy body is unknown, although they are related to both normal cytoskeletal elements and paired helical filaments of Alzheimer neurofibrillary tangles. From the Lewy body-rich cerebral cortex of patients with diffuse Lewy body disease we have isolated intact Lewy bodies using a high salt buffer/nonionic detergent gradient centrifugation procedure and extracted the constitutive fibrils with urea and sodium dodecyl sulfate. Urea/detergent-resistant Lewy body fibrils were solubilized with formic acid and found to contain a single protein band of 68 kDa, which was not found in identically prepared normal brain homogenates. The Lewy body derived-polypeptide was recognized on immunoblots by a polyclonal antibody that reacted with both the 68-kDa neurofilament subunit and the microtubule-associated protein %%%tau%%%. The 68-kDa Lewy body protein was not labeled by the

%%monoclonal%%% antibody %%%tau%%%-1 despite prior in vitro enzymatic

dephosphorylation. We conclude that the detergent-insoluble component of the cortical Lewy body fibril shares epitopes with neurofilament and %%%tau%%% and may be a posttranslationally modified derivative of either neurofilament or %%%tau%%% with substantially altered biochemical and immunologic properties.

4/7/59 (Item 10 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

(c) 2002 Inst for Sci Info. All rts. reserv.

01584230 Genuine Article#: HK061 Number of References: 37

Title: THE 72-KDA MICROTUBULE-ASSOCIATED PROTEIN FROM PORCINE BRAIN

Author(s): TAKEUCHI M; HIRANAGA S; UMEYAMA T; HIROKAWA N

Corporate Source: UNIV TOKYO,FAC MED,DEPT ANAT & CELL

BIOL,HONGO,BUNKYO

KU/TOKYO 113/JAPAN/; UNIV TOKYO,FAC MED,DEPT ANAT & CELL BIOL,HONGO,BUNKYO KU/TOKYO 113/JAPAN/

Journal: JOURNAL OF NEUROCHEMISTRY, %%%1992%%%, V58, N4 (APR), P1510-1516

Language: ENGLISH Document Type: ARTICLE

Abstract: A microtubule-associated protein (MAP) with a molecular mass of 72-kDa that was purified from porcine brain by using its property of heat stability in a low pH buffer was characterized. Low-angle rotary shadowing revealed that the 72-kDa protein was a rodlike protein approximately 55-75 nm long. The 72-kDa protein bound to microtubules polymerized from phosphocellulose column-purified tubulin (PC-tubulin) with taxol and promoted the polymerization of PC-tubulin in the absence of taxol. Microtubules polymerized by the 72-kDa protein showed a tendency to form bundles of several microtubules. Quick-freeze, deep-etch electron microscopy revealed that the 72-kDa protein formed short crossbridges between microtubules. We performed peptide

mapping

to analyze the relationship of the 72-kDa protein to other heatstable MAPs, and the results showed some resemblance of the 72-kDa protein to MAP2. Cross-reactivity with a %%%monoclonal%%% anti-MAP2 antibody further suggested that the 72-kDa protein and MAP2 are immunologically related. To study the relationship between the 72-kDa protein and MAP2c, a smaller molecular form of MAP2 identified in juvenile rat brain, we prepared the 72-kDa protein from rat brain by the same method

as that used for porcine brain. The fact that the 72-kDa protein from juvenile rat brain was also stained with our %%%monoclonal%%% anti-MAP2

antibody also suggested that the 72-kDa protein is an MAP2C homologue of the porcine brain.

4/7/60 (Item 11 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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01512952 Genuine Article#: HE275 Number of References: 35

Title: %%%TAU%%%-2 - A PROBE FOR A SER CONFORMATION IN THE AMINO TERMINUS

OF %%%TAU%%%

Author(s): WATANABE N; TAKIO K; HASEGAWA M; ARAI T; TITANI K; IHARA Y

Corporate Source: UNIV TOKYO,FAC MED,INST BRAIN RES,DEPT NEUROPATHOL,7-3-1

HONGO,BUNKYO KU/TOKYO 113/JAPAN/; UNIV TOKYO,FAC MED,INST BRAIN

RES,DEPT NEUROPATHOL,7-3-1 HONGO,BUNKYO KU/TOKYO 113/JAPAN/; SCI UNIV

TOKYO,FAC SCI & TECHNOL,DEPT APPL BIOLSCI/NODA/CHIBA 278/JAPAN/;

RIKEN,AGING PROC RES LAB,FRONTIER RES

PROGRAM/WAKO/JAPAN/; FUJITA HLTH

UNIV,SCH MED,INST COMPREHENS MED SCI,DIV BIOMED POLYMER SCI/TOYOAKE/JAPAN/; TOKYO METROPOLITAN GERIATR HOSP & INST

GERONTOL,DEPT NEUROPHYSIOL/TOKYO 173/JAPAN/

Journal: JOURNAL OF NEUROCHEMISTRY, %%%1992%%%, V58, N3 (MAR), P960-966

Language: ENGLISH Document Type: ARTICLE

Abstract: We have determined the epitope for %%%Tau%%% 2, a %%%monoclonal%%% antibody that intensely stained tangles, plaque neurites, and curly fibers in the tissue section, and strongly labeled bovine %%%tau%%%, but only very weakly labeled human %%%tau%%% on the

blot. The epitope has been localized to Ala95 through Ala108 of bovine %%%tau%%%. Ser101 is critical for %%%Tau%%% 2 reactivities; the replacement of Ser by Pro, which is found in rat, mouse, and human %%%tau%%%, brings about very weak %%%Tau%%% 2 reactivities. The strong %%%Tau%%% 2 staining of tangles and its effective absorption with a synthetic Ser peptide (Ala95 through Ala108) suggest that the %%%tau%%%

in paired helical filaments takes a Ser conformation, rather than a Pro conformation, in its amino-terminal portion.

4/7/61 (Item 12 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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01501607 Genuine Article#: HE042 Number of References: 37
Title: COMMON EPITOPES OF HUMAN AND MURINE MALLORY BODIES AND LEWY BODIES

AS REVEALED BY A NEUROFILAMENT ANTIBODY
Author(s): PREISEGGER KH; ZATLOUKAL K; SPUREJ G; RIEGELNEGG D; DENK H

Corporate Source: GRAZ UNIV,SCH MED,INST PATHOL,DIV MOLEC PATHOL,MOLEC
PATHOL LAB,AUENBRUGGERPL 25/A-8036 GRAZ//AUSTRIA// GRAZ UNIV,SCH

MED,INST PATHOL,DIV MOLEC PATHOL,MOLEC PATHOL LAB,AUENBRUGGERPL
25/A-8036 GRAZ//AUSTRIA/

Journal: LABORATORY INVESTIGATION, %%%1992%%, V66, N2 (FEB), P193-199

Language: ENGLISH Document Type: ARTICLE

Abstract: The antibody SMI 31, which is directed against a %%%phosphorylated%% epitope, associated with neurofilaments and recognizes Lewy bodies in brains of patients with Parkinson's disease (Banerjee C, Lassmann H, Budka H, Jellinger K, Grundge-Iqbal I, Iqbal K, Wiche G, Seitelberger F, Wisniewski H: J Neuropathol Exp Neurol 1:81, 1989), decorated in immunofluorescence microscopy Mallory bodies (MBs) present in livers of mice chronically treated with griseofulvin and 3,5-diethoxycarbonyl-1,4-dihydrocollidine. In immunoblots it recognized very acidic MB components in a molecular weight range between 55 and 69.5 kilodaltons in addition to poorly soluble high molecular weight material. Moreover, an antibody to %%%tau%% protein

showed similar reactivities in immunofluorescence microscopy and immunoblotting experiments. Both antibodies also stained MBs in human liver with alcoholic hepatitis. These observations support and extend earlier findings which indicate that several intermediate filament-related cellular inclusion bodies, including MBs, share a variety of morphologic, structural and antigenic features. They also suggest the involvement of %%%tau%% or %%%tau%%-like proteins in MB formation.

4/7/62 (Item 13 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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01483122 Genuine Article#: HC201 Number of References: 49
Title: IMMUNOCYTOCHEMICAL STUDY OF BALLOONED NEURONS IN CORTICAL

DEGENERATION WITH NEURONAL ACHROMASIA

Author(s): SMITH TW; LIPPA CF; DEGTOLAMI U

Corporate Source: UNIV MASSACHUSETTS,MED CTR,DEPT PATHOL NEUROPATHOL,55

LAKE AVE N/WORCESTER//MA/01655: UNIV MASSACHUSETTS,MED CTR,DEPT

NEUROL/WORCESTER//MA/01605

Journal: CLINICAL NEUROPATHOLOGY, %%%1992%%, V11, N1 (JAN-FEB), P28-35

Language: ENGLISH Document Type: ARTICLE

Abstract: We studied the immunocytochemical characteristics of the ballooned neurons (BN) in three patients with cortical degeneration with neuronal achromasia (CDNA) using antibodies to %%%phosphorylated%% neurofilaments (PNF), %%%tau%%, Alz-50, ubiquitin, beta (A4) amyloid, and glial fibrillary acidic protein. All BN exhibited intense perikaryal staining for PNF protein. Most BN and some normal-appearing neurons also stained for ubiquitin and Alz-50. The BN did not immunostain for %%%tau%% protein, and none of the cases

had %%%tau%%-reactive neocortical neurofibrillary tangles or Pick bodies. One case had occasional senile plaques that stained for beta amyloid; no case had amyloid angiopathy. Our findings suggest that the pathophysiologic basis of the cortical degeneration in CDNA involves an alteration of neuronal cytoskeletal metabolism affecting neurofilament and possibly microtubular proteins in conjunction with activation of the ubiquitin proteolytic system.

4/7/63 (Item 14 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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01428655 Genuine Article#: GY439 Number of References: 46
Title: HYDROFLUORIC ACID-TREATED %%%TAU%%-PHF PROTEINS DISPLAY THE SAME

BIOCHEMICAL-PROPERTIES AS NORMAL %%%TAU%%

Author(s): GREENBERG SG; DAVIES P; SCHEIN JD; BINDER LI

Corporate Source: WM BURKE MED RES INST,785 MAMARONECK AVE/WHITE

PLAINS//NY/10605: YESHIVA UNIV ALBERT EINSTEIN COLL MED,DEPT

PATHOL/BRONX//NY/10461: UNIV ALABAMA,SCH MED & DENT,DEPT CELL

BIOL/BIRMINGHAM//AL/35294

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, %%%1992%%, V267, N1 (JAN 5), P

564-569

Language: ENGLISH Document Type: ARTICLE

Abstract: %%%Tau%% (%%tau%%) is a major constituent of paired helical

filaments (PHF) found in Alzheimer's disease. The current study examines the possibility that the distinct properties of PHF-associated %%%tau%%-proteins (%%tau%%(PHF)) result from post-translational

modifications of normal soluble-%%tau%% (%%tau%%(s)).

Following

hydrofluoric acid (HF) treatment, %%%tau%%(PHF) proteins are heat-

and

acid-stable, soluble in 2-(N-morpholino)ethanesulfonic acid buffers and display the same molecular weight, pI, and immunochemical properties as normal %%%tau%%(s). Alkaline phosphatase treatment of dissociated PHF

results in similar, although less extensive, electrophoretic changes and a reduction in PHF-1 immunoreactivity. Therefore, %%%phosphorylation%% of normal %%%tau%%(s) appears to be responsible

for the distinct properties of %%%tau%%(PHF). Although our results suggest that all of the normal %%%tau%%-isoforms are in PHF, the relative abundance of individual %%%tau%%-species differs in HF-treated PHF and %%%tau%%(s) samples. Moreover, the loss of PHF following HF treatment suggests that post-translational modifications contribute to the structural stability of PHF.

4/7/64 (Item 15 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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01332783 Genuine Article#: GP898 Number of References: 71
Title: 2 NOVEL KINASES %%%PHOSPHORYLATE%%-%%TAU%% AND THE KSP SITE OF

HEAVY NEUROFILAMENT SUBUNITS IN HIGH STOICHIOMETRIC RATIOS

Author(s): RODER HM; INGRAM VM

Corporate Source: MIT,DEPT BIOL,ROOM

56-601/CAMBRIDGE//MA/02139; MIT,DEPT

BIOL,ROOM 56-601/CAMBRIDGE//MA/02139

Journal: JOURNAL OF NEUROSCIENCE, %%%1991%%, V11, N11, P3325-3343

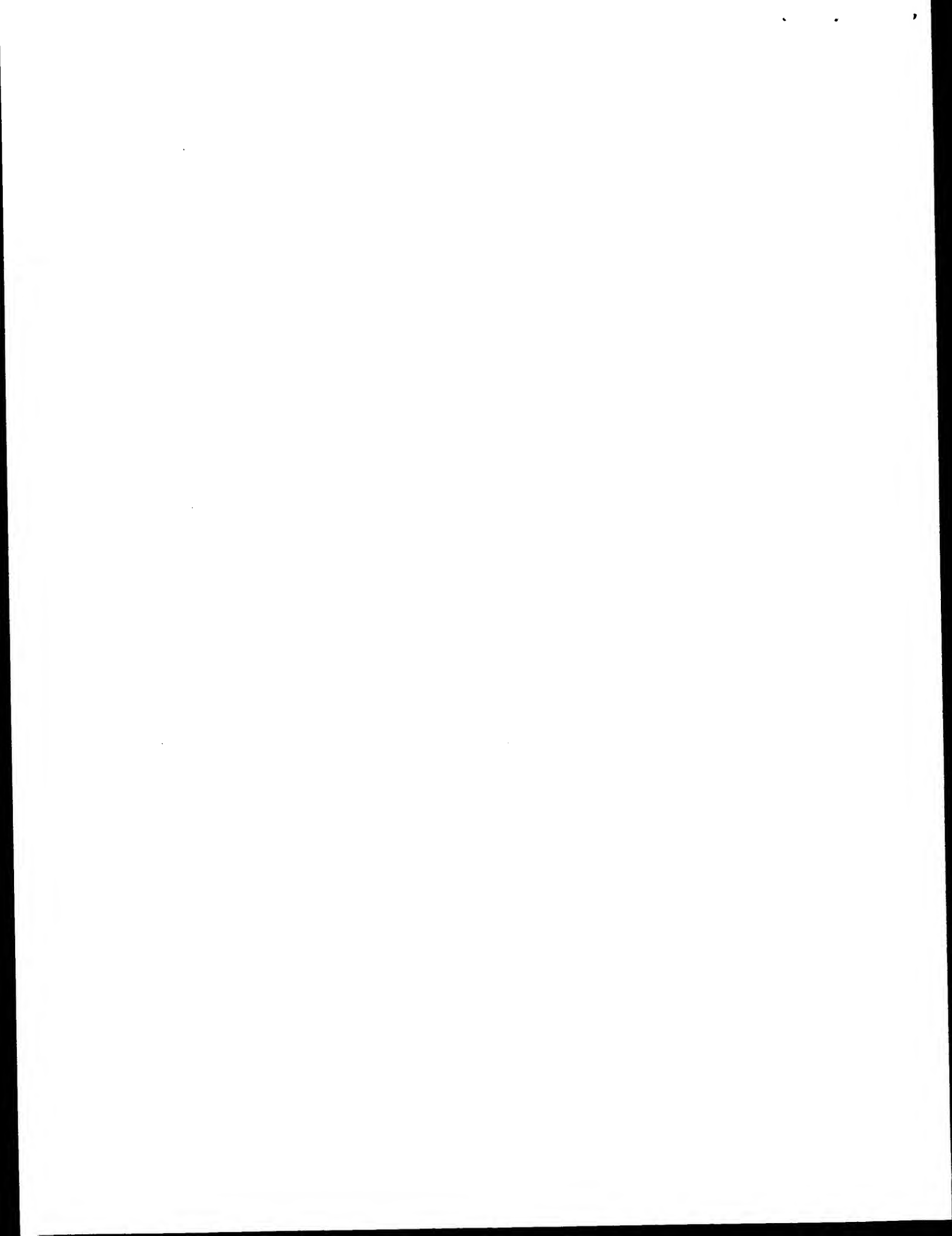
Language: ENGLISH Document Type: ARTICLE

Abstract: We have identified, purified, and characterized two neurofilament/%%tau%% kinases from bovine brain, PK36 and PK40, with

apparent M(r) of 36,000 and 40,000 and with novel biochemical properties. A specially designed immunoassay for %%%phosphorylated%%

epitopes in neurofilament (NF) proteins was used in the early stages of the purification. Neither kinase is closely associated with the cytoskeleton. Both kinases %%%phosphorylate%% bovine intermediate (NF-M) and heavy (NF-H) NF subunits and also bovine %%%tau%% at the

expected KSP sequences, though other sites cannot be ruled out. In human paired helical filaments, %%%tau%%, %%%phosphorylated%% at



these same KSP sites, is a major characterized constituent. Neither kinase is activated by the usual second messengers. τ and the above NF subunits are τ -phosphorylated in high stoichiometric ratios. In the intermediate NF subunit, all the expected sites appear to be τ -phosphorylated, but in the heavy NF subunit only 7 out of the > 40 expected sites can be τ -phosphorylated by our kinases.

We

demonstrate that both kinases can induce considerable shifts of apparent $M(r)$ with SDS-PAGE for τ and, for the first time in vitro, also for the intermediate NF subunit.

Interestingly, PK36 and particularly PK40 are strongly inhibited by an excess of free ATP. We propose that during normal aging, and in Alzheimer's disease, age-related mitochondrial dysfunction would reduce ATP levels, which in turn might release the neurofilament/ τ kinase from inhibition with consequent paired helical filament formation.

4/7/65 (Item 16 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01261754 Genuine Article#: GK042 Number of References: 51
Title: EVIDENCE FOR DIRECT COUPLING OF PRIMARY AGONIST RECEPTOR INTERACTION

TO THE EXPOSURE OF FUNCTIONAL IIB-IIIA COMPLEXES IN HUMAN

BLOOD-PLATELETS - RESULTS FROM STUDIES WITH THE ANTIPLATELET COMPOUND

AJOENE

Author(s): APITZCASTRO R; JAIN MK; BARTOLI F; LEDEZMA E; RUIZ MC; SALAS R

Corporate Source: INST VENEZOLANO INVEST CIENT,CTR BIOFIS & BIOQUIM,TROMBOSIS EXPTL LAB,APARTADO 21827/CARACAS 1020A/VENEZUELA/;

UNIV DELAWARE,DEPT CHEM/NEWARK//DE/19711

Journal: BIOCHIMICA ET BIOPHYSICA ACTA, 1991, V1094, N3, P269-280

Language: ENGLISH Document Type: ARTICLE

Abstract: Ajoene, (E,Z)-4,5,9-trithiadodeca-1,6,11-triene 9-oxide, is a potent antiplatelet compound isolated from alcoholic extracts of garlic. In vitro, ajoene reversibly inhibits platelet aggregation as well as the release reaction induced by all known agonists. In this paper we show that ajoene has a unique locus of action, that is not shared by any other known antiplatelet compound. For example, ajoene inhibits agonist-induced exposure of fibrinogen receptors, as well as intracellular responses such as activation of protein kinase C and the increase in cytoplasmic free calcium induced by receptor-dependent agonists (collagen, ADP, PAF, low-dose thrombin). On the other hand, with agonists that can by-pass (at least partially) the receptor-transducer-effector sequence, such as high-dose thrombin, PMA, NaF, only the exposure of fibrinogen receptors is blocked by ajoene. Binding of fibrinogen to chymotrypsin-treated platelets is only slightly inhibited by ajoene. The results reported here also show that: (a) ajoene does not act as a calcium chelator, does not impair the initial agonist-receptor interaction and does not influence the basal levels of intracellular inhibitors of platelet activation such as cyclic GMP; (b) the locus of action of ajoene is a yet unknown molecular step that links, in the case of physiological agonists, specific agonist-receptor complexes to the sequence of the signal transduction system on the plasma membrane of platelets. In the case of the non-physiological, receptor-independent agonists (PMA, NaF), we can only speculate on the hypothesis that they somehow mimic the effect of the agonist-receptor complexes on the signal transduction system; and (c) the exposure of fibrinogen receptors is not a direct consequence of other intracellular processes. These observations clearly show, for the first time, that the exposure of fibrinogen receptors is a membrane event proximally and obligatorily coupled to the occupancy of other membrane receptors by their agonists without any intervention by the cytoplasmic biochemical processes. Additional results support the involvement of G-proteins in these early events of platelet activation. Furthermore, a role of the β - τ -subunits of G-proteins in the exposure of fibrinogen receptors is proposed.

4/7/66 (Item 17 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

01212160 Genuine Article#: GE895 Number of References: 46
Title: DEMONSTRATION OF A NOVEL NEUROFILAMENT ASSOCIATED ANTIGEN WITH THE

NEUROFIBRILLARY PATHOLOGY OF ALZHEIMER AND RELATED DISEASES

Author(s): GHEUENS J; CRAS P; PERRY G; BOONS J;

CEUTERICKDEGROOTE C; LUBKE

U; MERCKEN M; TABATON M; GAMBETTI PL; VANDERMEEREN M; MULVIHILL P;

SIEDLAK S; VANHEUVERSWIJN H; MARTIN JJ

Corporate Source: UNIV INSTELLING ANTWERP,BORN BUNGE FDN,NEUROBIOL

LAB/B-2610 WILRIJK//BELGIUM/; UNIV INSTELLING

ANTWERP,NEUROPATHOL

LABS/B-2610WILRIJK//BELGIUM/; CASE WESTERN RESERVE

UNIV,INST PATHOL,DIV

NEUROPATHOL/CLEVELAND//OH/44106;

INNOGENET/GHENT//BELGIUM/

Journal: BRAIN RESEARCH, 1991, V558, N1, P43-52

Language: ENGLISH Document Type: ARTICLE

Abstract: A τ -monoclonal antibody, termed NFT200, was raised after in

vitro immunization with sonicated neurofibrillary tangle (NFT)-enriched fractions prepared from Alzheimer brain. The antigen to which NFT200 is directed was expressed in the paired helical filaments of NFT in sporadic and familial Alzheimer disease (AD), in the straight filaments of NFT in AD, progressive supranuclear palsy and of Pick bodies, and the NFT in several other conditions such as Parkinson-dementia complex of Guam and subacute sclerosing panencephalitis. Granulovacuolar degeneration of AD was also labeled with NFT200. Hirano bodies and amyloid deposits in AD, as well as Lewy bodies of idiopathic Parkinson disease lacked in the antigen. The NFT200-antigen was also expressed as a phosphatase-insensitive antigen in normal neurofilaments found in spinal cord and peripheral nerve axons but was absent from the perikaryal accumulation of neurofilaments induced by aluminum intoxication. Nevertheless, immunoblot studies failed to detect the NFT200 in isolated preparations of the neurofilament proteins, MAP-2, τ , ubiquitin or A4-amyloid peptide. The results indicate that the NFT200 τ -monoclonal antibody is directed against a phosphatase-insensitive epitope of an axonal protein associated with neurofilaments but is labile to isolation and expressed as a stable epitope of a 200 kDa component of NFT.

4/7/67 (Item 18 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01199639 Genuine Article#: GD742 Number of References: 34
Title: EFFECTS OF ALUMINUM ON τ -PROTEINS IN HUMAN

NEUROBLASTOMA-CELLS

Author(s): MESCO ER; KACHEN C; TIMIRAS PS

Corporate Source: NIA,FRANCIS SCOTT KEY MED CTR,GERONTOL RES CTR,4940

EASTERN AVE/BALTIMORE//MD/21224; UNIV CALIF BERKELEY,DEPT MOLEC &

CELLULAR BIOL/BERKELEY//CA/94720

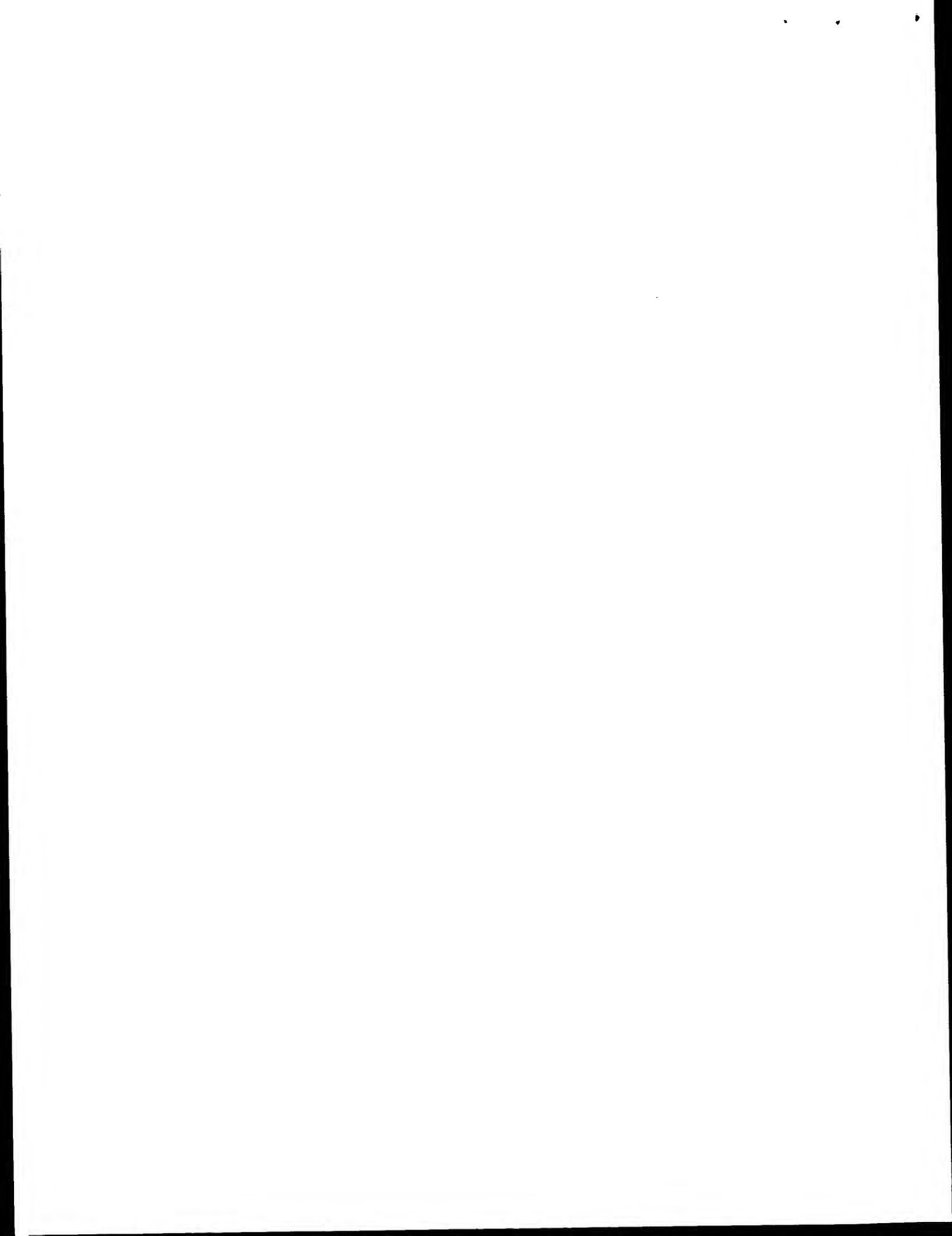
Journal: MOLECULAR AND CHEMICAL NEUROPATHOLOGY, 1991, V14, N3, P

199-212

Language: ENGLISH Document Type: ARTICLE

Abstract: The presence of the trivalent metallic cations, aluminum and boron, in the culture medium of differentiated human LAN-5 neuroblastoma cells results in increased amounts of specific isomers of microtubule-associated τ proteins. The cells were differentiated to a neuronal phenotype by the addition of retinoic acid. Six-day exposures of the differentiated cells to a 1-mM dose of aluminum or boron yielded increases in τ protein immunoreactivity to the τ -monoclonal antibodies τ -1 and

Alz-50. Significant increases in immunoreactivity were seen at



treatment levels of aluminium down to 100- μ M. The increases in τ proteins were independent from increases in levels of total cell protein. Control cultures treated with the divalent cations zinc and iron showed no increases in levels of τ proteins.

4/7/68 (Item 19 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

01117971 Genuine Article#: FX450 Number of References: 22
Title: INCREASED CYTOSOLIC FREE CALCIUM IN LYMPHOCYTES OF ALZHEIMER PATIENTS

Author(s): ADUNSKY A; BARAM D; HERSHKOWITZ M; MEKORI YA
Corporate Source: MEIR HOSP, ALLERGY IMMUNOL UNIT/IL-44281 KEFAR

SAVA//ISRAEL/; MEIR HOSP, ALLERGY IMMUNOL UNIT/IL-44281 KEFAR

SAVA//ISRAEL/; CHAIM SHEBA MED CTR, DEPT GERIATR MED/TEL AVIV//ISRAEL/;

CHAIM SHEBA MED CTR, DEMENTIA CLIN/TEL AVIV//ISRAEL/; TEL AVIV

UNIV, SACKLER SCH MED/TEL AVIV//ISRAEL/

Journal: JOURNAL OF NEUROIMMUNOLOGY, %1991%, V33, N2, P167-172

Language: ENGLISH Document Type: ARTICLE

Abstract: Free cytosolic calcium content $[Ca^{2+}]_i$ was determined in peripheral blood mononuclear cells (PBMC) from healthy volunteers, Alzheimer's disease and multi-infarct dementia patients. Measurement of $[Ca^{2+}]_i$ by the fluorescent dye quin-2, before and at several time intervals during incubation with phytohemagglutinin (PHA), showed a higher resting $[Ca^{2+}]_i$ in PBMC of Alzheimer's disease patients as compared to controls and multi-infarct dementia patients. However, the addition of supra-optimal PHA doses (100- μ g/ml) induced strikingly higher $[Ca^{2+}]_i$ levels in Alzheimer's disease patients (1647 \pm 200 nM versus 398 \pm 27 nM in controls, and 346 \pm 40 nM in multi-infarct dementia patients). The increased $[Ca^{2+}]_i$ concentration was also found after a specific stimulation with a %monoclonal% anti-CD3 antibody.

The results may have important implications in understanding the pathophysiology of Alzheimer's disease and suggest that $[Ca^{2+}]_i$ may prove diagnostically valuable.

4/7/69 (Item 20 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01106841 Genuine Article#: FW806 Number of References: 50
Title: A PROGRESSIVE DEPOSITION OF PAIRED HELICAL FILAMENTS (PHF) IN THE

BRAIN CHARACTERIZES THE EVOLUTION OF DEMENTIA IN ALZHEIMERS-DISEASE -

AN IMMUNOCYTOCHEMICAL STUDY WITH A %MONOCLONAL%-ANTIBODY AGAINST THE PHF CORE

Author(s): MENA R; WISCHIK CM; NOVAK M; MILSTEIN C; CUELLO AC
Corporate Source: MCGILL UNIV, DEPT PHARMACOL & THERAPEUT, MCINTYRE MED SCI

BLDG, 3655 DRUMMOND ST/MONTREAL H3G 1Y6/QUEBEC/CANADA/; MCGILL UNIV, DEPT

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PSYCHIAT/CAMBRIDGE CB2 2QQ//ENGLAND/; SLOVAK ACAD SCI/CS-80936

BRATISLAVA//CZECHOSLOVAKIA/; MRC, MOLEC BIOL LAB/CAMBRIDGE//ENGLAND/

Journal: JOURNAL OF NEUROPATHOLOGY AND EXPERIMENTAL NEUROLOGY, %1991%, V50, N4, P474-490

Language: ENGLISH Document Type: ARTICLE

Abstract: Using the %monoclonal% antibody (%mAb%) 6.423 which

recognizes epitopes of the pronase-resistant core of paired helical filaments (PHF), we studied postmortem frontal cortex from Alzheimer's disease (AD) patients with short (Group II) and long (Group III) histories of clinical dementia. Four cases with clinically unconfirmed dementia and a postmortem diagnosis of AD (Group I) were also studied. In Group I, the 6.423 %mAb% was negative whereas in Group II, the

antibody recognized primarily neurofibrillary tangles (NFT). In contrast, brains in Group III contained a dense network of 6.423-immunoreactive (IR) thread-like structures ("ghost" neurites) and plaque-like structures with granular appearance, in addition to NFT. The number of 6.423-IR structures appeared to be related to the duration of clinical dementia and the age of onset. Furthermore, "ghost" neurites were more abundant in young AD cases. The possible significance of the 6.423-IR pattern in the pathogenesis of AD is discussed.

4/7/70 (Item 21 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01092219 Genuine Article#: FV816 Number of References: 52
Title: EPITOPE MAP OF NEUROFILAMENT PROTEIN DOMAINS IN CORTICAL AND

PERIPHERAL NERVOUS-SYSTEM LEWY BODIES

Author(s): SCHMIDT ML; MURRAY J; LEE VMY; HILL WD; WERTKIN A; TROJANOWSKI

JQ

Corporate Source: HOSP UNIV PENN, DIV ANAT PATHOL, MALONEY BLDG BASEMENT, ROOM

A009, 3400 SPRUCE ST/PHILADELPHIA//PA/19104; UNIV PENN, SCH MED, DEPT

PATHOL & LAB MED, DIV ANAT PATHOL/PHILADELPHIA//PA/19104; UNIV PENN, SCH

MED, DEPT ANAT/PHILADELPHIA//PA/19104

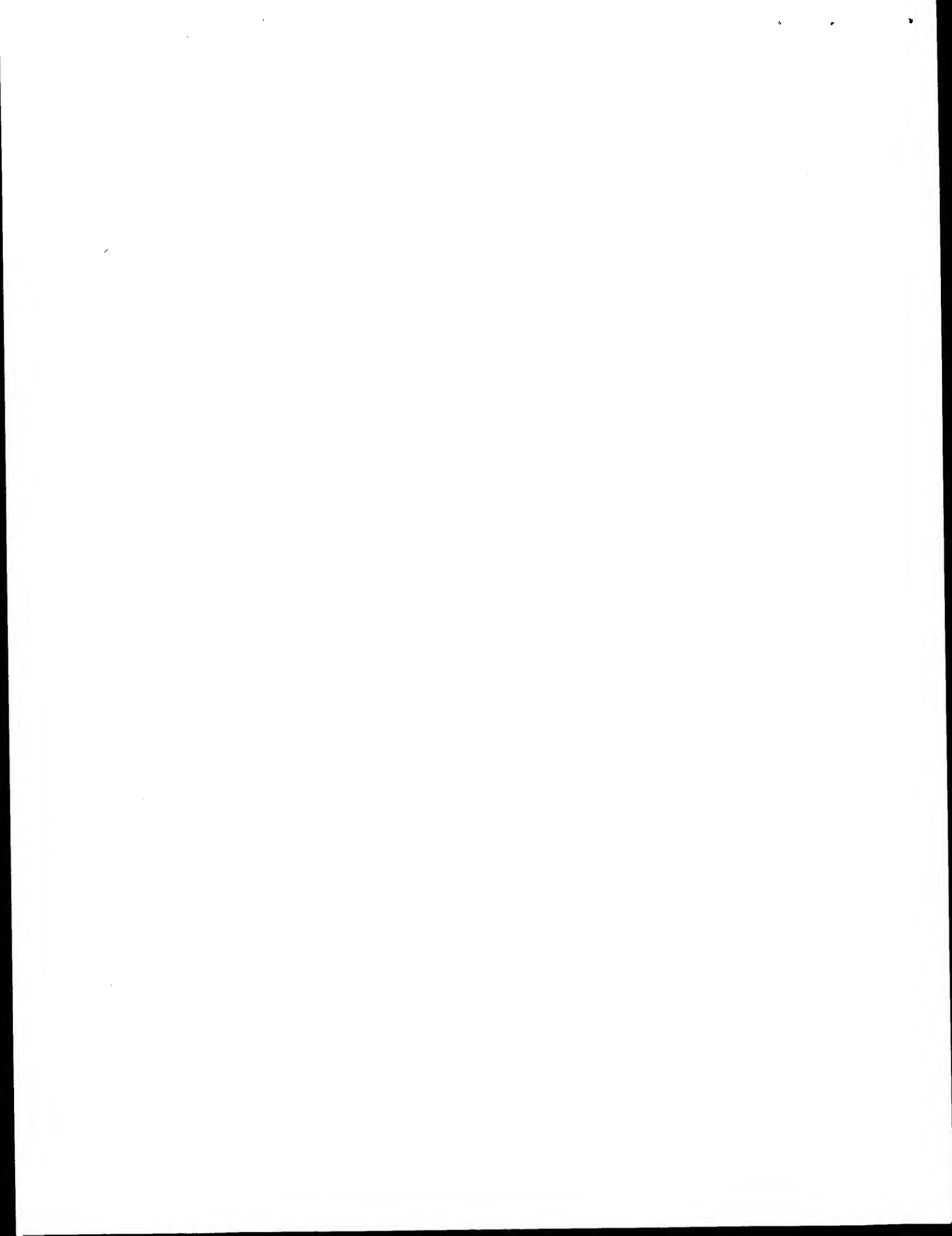
Journal: AMERICAN JOURNAL OF PATHOLOGY, %1991%, V139, N1, P53-65

Language: ENGLISH Document Type: ARTICLE

Abstract: A subset of demented elderly patients exhibit large numbers of cortical intraneuronal inclusions similar to the neurofilament (NF)-rich Lewy bodies (LB) found in pigmented subcortical neurons of patients with Parkinson's disease (PD). Because these cortical inclusions may contribute to the emergence of cognitive impairments in afflicted individuals, the authors mapped the distribution of NF epitopes in these so-called cortical LBs. This was done using ethanol-fixed tissues and a large library of %monoclonal% antibodies (MAbs) with well-characterized binding specificities to various regions of each NF triplet protein. Cortical LBs were examined by light, confocal, and electron microscopy, and they were compared with the subcortical LBs of PD and LBs in the peripheral nervous system (PNS). %Monoclonal% antibodies specific for the rod regions of each of the three NF subunits, or for phosphate-dependent and independent antigenic sites in the tail region of the high-(NF-H) and middle-(NF-M) molecular weight (M(r)) NF subunits as well as other MAbs to the extreme COOH terminus of NF-L and NF-M or the head region

of NF-M labeled a variable number of cortical LBs. Remarkably one of these anti-NF MAbs, RMO32, which recognized a %phosphorylated% epitope in the tail region of NF-M, immunolabeled nearly all cortical LBs, whereas each of the other anti-NF MAbs never labeled more than

10% of ubiquitin- or RMO32-positive cortical LBs. Further LBs in the PNS resembled those in the central nervous system (CNS) in their immunologic properties, and LBs in both sites were dominated by filamentous aggregates at the ultrastructural level. These findings suggest that NF proteins are profoundly altered during their incorporation into cortical and PNS LBs. Further the authors here identified immunologic and ultrastructural properties common to cortical LBs, PNS LBs, and classic substantia nigra LBs in PD. The accumulation of filamentous, perikaryal inclusions rich in NF proteins at diverse sites in the CNS and PNS of patients with a variety of neurodegenerative disorders suggests a widespread disruption of NF metabolism or transport.



4/7/71 (Item 22 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01079585 Genuine Article#: FU901 Number of References: 44
Title: DIFFERENCE BETWEEN THE TAU-PROTEIN OF
ALZHEIMER PAIRED HELICAL
FILAMENT CORE AND NORMAL TAU REVEALED BY EPTOPE
ANALYSIS OF

MONOCLONAL ANTIBODIES-423 AND ANTIBODIES-7.51
Author(s): NOVAK M; JAKES R; EDWARDS PC; MILSTEIN C; WISCHIK
CM

Corporate Source: MRC,MOLEC BIOL LAB,HILLS RD/CAMBRIDGE CB2
2QH/ENGLAND/

UNIV CAMBRIDGE,DEPT PSYCHIAT,CTR MRC,CAMBRIDGE BRAIN
BANK LAB/CAMBRIDGE
CB2 2QH/ENGLAND/

Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF
THE UNITED

STATES OF AMERICA, 1991, V88, N13, P5837-5841

Language: ENGLISH Document Type: ARTICLE

Abstract: The microtubule-associated protein tau that is
incorporated

into paired helical filaments (PHFs) undergoes some form of aberrant
posttranslational processing in Alzheimer disease. Difficulties in
deciding which changes are critical for PHF formation stem in part from
the lack of immunochemical markers specific for PHF tau. The
only

monoclonal antibody (mAb) that is known to react
with PHF

tau but not with the predominant normal adult tau
species

is mAb 423. Another mAb (7.51), described in this
paper)

recognizes a segment of tau that is included in the minimal
recognition unit required by mAb 423. Unlike 423, which is PHF
tau-specific, mAb 7.51 recognizes all PHF

core-derived
tau as well as native soluble tau and recombinant
tau

expressed in bacteria and so serves as a generic tau marker.
Both

epitopes are in the 12-kDa fragment released from the Pronase-resistant
core of the PHF (which encompasses the tandem repeat region). The
mAb 7.51 epitope requires segments located in the last two
repeats, which are common to all tau isoforms. The
mAb 423

epitope requires sequences located near both the N and the C terminus
of the 12-kDa fragment common to three- and four-repeat tau
isoforms. Fragments denatured by concentrated formic acid and SDS
regain 423 reactivity when denaturing agents are removed. Since the
primary amino acid sequences of PHF tau and normal
tau are

identical in the repeat region, we conclude that 423 reactivity also
requires a modification(s) occurring within an almost-equal-to
90-residue segment that are not present in tau proteins so far
described in the human brain.

4/7/72 (Item 23 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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00855645 Genuine Article#: FB769 Number of References: 43
Title: ALUMINUM MALTOL-INDUCED NEUROCYTOSKELETAL CHANGES
IN FETAL RABBIT

MIDBRAIN IN MATRIX CULTURE

Author(s): HEWITT CD; HERMAN MM; LOPES MBS; SAVORY J; WILLS
MR

Corporate Source: UNIV VIRGINIA,HLTH SCI CTR,DEPT
PATHOL/CHARLOTTESVILLE/VA/22908; UNIV VIRGINIA,HLTH SCI
CTR,DEPT

PATHOL/CHARLOTTESVILLE/VA/22908; UNIV VIRGINIA,HLTH SCI
CTR,DEPT

INTERNAL MED/CHARLOTTESVILLE/VA/22908; UNIV
VIRGINIA,HLTH SCI CTR,DEPT

BIOCHEM/CHARLOTTESVILLE/VA/22908
Journal: NEUROPATHOLOGY AND APPLIED NEUROBIOLOGY,
1991, V17, N1, P
47-60

Language: ENGLISH Document Type: ARTICLE

Abstract: We have developed a neuronal culture system to evaluate the
neurotoxic effects of aluminium maltol on fetal rabbit midbrain
sections containing the oculomotor nucleus. Cultures were treated with
5, 7, 9, 11, 13 and 15-mu-mol/l aluminium maltol or 39 and 45-mu-mol/l
maltol (molar equivalents to 13 and 15-mu-mol/l aluminium maltol).
Control cultures were maintained in nutrient medium alone.
Silver-positive neuritic swellings and occasional perikaryal
neurofibrillary tangles were observed in cultures treated with 11, 13
and 15-mu-mol/l aluminium maltol. The number of tangles (involved
neurons) produced in aluminium maltol treated cultures were counted and
compared to (untreated) controls. We observed a total of 3, 7 and 7%
of involved neurons following treatment with 11, 13 and 15-mu-mol/l
aluminium maltol respectively, and none in the control group. By
immunohistochemistry, neurofibrillary tangles were immunoreactive with
MAbs to phosphorylated (SMI-31),
non-phosphorylated,
phosphorylation dependent (SMI-32) and
phosphorylation
independent (SMI-33) epitopes of the high (-H) and middle (-M)
molecular weight neurofilament subunits (NF-H/M). By contrast these
lesions were nonreactive with MAbs recognizing tau, MAP2 or
different beta-tubulin isotypes. The perikaryal tangles consisted of
focal accumulations of 10 nm straight filaments by electron microscopy.

These findings are in agreement with previous data from rabbit in
vivo studies after the administration of aluminium maltol intravenously
(Bertholf et al., 1989) or intraventricularly (Katsetos et al., 1990).
Using this in vitro system, aluminium-induced neurofibrillary tangles
can be consistently produced, and changes in the distribution of
neurofilament proteins evaluated. These studies may aid in the
assessment of the possible role of aluminium in the aetiology of human
neurodegenerative disorders.

4/7/73 (Item 24 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

00755432 Genuine Article#: EU300 Number of References: 38
Title: ABNORMAL PHOSPHORYLATION OF
TAU-PRECEDES UBIQUITINATION
IN NEUROFIBRILLARY PATHOLOGY OF ALZHEIMER-DISEASE
Author(s): BANCHER C; GRUNDKEI QBAL I; IQBAL K; FRIED VA; SMITH
HT;

WISNIEWSKI HM

Corporate Source: NEW YORK STATE INST BASIC RES DEV
DISABILITIES,1050

FOREST HILL RD/STATEN ISL/NY/10314; NEW YORK STATE INST
BASIC RES DEV

DISABILITIES,1050 FOREST HILL RD/STATEN ISL/NY/10314; ST
JUDE

CHILDRENS HOSP,DEPT BIOCHEM/MEMPHIS/TN/38101

Journal: BRAIN RESEARCH, 1991, V539, N1, P11-18

Language: ENGLISH Document Type: ARTICLE

4/7/74 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE
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05246208 EMBASE No: 1993014293

The antineoplastic agent estramustine and the derivative estramustine-
phosphate inhibit secretion of interleukin-3 in leukemic cells. Possible
roles of MAPs

Martinez J.; Santibanez J.F.; Vial C.; Maccioni R.B.

INTA, Universidad de Chile, Casilla 138-11, Santiago Chile
Molecular and Cellular Biochemistry (MOL. CELL. BIOCHEM.) (United
States) 1992, 117/2 (165-173)

CODEN: MCBIB ISSN: 0300-8177

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The antineoplastic drug estramustine is an adduct of estradiol and nitrogen mustard. It has been shown that this drug interferes with microtubule assembly, an effect mediated by estramustine interaction with microtubule-associated proteins (MAPs). In the present report we demonstrate that estramustine and the τ -phosphorylated derivative of

the drug, estramustine-phosphate, inhibit the secretion of interleukin-3 by WEHI-3B cells. These studies also show that the estramustine derivative specifically interacts with a MAPs component found in these cells, which exhibited characteristics resembling those of τ protein isoforms.

Western blots using a unique τ -monoclonal antibody MT86.22 that recognizes microtubule-binding domains on MAPs, indicated that this WEHI protein factor contained the antigenic determinant that are functionally significant for microtubule assembly. ELISA assays using this antibody, also showed a decrease in the levels of the immunoreactive protein in WEHI cells after treatment with EMP. Interestingly, it has been recently described that the action of estramustine-phosphate is mediated by a direct interaction with MAP-binding sites on the microtubule surface, which are recognized by the site-specific τ -monoclonal antibody. These findings

together with immuno-precipitation experiments using anti-interleukin-3 antibodies and the inhibitory effect of the estramustine derivative on WEHI

secretion process suggest that this anti-mitotic agent may block IL-3 secretion by a mechanism involving its interaction with a τ -like MAPs component present in these cells.

4/7/75 (Item 2 from file: 73)

DIALOG(R)File 73:EMBASE

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05205388 EMBASE No: 1992345622

A serine \rightarrow proline change in the Alzheimer's disease-associated epitope τ 2 results in altered secondary structure, but τ -phosphorylation overcomes the conformational gap

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Wistar Institute of Anatomy/Biology, 3601 Spruce Street, Philadelphia, PA 19104 United States

Biochemical and Biophysical Research Communications (BIOCHEM. BIOPHYS.

RES. COMMUN.) (United States) 1992, 188/1 (162-169)

CODEN: BBRCA ISSN: 0006-291X

DOCUMENT TYPE: Journal: Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

τ -monoclonal antibody τ 2 was raised against bovine τ

protein, was reported to recognize a conformational epitope, and stained τ was found in neurofibrillary tangles of Alzheimer's disease, but

not normal human τ . We synthesized tetradecapeptides corresponding

to the original bovine sequence, its serine \rightarrow proline substituted analog, the genuine human sequence of this region, and the bovine epitope τ -phosphorylated on the crucial serine. The secondary structure of the

peptides was determined by circular dichroism. It was found that only the original bovine epitope showed a tendency to form the beta-pleated sheets characteristic of the neurofibrillary tangles. The spectra of the human peptide, its analog, and the τ -phosphorylated bovine sequence were very

similar, featuring a weak, helical beta-turn character. Eventual τ -phosphorylation of epitopes of this otherwise heavily τ -phosphorylated protein may overcome inter-species conformational gaps.

4/7/76 (Item 3 from file: 73)

DIALOG(R)File 73:EMBASE

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04979949 EMBASE No: 1992120165

Fragmentation of the Golgi apparatus of motor neurons in amyotrophic lateral sclerosis

Gonatas N.K.; Stieber A.; Mourelatos Z.; Chen Y.; Gonatas J.O.; Appel S.H.; Hays A.P.; Hickey W.F.; Haug J.-J.

Department of Pathology, University of Pennsylvania, School of Medicine, 418 Johnson Pavilion, Philadelphia, PA 19104-6079 United States

American Journal of Pathology (AM. J. PATHOL.) (United States) 1992, 140/3 (731-737)

CODEN: AJPA ISSN: 0002-9440

DOCUMENT TYPE: Journal: Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The Golgi apparatus (complex) is at the center stage of important functions of processing and transport of plasma membrane, lysosomal, and secreted proteins. The involvement of the Golgi apparatus in the pathogenesis of chronic degenerative diseases of neurons is virtually unknown. In the present study, fragmentation and atrophy of the Golgi apparatus of motor neurons in amyotrophic lateral sclerosis (ALS), has been detected with organelle specific antibodies. Approximately 30% of motor neurons in five ALS patients showed a fragmented Golgi apparatus whereas only about 1% of motor neurons from seven controls with neurologic or systemic disease showed a similar change. Morphometric studies are consistent with the hypothesis that the alteration of the Golgi apparatus is an early event in the pathogenesis of the neuronal degeneration in ALS. Immunocytochemical studies with antibodies against alpha tubulin, τ

, and τ -phosphorylated subunits of neurofilament polypeptides did not

disclose differences in the staining of neurons with fragmented or normal Golgi apparatus, suggesting that the alteration of the organelle is not secondary to a gross lesion of the cytoskeleton. However, these observations do not rule out the hypothesis that the fragmentation of the Golgi apparatus is secondary to subtle changes of the polypeptides involved in the attachment of membranes of the organelle to the cytoskeleton.

4/7/77 (Item 4 from file: 73)

DIALOG(R)File 73:EMBASE

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04919752 EMBASE No: 1992059968

τ proteins of Alzheimer paired helical filaments: Abnormal τ -phosphorylation of all six brain isoforms

Goedert M.; Spillantini M.G.; Cairns N.J.; Crowther R.A.

Laboratory of Molecular Biology, Medical Research Council, Hills Road, Cambridge CB2 2QH United Kingdom

Neuron (NEURON) (United States) 1992, 8/1 (159-168)

CODEN: NERNE ISSN: 0896-6273

DOCUMENT TYPE: Journal: Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Preparations of dispersed paired helical filaments (PHFs) from the brains of Alzheimer's disease and Down's syndrome patients display on gels three principal bands corresponding to abnormally modified forms of the microtubule-associated protein τ . Interpretation of the pattern is

difficult because there are six τ isoforms in normal brain and τ -phosphorylation changes their mobility. By enzymatic dephosphorylation at high temperature, we have shifted the three abnormal bands obtained from dispersed PHFs to align with the six nonphosphorylated τ isoforms. By using antibodies specific for some of the inserts that distinguish the various isoforms and label PHFs, we have established a correspondence between PHFs, abnormal bands, and isoforms. This identification of isoforms is a necessary step in unravelling the molecular pathogenesis of PHFs.

4/7/78 (Item 5 from file: 73)

DIALOG(R)File 73:EMBASE

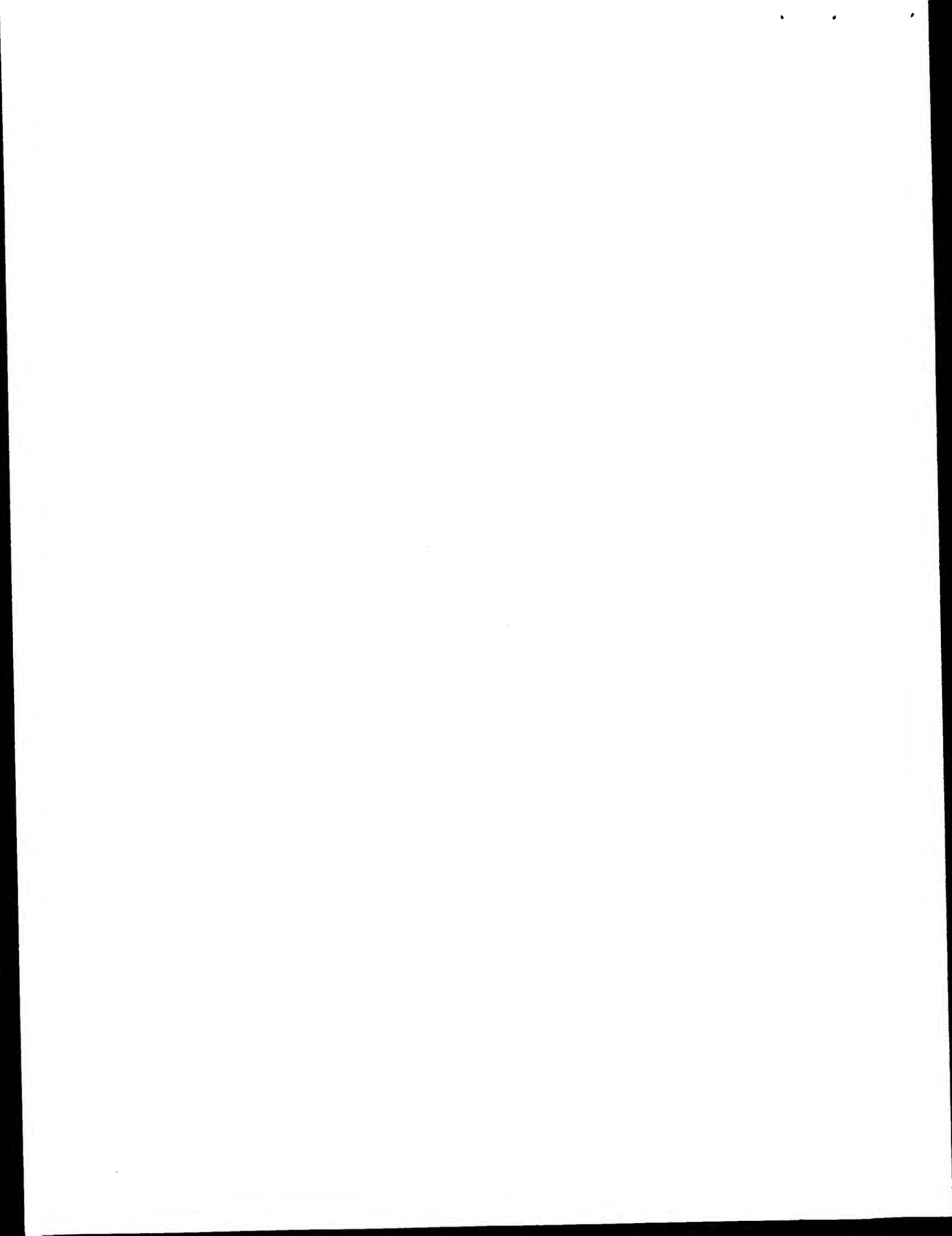
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04919418 EMBASE No: 1992059634

Effects of elevated intracellular calcium levels on the cytoskeleton and τ in cultured human cortical neurons

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Sanders-Brown Research Center on Aging, and Department of Anatomy and



Neurobiology, University of Kentucky Medical Center, Lexington, KY
40536-0230 United States
Molecular and Chemical Neuropathology (MOL. CHEM. NEUROPATHOL.)
(United States) 1991, 15/2 (117-142)
CODEN: MCHNE ISSN: 1044-7393
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Considerable evidence suggests that altered neuronal calcium homeostasis plays a role in the neuronal degeneration that occurs in an array of neurological disorders. A reduction in microtubules, the accumulation of 8-15 nm straight filaments, and altered antigenicity toward antibodies to the microtubule-associated protein τ and ubiquitin, as well as granulovacuolar degeneration, are observed in many human neurodegenerative disorders. Progress toward understanding how and why human neurons degenerate has been hindered by the inability to examine living human neurons under controlled conditions. We used cultured human fetal cerebral cortical neurons to examine ultrastructural and antigenic changes resulting from elevations in intracellular calcium levels. Elevation of intracellular calcium by exposure to a calcium ionophore or a reduced level of extracellular Na^+ for periods of hours to days caused a loss of microtubules, an increase in 8-15 nm straight filaments, and increased immunostaining with Alz-50 and 5E2 (τ antibodies) and ubiquitin antibodies. Granulovacuolar degeneration was also observed. Antigenic changes in τ were sensitive to phosphatases, and the electrophoretic mobility of τ was altered in cells exposed to calcium ionophore, indicating that τ was excessively phosphorylated as the result of elevated intracellular calcium levels. Colchicine also caused an accumulation of straight filaments and altered τ immunoreactivity, suggesting that a disruption of microtubules secondary to altered calcium homeostasis may be a key event leading to altered τ disposition and neuronal degeneration. These

data demonstrate that aberrant rises in intraneuronal calcium levels can result in changes in the neuronal cytoskeleton similar to those seen in neurodegenerative disorders, and suggest that this experimental system will be useful in furthering our understanding of the cellular and molecular mechanisms of human neurological disorders.

4/7/79 (Item 6 from file: 73)
DIALOG(R)File: 73:EMBASE
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04837910 EMBASE No: 1991332646
A68 proteins in Alzheimer's disease are composed of several τ isoforms in a phosphorylated state which affects their electrophoretic mobilities
Brian J.-P.; Hanger D.P.; Couck A.-M.; Anderton B.H.
Laboratory of Pathology, Universite Libre de Bruxelles, 808, route de Lennik, Bldg C-10, 1070-Brussels Belgium
Biochemical Journal (BIOCHEM. J.) (United Kingdom) 1991, 279/3 (831-836)
CODEN: BIJOA ISSN: 0264-6021
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The τ -immunoreactive A68 polypeptides found in brains from patients with Alzheimer's disease have been studied by Western blotting using (1) antibodies to synthetic peptides corresponding to sequences that span the complete human τ molecule, and (2) antibodies specific for inserts 1 and 2 found towards the N-terminus of some τ isoforms.

The three major A68 polypeptides were labelled by all of the antibodies to sequences common to all τ isoforms, but the faster-migrating A68 polypeptide was not labelled by either of the two antibodies specific for inserts 1 and 2. Treatment with alkaline phosphatase of non-solubilized A68 did not change its electrophoretic mobility on SDS/PAGE under the conditions described here. However, A68 that was solubilized before treating it with alkaline phosphatase was found to move faster on SDS/PAGE than untreated A68, to a position similar to that of normal τ .

We also confirmed that A68 preparations contain numerous paired helical filaments (PHF). These PHF were labelled by all anti- τ antibodies, including insert-specific antibodies. Our results further support the notion that PHF contain abnormally phosphorylated τ in an aggregated state, and indicate that these abnormally phosphorylated τ forms are composed of several τ isoforms and that the full length of the τ molecule is present in these polypeptides.

4/7/80 (Item 7 from file: 73)
DIALOG(R)File: 73:EMBASE
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03970271 EMBASE No: 1989139267
Selective expression of epitopes in multiphosphorylation repeats of the high and middle molecular weight neurofilament proteins in Alzheimer neurofibrillary tangles
Trojanowski J.Q.; Schmidt M.L.; Otvos Jr. L.; Gur R.C.; Gur R.E.; Hurtig H.; Lee V.M.Y.
Department of Pathology and Laboratory Medicine, University of Pennsylvania School of Medicine, Hospital of University of Pennsylvania, Philadelphia, PA 19104-4283 United States
Annals of Medicine (ANN. MED.) (Finland) 1989, 21/2 (113-116)
CODEN: ANMDE ISSN: 0785-3890
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Here we review our recent 'epitope analyses' of a few of the fibrous intraneuronal inclusions that are distinctive hallmarks of human neurodegenerative conditions using a large library of monoclonal antibodies (MAbs) raised to normal neuronal cytoskeletal proteins. Analyses of the low (NF-L), middle (NF-M), and high (NF-H) molecular weight neurofilament (NF) proteins with > 500 MAbs enumerated epitopes shared by NF proteins and the intraneuronal neurofibrillary tangles (NFTs) that occur in the hippocampus and brainstem of Alzheimer's disease (AD) subjects. We identified the NF-H multi-phosphorylation repeat domain, i.e. repeats of Lys-Ser-Pro-X (where X is a small uncharged amino acid and Ser acts as a phosphate acceptor), as the determinant recognized by 15/16 MAbs that detected NFTs in sections of AD hippocampus, and 11 of the same 16 MAbs recognised NF-M multi-phosphorylation repeats. Further, the antigen binding regions of these MAbs were shown to comprise 13 separate classes based on their differential binding to 12 synthetic peptides derived from the NF-H and NF-M multi-phosphorylation sites. NF subunits of 10 diverse mammalian and sub-mammalian species, and normal human τ (τ). None of these anti-NF MAbs recognized NFTs in the brainstem of subjects with progressive supranuclear palsy (PSP), but NFTs in AD brainstem sections were reactive with five of these MAbs. Both PSP and AD brainstem NFTs were recognized by MAbs specific for τ and paired helical filament antigens. Hirano bodies (HBs), another intraneuronal inclusion in the hippocampus of AD and non-AD subjects, were immunostained by 4 anti-NF MAbs, but none of these MAbs were specific for the NF-H and NF-M multi-phosphorylation repeats. These studies indicate that NF-H and NF-M multi-phosphorylation repeats are the most likely sequences in NF-H and NF-M present in NFTs, while τ -like determinants are more substantially represented in both AD and PSP NFTs. In contrast, HBs are immunologically distinct from NFTs. Thus, different pathological events are likely to account for the formation of each of these distinct lesions.

4/7/81 (Item 8 from file: 73)

DIALOG(R)File 73:EMBASE
(c) 2002 Elsevier Science B.V. All rts. reserv.

03944470 EMBASE No: 1989113463

Aluminum-induced neurofibrillary degeneration affects a subset of neurons in rabbit cerebral cortex, basal forebrain and upper brainstem
Kowall N.W.; Pendlebury W.W.; Kessler J.B.; Perl D.P.; Beal M.F.
Department of Neurology, Massachusetts General Hospital, Boston, MA 02114
United States
Neuroscience (NEUROSCIENCE) (United Kingdom) 1989, 29/2 (329-337)
CODEN: NRSCD ISSN: 0306-4522
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Neurofibrillary tangles in Alzheimer's disease show a predilection for cortical pyramidal and subcortical projection neurons. The antigenic composition, neuronal specificity and distribution of aluminum-induced neurofibrillary degeneration were examined in regions of rabbit brain analogous to those that develop neurofibrillary tangles in Alzheimer's disease. Neurofibrillary degeneration was induced by intraventricular instillation of aluminum chloride. In aluminum-treated rabbits, intensely immunoreactive filamentous aggregates were seen in affected neuronal perikarya after staining with an anti- τ -phosphorylated neurofilament antibody (SMI 31), while in controls immunoreactivity was confined to axon-like elements. Monoclonal antibodies against Microtubule-associated protein 2 and τ , which stain human neurofibrillary tangles, did not stain aluminum-induced neurofibrillary degeneration. Pyramidal neurons exhibiting neurofibrillary degeneration formed a discrete linear pattern in layers III and V of cortex. Cortical somatostatin and nicotinamide adenine dinucleotide phosphate diaphorase-reactive neurons identified in double-stained sections were unaffected. Large perikarya in the vicinity of the globus pallidus, some of which contained acetylcholinesterase, were frequently SMI 31-immunoreactive. Among the cell groups affected in the upper brainstem were the nucleus raphe dorsalis and locus coeruleus. These findings show that aluminum-induced neurofibrillary degeneration differs antigenically from neurofibrillary tangles in Alzheimer's disease. Nevertheless, many neuronal subsets that are particularly susceptible to Alzheimer's disease, including cortical pyramidal neurons, basal forebrain cholinergic neurons and upper brainstem catecholaminergic neurons, are also affected by aluminum-induced neurofibrillary degeneration.

4/7/82 (Item 9 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2002 Elsevier Science B.V. All rts. reserv.

03882293 EMBASE No: 1989051249

Immunocytochemical characterization of neurofibrillary tangles in amyotrophic lateral sclerosis and parkinsonism-dementia of Guam
Shankar S.K.; Yanagihara R.; Garruto R.M.; Grundke-Iqbal I.; Kosik K.S.; Gajdusek D.C.
Laboratory of Central Nervous System Studies, National Institute of Neurological and Communicative Disorders and Stroke, National Institutes of Health, Bethesda, MD United States
Annals of Neurology (ANN. NEUROL.) (United States) 1989, 25/2 (146-151)
CODEN: ANNEJ ISSN: 0364-5134
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Cryostat-cut sections of formalin-fixed and unfixed hippocampus from 23 Guamanian Chamorros with clinically and neuropathologically verified amyotrophic lateral sclerosis (ALS) (8 cases) and parkinsonism-dementia (PD) (15 cases) and from 12 neurologically normal Guamanians (5 with and 7 without neurofibrillary degeneration) were evaluated by the immunoperoxidase technique, using τ -monoclonal antibodies against τ -phosphorylated neurofilament, human fetal microtubule-associated protein τ , and paired helical filaments. On immunostaining, all three antibodies showed intracellular tangles in the hippocampal neurons of patients with ALS, patients with PD, and in neurologically normal Guamanians with neurofibrillary pathology, but the correlation of immunostaining between these antibodies was not absolute. Extracellular or

ghost tangles were immunostained only with the antibody against paired helical filaments. Our immunocytochemical data indicate that the antigenic composition of neurofibrillary tangles in Guamanian ALS and PD is similar to that Alzheimer's disease, suggesting a common pathogenic pathway for neurofibrillary tangle formation in these neurodegenerative disorders.

4/7/83 (Item 10 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2002 Elsevier Science B.V. All rts. reserv.

03131993 EMBASE No: 1986199570

Abnormal τ -phosphorylation of the microtubule-associated protein τ in Alzheimer cytoskeletal pathology
Grundke-Iqbal I.; Iqbal K.; Tung Y.-C.; et al.
New York State Institute for Basic Research in Developmental Disabilities, Staten Island, NY 10314 United States
Proceedings of the National Academy of Sciences of the United States of America (PROC. NATL. ACAD. SCI. U. S. A.) (United States) 1986, 83/13 (44913-4917)
CODEN: PNASA
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH

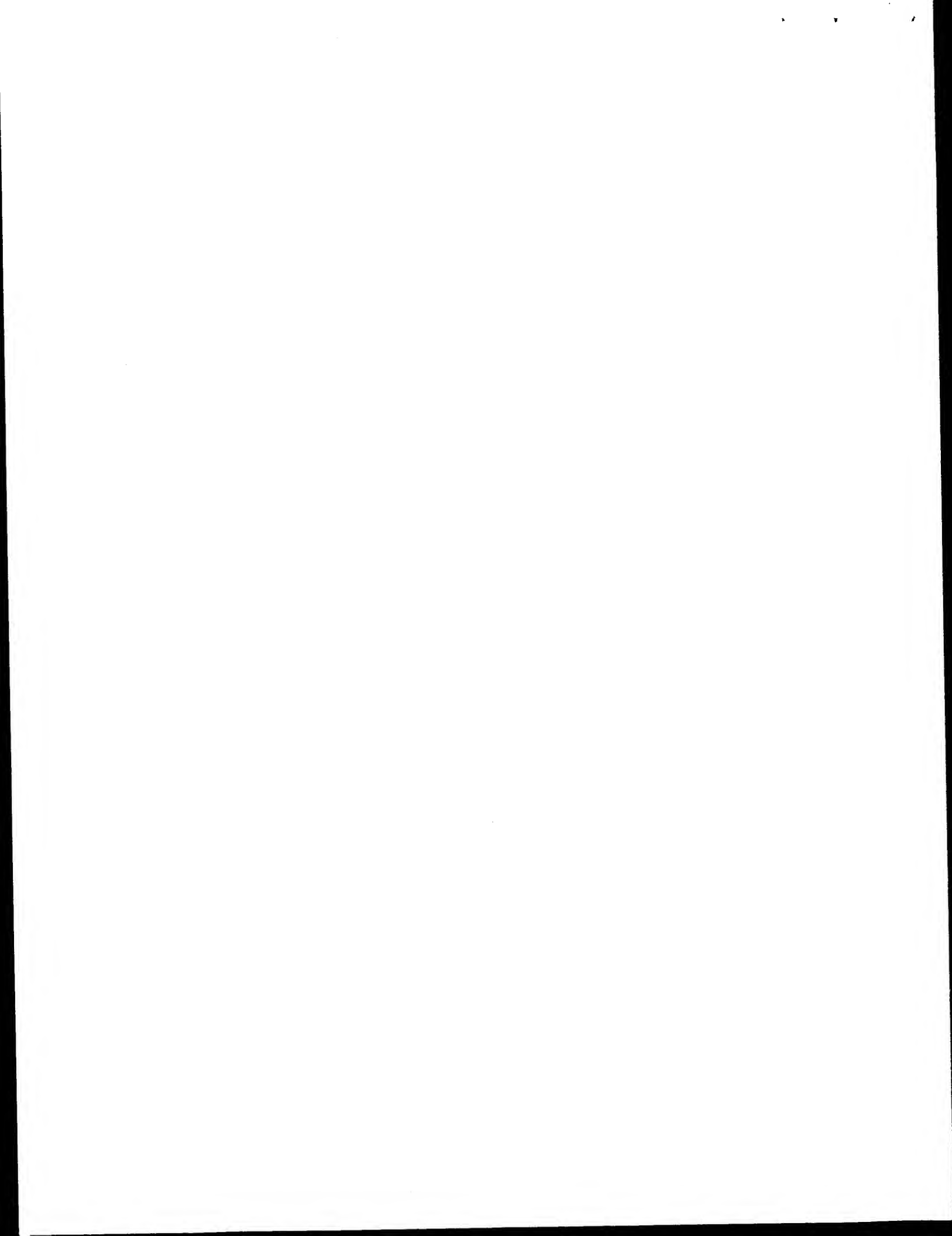
A monoclonal antibody to the microtubule-associated protein τ labeled some neurofibrillary tangles and plaque neurites, the two major locations of paired-helical filaments (PHF), in Alzheimer disease brain. The antibody also labeled isolated PHF that had been repeatedly washed with NaDodSO₄. Dephosphorylation of the tissue sections with alkaline phosphatase prior to immunolabeling dramatically increased the number of tangles and plaques recognized by the antibody. The plaque core amyloid was not stained in either dephosphorylated or nondephosphorylated tissue sections. On immunoblots PHF polypeptides were labeled readily only when dephosphorylated. In contrast, a commercially available τ -monoclonal antibody to a τ -phosphorylated epitope of neurofilaments that labeled the tangles and the plaque neurites in tissue did not label any PHF polypeptides on immunoblots. The PHF polypeptides, labeled with the τ -monoclonal antibody to τ , electrophoresed with those polypeptides recognized by antibodies to isolated PHF. The antibody to τ -labeled microtubules from normal human brains assembled in vitro but identically treated Alzheimer brain preparations had to be dephosphorylated to be completely recognized by this antibody. These findings suggest that τ in Alzheimer brain is an abnormally τ -phosphorylated protein component of PHF.

4/7/84 (Item 1 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

01843449 3633759

τ -phosphorylation-dependent epitopes of neurofilament antibodies on τ protein and relationship with Alzheimer τ
Lichtenberg Kraag, B.; Mandelkow, E. M.; Biernat, J.; Steiner, B.; Schroeter, C.; Gustke, N.; Meyer, H.E.; Mandelkow, E.
Max-Planck-Unit for Struct. Mol. Biol., c/o DESY, Notkestr. 85, D-2000 Hamburg 52, FRG
PROC. NATL. ACAD. SCI. USA vol. 89, no. 12, pp. 5384-5388 (1992)
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Immunology Abstracts; CSA Neurosciences Abstracts

We have studied the τ -phosphorylation of τ protein from Alzheimer paired helical filaments, of τ from normal human brain, and of recombinant τ isoforms. As a tool we used τ -monoclonal antibodies against neurofilament protein that crossreact with τ in



a %phosphorylation%-dependent manner. This allowed us to deduce the state of %phosphorylation% in normal and pathological %tau%, as well as antibody epitopes. The results suggest a role for the %phosphorylation% sites in Alzheimer disease, as well as the involvement of a Ser-Pro-directed protein kinase.

4/7/85 (Item 2 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

01819917 3600945

A serine arrow right proline change in the Alzheimer's disease-associated epitope %Tau% 2 results in altered secondary structure, but %phosphorylation% overcomes the conformational gap

Lang, E.; Otvos, L., Jr.

Wistar Inst. Anat. and Biol., 3601 Spruce St., Philadelphia, PA 19104, USA
BIOCHEM. BIOPHYS. RES. COMMUN. vol. 188, no. 1, pp. 162-169
(%1992%)

ISSN: 0006-291X

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: CSA Neurosciences Abstracts

%Monoclonal% antibody %Tau% 2 was raised against bovine %tau% protein, was reported to recognize a conformational epitope, and

stained %tau% was found in neurofibrillary tangles of Alzheimer's disease, but not normal human %tau%. We synthesized tetradeca peptides corresponding to the original bovine sequence, its serine arrow right proline substituted analog, the genuine human sequence of this region, and the bovine epitope %phosphorylated% on the crucial serine.

The secondary structure of the peptides was determined by circular dichroism. It was found that only the original bovine epitope showed a tendency to form the beta-pleated sheets characteristic of the neurofibrillary tangles. The spectra of the human peptide, its analog, and the %phosphorylated% bovine sequence were very similar, featuring a weak, helical beta-turn character.

4/7/86 (Item 1 from file: 94)
DIALOG(R)File 94:JICST-EPlus
(c)2002 Japan Science and Tech Corp(JST). All rts. reserv.

01734301 JICST ACCESSION NUMBER: 92A0755126 FILE SEGMENT: JICST-E

Anti-PHF %monoclonal% antibody M4 and C5 recognize fetal type %phosphorylation% of the %tau%.

WATANABE ATSUSHI (1); HASEGAWA SHIGETO (1); IHARA YASUO (1); ARAI TAKAO (2)

; TAKIO HIROSHI (3); SUZUKI MASAMI (4); CHITANI KOICHI (4)
(1) Univ. of Tokyo; (2) Science Univ. of Tokyo; (3) Inst. of Physical and Chemical Res.; (4) Fujitahoken'eiseidai

Shinkei Kagaku(Bulletin of the Japanese Society for Neurochemistry), %1992%, VOL.31,NO.1, PAGE.206-207, FIG.1, REF.6

JOURNAL NUMBER: Y0225AAP ISSN NO: 0037-3796
UNIVERSAL DECIMAL CLASSIFICATION: 616.8 591.18.05+591.481 576.311/316

LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan

DOCUMENT TYPE: Conference Proceeding

ARTICLE TYPE: Short Communication

MEDIA TYPE: Printed Publication

4/7/87 (Item 2 from file: 94)
DIALOG(R)File 94:JICST-EPlus
(c)2002 Japan Science and Tech Corp(JST). All rts. reserv.

01626289 JICST ACCESSION NUMBER: 92A0522921 FILE SEGMENT: JICST-E

Confocal microscopic immunocytochemistry of neuropil threads and neurofibrillary tangles in aged and Alzheimer's disease brains.

IWATSUBO TAKESHI (1)

(1) Univ. of Tokyo, Faculty of Medicine, Inst. of Brain Res.

Shinkei Kenkyu no Shinpo(Advances in Neurological Sciences), %1992%,

VOL.36,NO.3, PAGE.511-523, FIG.5, TBL.2, REF.42

JOURNAL NUMBER: Z0693AAP ISSN NO: 0001-8724

UNIVERSAL DECIMAL CLASSIFICATION: 616.83/.89

LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan

DOCUMENT TYPE: Journal

ARTICLE TYPE: Original paper

MEDIA TYPE: Printed Publication

ABSTRACT: I studied immunocytochemically the neuropil threads and neurofibrillary tangles in aged and Alzheimer's disease brains using a confocal laser scanning fluorescence microscope. Some of the neuropil threads visualized by %tau% antibodies were shown to occur in small

dendrites, although the majority of the threads were not continuous with dendritic branches. This may suggest that normal neuronal cytoskeletons are liable to disappear in thread-bearing neurites. Double-labelling with %tau%/ubiquitin antibodies revealed that ubiquitin-immunoreactivities were lacking at one, or more often, both ends of the %tau%-positive threads. It is reasonable to speculate that the thread ends were newly formed portions, and thus the threads grow bidirectionally in dendritic branches. A PHF %monoclonal% antibody C5, which recognizes a %phosphorylated% epitope in the carboxyl third of %tau%, stained both intra- and extracellular NFTs, while antibodies to N-terminus of %tau% stained only the intracellular ones. N-terminus of %tau% appears to be removed, once

PHFs are exposed to extracellular environment. (author abst.)

4/7/88 (Item 3 from file: 94)
DIALOG(R)File 94:JICST-EPlus
(c)2002 Japan Science and Tech Corp(JST). All rts. reserv.

01541804 JICST ACCESSION NUMBER: 92A0298363 FILE SEGMENT: JICST-E

Molecular Biology in the Investigation of Dementia. PHF: From the Viewpoint of A68 (Abnormally %Phosphorylated% %tau%).

ENDO RIUKO (1); MORI HIROSHI (1)

(1) Univ. of Tokyo, Faculty of Medicine, Inst. of Brain Res.

Saishin Igaku, %1992%, VOL.47,NO.4, PAGE.593-601, FIG.5, TBL.2, REF.26

JOURNAL NUMBER: Z0358AAR ISSN NO: 0370-8241 CODEN: SAIGA

UNIVERSAL DECIMAL CLASSIFICATION: 616.831/.832+85

LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan

DOCUMENT TYPE: Journal

ARTICLE TYPE: Commentary

MEDIA TYPE: Printed Publication

ABSTRACT: Alzheimer's disease is the most common cause of dementia in elderly people. Severity of dementia correlates with brain content of two filamentous lesions: neurofibrillary tangles and senile plaques. Neurofibrillary tangles are made up of abnormal filaments, paired helical filaments composed of %tau% containing several isoforms (Mr

40,000 to Mr 60,000) that are associated with axonal microtubules. %Tau% forms in PHF are abnormally %phosphorylated% and show

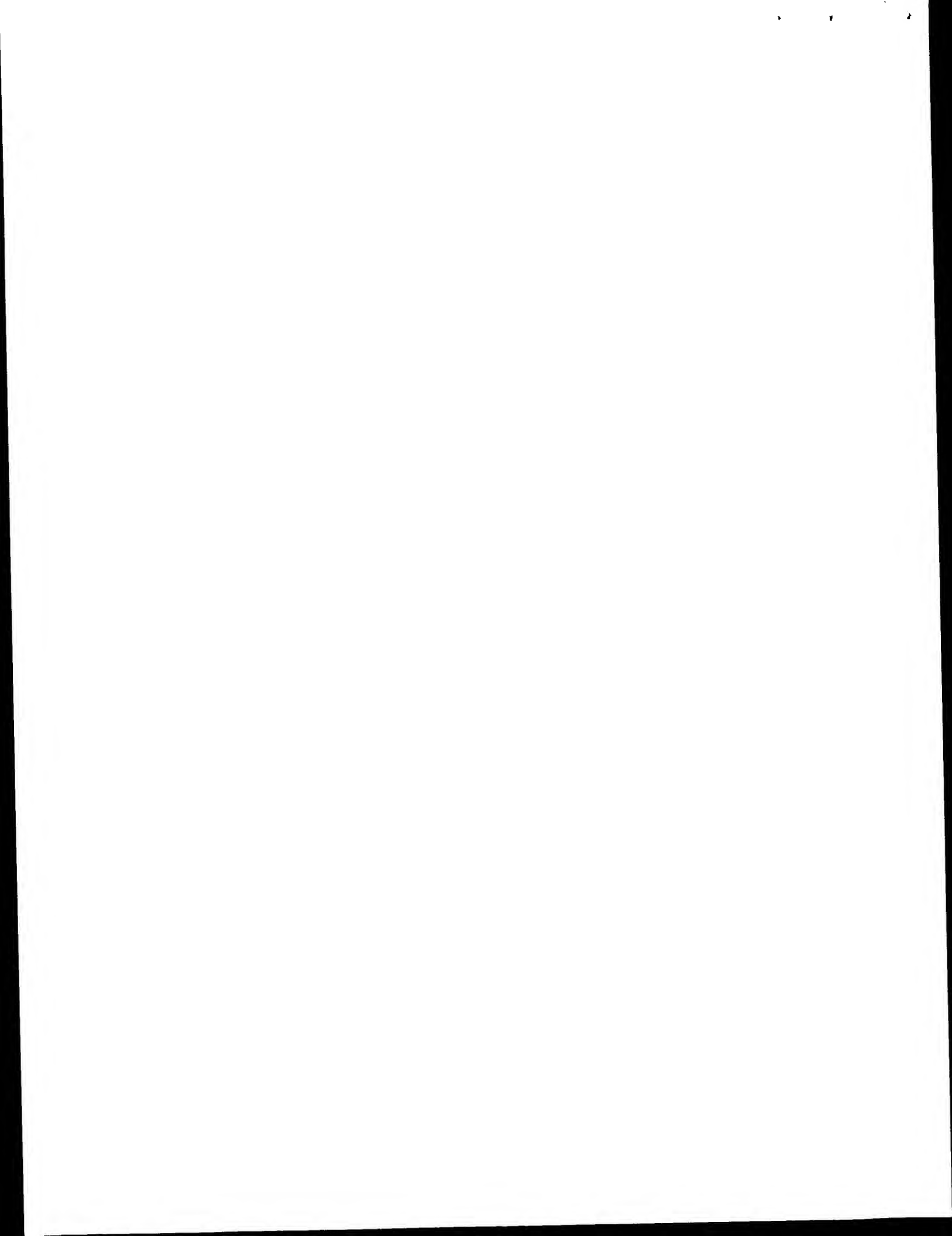
characteristic retarded mobility on SDS polyacrylamide gel electrophoresis. Because of its apparent molecular weight, %tau% in

PHF is referred to as A68; it has been identified as an antigen for Alz-50, a %monoclonal% antibody. A68 merits attention because it reveals the morphology of PHF on electron microscopy. Detailed examination for A68 may elucidate the mechanism of the pathogenesis of neurofibrillary tangles: further, prevention of abnormal %phosphorylation% of %tau% may suggest new therapeutic approaches. (author abst.)

4/7/89 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
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10511919 PASCAL No.: 93-0021170

A serine rightarrow proline change in the Alzheimer's disease-associated epitope %Tau% 2 results in altered secondary structure, but



phosphorylation overcomes the conformational gap
LANG E; OTVOS L JR
Wistar inst. anatomy biology, Philadelphia PA 19104, USA
Journal: Biochemical and biophysical research communications,
1992, 188 (1) 162-169
ISSN: 0006-291X CODEN: BBRC99 Availability: INIST-8252;
354000032123140240
No. of Refs.: 40 ref.

Document Type: P (Serial) ; A (Analytic)
Country of Publication: USA
Language: English
Monoclonal antibody τ 2 was raised against bovine
 τ protein, was reported to recognize a conformational epitope,
and
stained τ was found in neurofibrillary tangles of Alzheimer's
disease, but not normal human τ . We synthesized
tetradecapeptides corresponding to the original bovine sequence, its serine
rightarrow proline substituted analog, the genuine human sequence of this
region, and the bovine epitope phosphorylated on the crucial
serine.
The secondary structure of the peptides was determined by circular
dichroism

4/7/90 (Item 2 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2002 INIST/CNRS. All rts. reserv.

10447395 PASCAL No.: 92-0650878
Immunological and conformational characterization of a
phosphorylated immunodominant epitope on the paired helical
filaments
found in Alzheimers's disease
LANG E; SZENDREI G I; LEE V M Y; OTVOS L JR
Wistar inst. anatomy biology, Philadelphia PA 19104, USA
Journal: Biochemical and biophysical research communications,
1992, 187 (2) 783-790
ISSN: 0006-291X CODEN: BBRC99 Availability: INIST-8252;
354000031587310340
No. of Refs.: 28 ref.
Document Type: P (Serial) ; A (Analytic)
Country of Publication: USA
Language: English

The immunological recognition pattern of one of the most commonly used
monoclonal antibodies, PHF-1, which detects the paired
helical
filaments of Alzheimer's disease, exhibits a high degree of similarity with
the recognition of a polyclonal antibody, anti-T3P, raised against a
synthetic phosphopeptide, GAETVYK(Phospho)PVVSGD, corresponding to amino
acids 389-402 of the microtubule-associated protein τ . A
panel of
16 synthetic non-phosphorylated and phosphorylated
peptides,
excised from different regions of τ and peptide analogs
thereof,
were used to show that PHF-1 is indeed directed against the T3 fragment

4/7/91 (Item 3 from file: 144)
DIALOG(R)File 144:Pascal
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09353966 PASCAL No.: 91-0144344
Cyclic AMP agonists induce the phosphorylation of phospholipase
C-
 τ and of a 76kDa protein co-precipitated by
anti-(phospholipase C-
 τ) monoclonal antibodies in BALB/c-3T3 cells :
relationship
to inositol phosphate formation
OLASHAW N E; RHEE S G; PLEDGER W J

Vanderbilt univ. school medicine, dep. cell biology, Nashville TN 37232,
USA

Journal: Biochemical journal : (London, 1984), 1990, 272 (2)
297-303

ISSN: 0264-6021 Availability: INIST-5003;
354000018336160020/NUM;
INSERM-032

No. of Refs.: 38 ref.
Document Type: P (Serial) ; A (Analytic)
Country of Publication: United Kingdom
Language: English

Previous studies have demonstrated enhanced phosphorylation of
phospholipase C- τ (PLC- τ), a key regulatory
enzyme in
phosphoinositide metabolism, in cells treated with platelet-derived growth
factor (PDGF) and epidermal growth factor, both of which act via specific
receptor tyrosine kinases. Our studies on BALB/c-3T3 cells show that
agents
that promote cellular cyclic AMP accumulation also increase the
phosphorylation, specifically the serine
phosphorylation, of
this enzyme. Increased phosphorylation of PLC- τ
(2-3-fold)
was evident within 5-10 min of addition of isobutylmethylxanthine (IBMX)
and either cholera toxin or forskolin to cells, and persisted for at least
3 h. Treatment of cells with cyclic AMP agonists also enhanced, with
similar kinetics, the phosphorylation of a 76 kDa protein
co-precipitated by anti-PLC- τ monoclonal
antibodies. Brief
exposure of cells to cholera toxin/IBMX or forskolin/IBMX decreased
inositol phosphate formation induced by the GTP-binding protein (G-protein)
activator aluminium fluoride by approx. 50 %, but was without effect on
PDGF-stimulated inositol phosphate formation. These findings suggest that
PLC- τ , and perhaps the 76 kDa co-precipitated protein,
are
substrates of cyclic AMP-dependent protein kinase in BALB/c-3T3 cells;
however, the lack of effect of cyclic AMP elevation on PDGF-stimulated
inositol phosphate formation indicates that the intrinsic activity of PLC-
 τ is unaltered by cyclic AMP-mediated
phosphorylation

4/7/92 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07582712 93111483 PMID: 1471723
Cytoskeletal immunohistochemistry of central neurocytomas.
Hessler R B; Lopes M B; Frankfurter A; Reidy J; VandenBerg S R
Department of Pathology, University of Virginia, Charlottesville.
American journal of surgical pathology (UNITED STATES) Nov
1992, 16 (11) p1031-8, ISSN 0147-5185 Journal Code: 7707904
Contract/Grant No.: T32 NS 7236; NS; NINDS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Central neurocytomas are rare intraventricular tumors. Patients with such
tumors have a favorable prognosis after surgical removal. These tumors may
be misdiagnosed as neuroblastomas or gliomas, risking the complications of
adjuvant therapy. Diagnosis of central neurocytoma requires that the tumor
shows the ultrastructural features of mature neuronal differentiation,
including the presence of synapses and dense-core and clear vesicles in
addition to profiles of neuritic processes with microtubules. The
cytoskeletal phenotype of central neurocytomas has not been previously
characterized, but it may facilitate their definitive recognition when
ultrastructural examination is not possible. Ten central neurocytomas were
examined by immunohistochemistry for phosphorylation-
dependent/independent neurofilament epitopes, neuron-associated class
III
beta-tubulin, microtubule-associated proteins (MAP2, τ), and
glial
fibrillary acidic protein (GFAP). The neuronal nature of all neoplasms was
documented by immunoreactivity for synaptophysin in nine tumors and for
phosphorylation-independent neurofilament-H/M in the remaining

case.

Electron microscopy in four cases showed synapses and dense core vesicles. All tumors were immunoreactive for class III beta-tubulin and MAP2, which

were seen in cytoskeletal structures by immunoelectron microscopy. Two thirds of the cases were immunohistochemically positive for neurofilament epitopes. None of the tumor cells displayed GFAP immunoreactivity, although reactive astrocytes were present. These data suggest that central neurocytomas may be recognized by synaptophysin immunoreactivity and that

the expression of cytoskeletal epitopes indicates that these tumors are well-differentiated neuronal neoplasms.

Record Date Created: 19930126

4/7/93 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07574924 93101309 PMID: 1465214

%%Tau%% pathology in a case of familial Alzheimer's disease with a valine to glycine mutation at position 717 in the amyloid precursor protein.

Hanger D P; Mann D M; Neary D; Anderton B H

Department of Neuroscience, Institute of Psychiatry, London, UK.

Neuroscience letters (NETHERLANDS) Oct 12 %%1992%%, 145 (2)

p178-80, ISSN 0304-3940 Journal Code: 7600130

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The brain tissue from a case of familial Alzheimer's disease (FAD) caused by a missense (valine to glycine) mutation at codon 717 of the amyloid precursor protein (APP) gene has been examined for the presence of abnormally %%phosphorylated%% paired helical filament

%%tau%% (PHF-%%tau%%). There was abundant PHF-%%tau%% present, which on Western

blots, was indistinguishable from the PHF-%%tau%% typical of cases of

sporadic Alzheimer's disease and that of another FAD mutation (valine to isoleucine), previously (Neurosci. Lett., 137 (1992) 221-224). This result implies that the cytoskeletal pathology in Alzheimer's disease is biochemically linked to abnormal APP processing and amyloid deposition.

Record Date Created: 19930119

4/7/94 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07513573 93038653 PMID: 1384476

A serine-->proline change in the Alzheimer's disease-associated epitope %%Tau%% 2 results in altered secondary structure, but %%phosphorylation%% overcomes the conformational gap.

Lang E; Otvos L

Wistar Institute of Anatomy and Biology, Philadelphia, PA 19104.

Biochemical and biophysical research communications (UNITED STATES)

Oct 15 %%1992%%, 188 (1) p162-9, ISSN 0006-291X Journal Code: 0372516

Contract/Grant No.: AG 10670; AG; NIA

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

%%Monoclonal%% antibody %%Tau%% 2 was raised against bovine

protein, was reported to recognize a conformational epitope, and stained %%tau%% was found in neurofibrillary tangles of Alzheimer's disease, but

not normal human %%tau%%. We synthesized tetrade peptides corresponding

to the original bovine sequence, its serine-->proline substituted analog, the genuine human sequence of this region, and the bovine epitope %%phosphorylated%% on the crucial serine. The secondary structure of the

peptides was determined by circular dichroism. It was found that only the original bovine epitope showed a tendency to form the beta-pleated sheets characteristic of the neurofibrillary tangles. The spectra of the human peptide, its analog, and the %%phosphorylated%% bovine sequence were very similar, featuring a weak, helical beta-turn character. Eventual %%phosphorylation%% of epitopes of this otherwise heavily %%phosphorylated%% protein may overcome inter-species conformational

gaps.

Record Date Created: 19921119

4/7/95 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07281845 92212933 PMID: 1557394

A protein kinase associated with paired helical filaments in Alzheimer disease.

Vincent I J; Davies P

Department of Pathology, Albert Einstein College of Medicine, Bronx, NY 10461.

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Apr 1 %%1992%%, 89 (7) p2878-82, ISSN

0027-8424 Journal Code: 7505876

Contract/Grant No.: AG06803; AG; NIA; MH38623; MH; NIMH

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We have identified a protein kinase in immunoaffinity-purified preparations of paired helical filaments from brain tissue of individuals with Alzheimer disease. The kinase %%phosphorylates%% the filament

proteins in vitro in a manner independent of second messenger regulation or of modulation by heparin and polyamines. Physiological concentrations of hemin, an oxidized heme porphyrin, inhibit the kinase and abolish Alz-50 immunoreactivity of the proteins. Since paired helical filaments are composed of hyperphosphorylated proteins, association of a protein kinase with the filaments provides a mechanism for abnormal processing of the proteins in disease.

Record Date Created: 19920506

4/7/96 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07237565 92177459 PMID: 1795405

Regional variation in the abundance of axonal cytoskeletal proteins.

Watson D

Department of Neurology, Wayne State University School of Medicine, Detroit, Michigan 48201.

Journal of neuroscience research (UNITED STATES) Sep %%1991%%, 30

(1) p226-31, ISSN 0360-4012 Journal Code: 7600111

Contract/Grant No.: NS00983; NS; NINDS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The relative abundance of several axonal cytoskeletal proteins was determined by immunoassay at various sites in the peripheral and central nervous systems of adult rats. Within the peripheral nervous system, the ratio of tubulin to neurofilaments was greatest for nerves composed of unmyelinated axons and least for nerves with large myelinated axons. MAP1 protein was more prominent in unmyelinated fibers; conversely

%%tau%% proteins were relatively more abundant in large myelinated axons. An immunochemical index of neurofilament %%phosphorylation%% was less for

unmyelinated fibers than for myelinated ones. In the fimbria-fornix, pyramidal tract, and superior cerebellar peduncle, similar trends were observed: small axons had more MAP1, less %%tau%%, and a greater ratio of

tubulin to neurofilament proteins. The %%phosphorylation%% index

test for the superior cerebellar peduncle, the tract with the largest
The immunohistochemical index of neurofilament
phosphorylation was
for the optic nerve than for axonal tracts in the brain proper.
results suggest that development of large myelinated axons is
ated with greater neurofilament content, neurofilament
phosphorylation, and with greater abundance of tau
proteins in
the CNS and the PNS; however, quantitative aspects of these relationships
differ in the PNS and the CNS.
Record Date Created: 19920408

4/7/97 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06829233 91126483 PMID: 1899488

A68: a major subunit of paired helical filaments and derivatized forms of
normal tau.

Lee V M; Balin B J; Otvos L; Trojanowski J Q
Department of Pathology and Laboratory Medicine, University of
Pennsylvania School of Medicine, Philadelphia 19104.

Science (UNITED STATES) Feb 8 1991; 251 (4994)
p675-8, ISSN

0036-8075 Journal Code: 0404511

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Putative Alzheimer disease (AD)-specific proteins (A68) were purified to
homogeneity and shown to be major subunits of one form of paired helical
filaments (PHFs). The amino acid sequence and immunological data indicate
that the backbone of A68 is indistinguishable from that of the protein
tau, but A68 could be distinguished from

normal human
tau by the degree to which A68 was phosphorylated and by the

specific residues in A68 that served as phosphate acceptors. The larger
apparent relative molecular mass (Mr) of A68, compared to normal human
tau, was attributed to abnormal phosphorylation of
A68 because

enzymatic dephosphorylation of A68 reduced its Mr to close to that of
normal tau. Moreover, the LysSerProVal motif in normal
human

tau appeared to be an abnormal phosphorylation site
in A68

because the Ser in this motif was a phosphate acceptor site in A68, but not
in normal human tau. Thus, the major subunits of a class of PHFs are

A68 proteins and the excessive or inappropriate

phosphorylation of

normal tau may change its apparent Mr, thus transforming
tau
into A68.

Record Date Created: 19910313

4/7/98 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06460368 90164679 PMID: 1689542

The neuroendocrine and neural profiles of neuroblastomas,
ganglioneuroblastomas, and ganglioneuromas.

Molenaar W M; Baker D L; Pleasure D; Lee V M; Trojanowski J Q
Department of Pathology and Laboratory Medicine, University of
Pennsylvania, Philadelphia 19104.

American journal of pathology (UNITED STATES) Feb 1990; 136 (2)

p375-82, ISSN 0002-9440 Journal Code: 0370502

Contract/Grant No.: CA-36245; CA: NCI; CA-47983; CA: NCI;

NS-08075; NS;

NINDS; +

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

To establish the neuroendocrine and neural features of peripheral
neuroblastic tumors, a prospectively collected group of 12 neuroblastomas
(NB), 2 ganglioneuroblastomas (GNB), and 4 ganglioneuromas (GN) was
probed

with a panel of monoclonal antibodies (MAbs) to neuroendocrine
and

neural antigens. All tumors expressed the pan-neuroendocrine markers
synaptophysin and chromogranin A. They also showed extensive expression
of

neuronal antigens, ie, of each of the neurofilament (NF) triplet proteins
and of the microtubule-associated proteins (MAPs) MAP2 and
tau

-protein. However, only in the GNBs and GNs was the pattern of NF
phosphoisoforms relatively mature. In the latter tumors glial fibrillary
acidic protein (GFAP) and myelin basic protein (MBP) could be demonstrated
as well, suggesting the presence of nonmyelinating and myelinating Schwann
cells, respectively. The glial markers did not colocalize with the neural
markers. On the basis of these data, it was concluded that all peripheral
neuroblastic tumors manifest molecular characteristics of neuroendocrine
cells and of neurons. The latter were most developed in GNBs and GNs, in
which they were accompanied by Schwann cell differentiation in a separate
population of cells. The above-outlined neuronal profile of peripheral
neuroblastic tumors, including NBs, distinguishes this group of tumors from
the much-less neuronally differentiated primitive neuroectodermal tumors
of

the central nervous system.

Record Date Created: 19900326

4/7/99 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06428736 90132789 PMID: 1688924

Modified Bielschowsky and immunocytochemical studies on cerebellar
plaques in Alzheimer's disease.

Suenaga T; Hirano A; Ilena J F; Ksiazek-Reding H; Yen S H; Dickson D W
Department of Pathology, Montefiore Medical Center, Bronx, NY 10467.

Journal of neuropathology and experimental neurology (UNITED STATES)
Jan 1990; 49 (1) p31-40, ISSN 0022-3069 Journal Code:
2985192R

Contract/Grant No.: AG06803; AG: NIA; AG4145; AG: NIA

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Senile plaques (SP) in the cerebellum of 23 cases of Alzheimer's disease
(AD), three with widespread amyloid angiopathy, were studied with a
modified Bielschowsky stain and immunocytochemical methods using
antibodies

to a beta-amyloid synthetic peptide (beta ASP),

phosphorylated

neurofilament proteins, ubiquitin, tau protein, and glial fibrillary
acidic protein (GFAP). The four subtypes of SP (diffuse plaques, compact

plaques, perivascular plaques, and subpial fibrillar deposits) that were
observed with the modified Bielschowsky stain were also stained with
antibodies to beta ASP. Many cerebellar SP contained ubiquitin-positive
granular elements resembling dystrophic neurites. In contrast to neuritic
elements in cerebral SP in AD, ubiquitin-positive elements in cerebellar SP
were not labeled with antibodies to phosphorylated
neurofilament or

tau proteins. Various degrees of glial reaction were observed in
all

subtypes of SP except diffuse plaques. The absence of

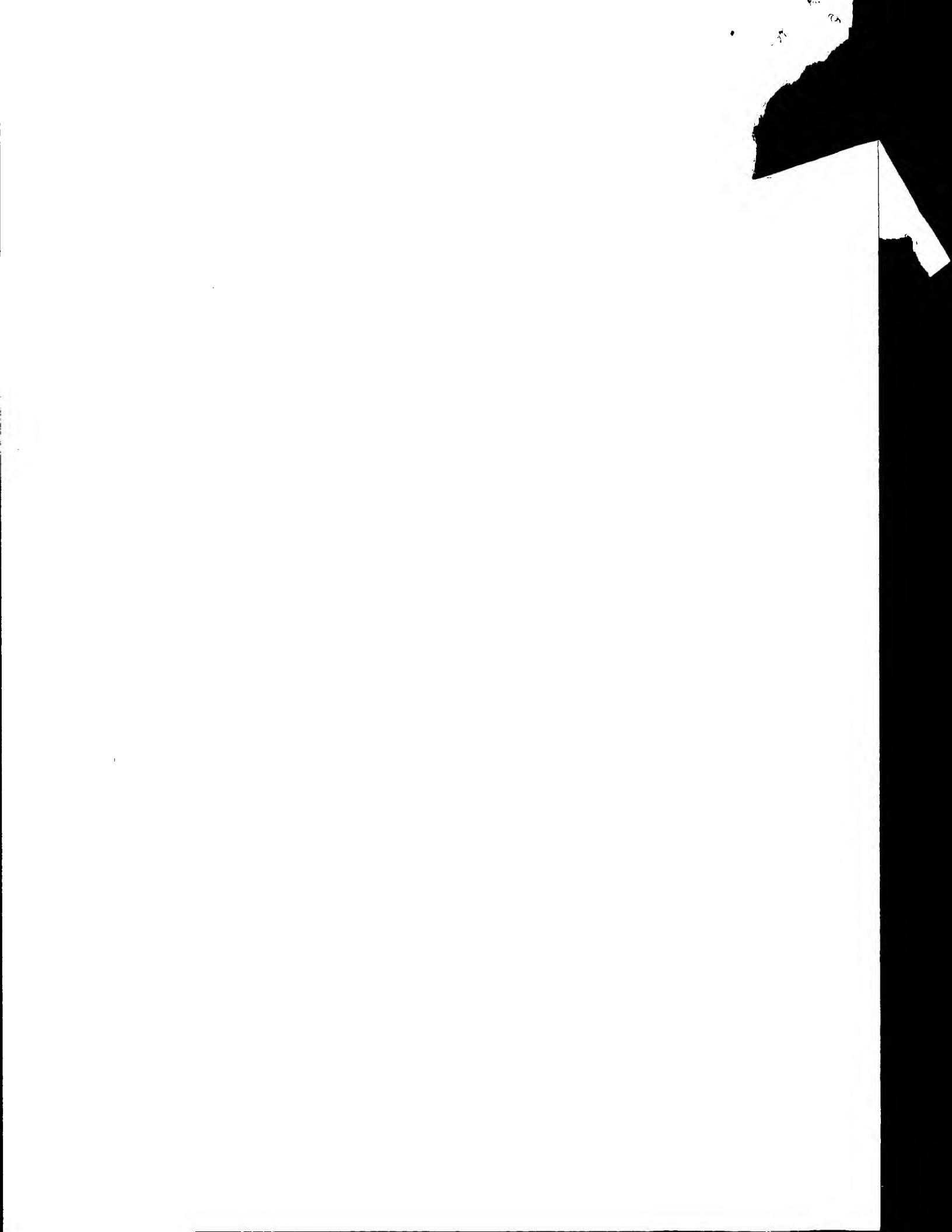
phosphorylated

neurofilament and tau epitopes in neuritic elements in cerebellar
SP

is not surprising since paired helical filaments have not been seen in the
cerebellum. Nevertheless, our results suggest that cerebellar SP are
frequently associated with dystrophic neurites.

Record Date Created: 19900226

4/7/100 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)



06409491 90099531 PMID: 2557644

%%tau%% and ubiquitin immunoreactivity at different stages of formation of Alzheimer neurofibrillary tangles.

Bancher C; Brunner C; Lassmann H; Budka H; Jellinger K; Seitelberger F; Grundke-Iqbal I; Iqbal K; Wisniewski H M

Neurological Institute, University of Vienna, Austria.
Progress in clinical and biological research (UNITED STATES)

%%1989%%

317 p837-48, ISSN 0361-7742 Journal Code: 7605701

Contract/Grant No.: AG 04220; AG: NIA; AG 05892; AG: NIA; NS 18105; NS;

NINDS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

In his original 1911 publication Alois Alzheimer classified neurofibrillary tangles (ANT) into three morphologically defined subgroups according to their stage of maturation. The present study shows that changes in the morphological appearance of ANT during their maturation process are accompanied by changes in their antigenic profile. As shown by several immunocytochemical studies these abnormal

microtubule-associated protein %%tau%% and of ubiquitin. In this study, immunoreactivity for the altered %%tau%% is not only seen in a subset of

tangles but also in the cytoplasm of some nerve cells lacking ANT, which we believe to be at a stage of neuronal alteration preceding the formation of compact tangles (Stage 0 tangles). Similar numbers of Stage 0 tangles are present in the brains of age-matched non-demented individuals as in Alzheimer cases, but are absent in young controls lacking ANT. In extracellular "ghost tangles", the ultimate stage of neurofibrillary degeneration, immunoreactivity for %%tau%% is accessible to antibodies

only when tissue sections are pretreated with formic acid to uncover the binding sites. In contrast to %%tau%%, presence/accessibility of an epitope residing on residues 50-65 of ubiquitin recognized by a %%monoclonal%% antibody raised to paired helical filaments (3-39) increases during the maturation of ANT and is most pronounced in "ghost tangles". Appearance/uncovering of the 3-39 epitope and masking of %%tau%% reactivity during tangle maturation may reflect degradation or

conformational changes in the pathological filaments due to their aging and the final loss of their parent nerve cells.

Record Date Created: 19900131

4/7/101 (Item 10 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

06272525 89351937 PMID: 2475148

The reinterpretation of the immunochemical study of Alzheimer neurofibrillary tangles.

Nukina N

Center for Neurologic Diseases, Harvard Medical School Brigham and Women's Hospital, Boston, Massachusetts.

Annals of medicine (FINLAND) %%1989%%, 21 (2) p117-9, ISSN

0785-3890 Journal Code: 8906388

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Many studies have been done on neurofibrillary tangles occurring in Alzheimer's disease using antibodies, but without agreement on the interpretation of the results. Immunochemical studies using antibodies to neurofilament and %%tau%% and the antibody, Alz50, were carried out to

establish a common view. The results suggest that: 1) antibodies to neurofilament recognizing tangles react with the %%phosphorylated%% epitope of %%tau%% in paired helical filaments; 2) Alz50 reacts with abnormal %%tau%%, which has slower electrophoretic mobility than normal

%%tau%%; and 3) a certain part of %%tau%% has the protease-resistant

property in brains affected by the disease. (19 Refs.)

Record Date Created: 19891005

4/7/102 (Item 11 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

05909622 88310474 PMID: 3136867

Alzheimer's disease: study of the distribution of %%tau%% proteins constituting helical filament pairs in human central nervous tissue] Maladie d'Alzheimer: Etude de la distribution des proteines

%%tau%% constitutives des paires de filaments en helice dans le tissu nerveux central humain.

Parent M; Delacourte A; Defossez A; Hemon B; Han K K; Petit H

Laboratoire de Neurosciences, I.N.S.E.R.M. U n. 16, A.D.E.R.M., Faculte de Medecine de Lille.

Comptes rendus de l'Academie des sciences. Serie III, Sciences de la vie (FRANCE) %%1988%%, 306 (13) p391-7, ISSN 0764-4469 Journal

Code: 8503078

Document type: Journal Article; English Abstract

Languages: FRENCH

Main Citation Owner: NLM

Record type: Completed

%%Tau%% proteins are the major components of Paired Helical Filaments

(PHF) of Alzheimer's disease. Using the immunoblot technique and an antiserum against PHF, we have studied the distribution of

%%Tau%% proteins in the different areas of normal human brains and Alzheimer brains. %%Tau%% proteins were clearly present in cortical grey matter but

were difficult to detect in the white matter. In Alzheimer brains, we observed two differences: first, there is an important background due to the partial dissociation of the lesions containing %%Tau%% aggregates. Second, the profile of %%Tau%% proteins is modified, due to

abnormal %%phosphorylation%%. Thus, %%Tau%% proteins are found in large amounts

in the grey matter of the cortical areas and are not exclusively distributed in the axonal domain. The normal cortical distribution of %%Tau%% in the human brain correlates well with the distribution of histological lesions that contain PHF (neurofibrillary tangles and neuritic plaques) in the Alzheimer cortex.

Record Date Created: 19880930

4/7/103 (Item 12 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

05219651 86267071 PMID: 3089107

%%Tau%% microheterogeneity: an immunological approach with %%monoclonal%% antibodies.

Fellous A; Ohayon R; Mazie J C; Rosa F; Luduena R F; Prasad V

Annals of the New York Academy of Sciences (UNITED STATES)

%%1986%%,

466 p240-56, ISSN 0077-8923 Journal Code: 7506858

Contract/Grant No.: CA 26276; CA; NCI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The family of %%tau%% polypeptides purified from mammalian brain

exhibit both extensive heterogeneity and large similarities in their chemical, physical, and functional properties. All the %%tau%% isoforms

generated at a transcriptional or posttranscriptional level share the property of interacting with tubulin dimers in a specific manner. They strengthen longitudinal interactions between tubulin dimers and thus may stabilize microtubules once they are formed. Mild proteolysis or %%phosphorylation%% does not remove but only modulates the %%tau%%

specific function that is probably related to the conserved sequences of the molecules. %%%Monoclonal%% antibodies raised against %%%tau%% were found to recognize epitopes conserved not only between species but also in different tissues. Using indirect immunofluorescence, a specific staining pattern was observed on rat neuronal cells and also on human skin fibroblasts. The same antibodies did not recognize glial cells, suggesting that these cells either do not contain detectable levels of %%%tau%% or contain %%%tau%% molecules different from the neuronal ones. These data suggest that %%%tau%% protein is widely distributed, highly conserved, and may be preferentially associated with special subclasses of microtubules.
Record Date Created: 19860814

4/7/104 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05026439 86105177 PMID: 2867809
Cultured neurons contain a variety of microtubule-associated proteins.
Peng I; Binder L I; Black M M
Brain research (NETHERLANDS) Dec 30 %%%1985%%, 361 (1-2)
p200-11,
ISSN 0006-8993 Journal Code: 0045503
Contract/Grant No.: NS17681; NS: NINDS: S 07 RR-0547; RR: NCR
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The non-tubulin proteins associated with microtubules (MAPs) in cultures of pure sympathetic neurons have been identified using a variety of biochemical and immunochemical methods. MAPs of cultured sympathetic neurons include proteins corresponding to brain MAP-1 (consisting of MAP-1a and MAP-1b species), MAP-2, MAP-3, %%%tau%%, 4 proteins that range in molecular weight from 60,000 to 76,000, and proteins with molecular weights of 210,000, 130,000 and 32,000. Many of the MAPs are %%%phosphorylated%% in situ. MAP-2 and %%%tau%% of cultured sympathetic neurons differ from their counterparts of brain in electrophoretic mobility. The observed variety of MAPs in sympathetic neurons together with the differences in MAPs of brain and sympathetic neurons are discussed in terms of microtubule heterogeneity in the nervous system.
Record Date Created: 19860324

4/7/105 (Item 1 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

09735631 Genuine Article#: AT454 Number of References: 37
Title: %%%TAU%%-PROTEIN BECOMES LONG AND STIFF UPON %%%PHOSPHORYLATION%%
- CORRELATION BETWEEN PARACRYSTALLINE STRUCTURE AND DEGREE OF %%%PHOSPHORYLATION%%
Author(s): HAGESTEDT T; LICHTENBERG B; WILLE H; MANDELKOW EM; MANDELKOW E
Corporate Source: MAX PLANCK UNIT STRUCT MOLEC BIOL/D-2000 HAMBURG 52//FED
REP GER/
Journal: JOURNAL OF CELL BIOLOGY, %%%1989%%, V109, N4, P1643-1651
Language: ENGLISH Document Type: ARTICLE

4/7/106 (Item 2 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

09539517 Genuine Article#: T0136 Number of References: 13

Title: DIRECT BIOCHEMICAL-EVIDENCE FOR AN ABNORMAL %%%PHOSPHORYLATION%% OF %%%TAU%% PROTEINS DURING ALZHEIMERS-DISEASE
Author(s): FLAMENT S; DELACOURTE A; HEMON B; DEFOSSEZ A
Corporate Source: FAC MED LILLE,ADERMA,NEUROSCI LAB,INSERM,UNITE 16/F-59045 LILLE//FRANCE/
Journal: COMPTES RENDUS DE L ACADEMIE DES SCIENCES SERIE III-SCIENCES DE LA VIE, %%%1989%%, V308, N3, P77-82
Language: FRENCH Document Type: ARTICLE

4/7/107 (Item 3 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

08836546 Genuine Article#: N7766 Number of References: 41
Title: ALZ-50, A %%%MONOCLONAL%%-ANTIBODY TO ALZHEIMERS-DISEASE ANTIGEN, CROSS-REACTS WITH %%%TAU%%-PROTEINS FROM BOVINE AND NORMAL HUMAN-BRAIN
Author(s): KSIEZAKREDING H; DAVIES P; YEN SH
Corporate Source: YESHIVA UNIV ALBERT EINSTEIN COLL MED,DEPT PATHOL/BRONX//NY/10461
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, %%%1988%%, V263, N17, P7943-7947
Language: ENGLISH Document Type: ARTICLE

4/7/108 (Item 4 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

08738468 Genuine Article#: N0443 Number of References: 20
Title: THE %%%MONOCLONAL%%-ANTIBODY, ALZ 50, RECOGNIZES %%%TAU%%-PROTEINS IN ALZHEIMERS-DISEASE BRAIN
Author(s): NUKINA N; KOSIK KS; SELKOE DJ
Corporate Source: BRIGHAM & WOMENS HOSP,CTR NEUROL DIS,DEPT MED NEUROL,75 FRANCIS ST/BOSTON//MA/02115; HARVARD UNIV,SCH MED,DEPT NEUROL NEUROSCI/BOSTON//MA/02115
Journal: NEUROSCIENCE LETTERS, %%%1988%%, V87, N3, P240-246
Language: ENGLISH Document Type: ARTICLE

4/7/109 (Item 5 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

06516517 Genuine Article#: AKC67 Number of References: 54
Title: DEPHOSPHORYLATION OF MICROTUBULE-ASSOCIATED PROTEIN-2, %%%TAU%%-FACTOR, AND TUBULIN BY CALCINEURIN
Author(s): GOTO S; YAMAMOTO H; FUKUNAGA K; IWASA T; MATSUKADO Y; MIYAMOTO E
Corporate Source: KUMAMOTO UNIV,SCH MED,DEPT PHARMACOL/KUMAMOTO 860//JAPAN/ ; KUMAMOTO UNIV,SCH MED,DEPT NEUROSURG/KUMAMOTO 860//JAPAN/
Journal: JOURNAL OF NEUROCHEMISTRY, %%%1985%%, V45, N1, P276-283
Language: ENGLISH Document Type: ARTICLE

4/7/110 (Item 6 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

06295666 Genuine Article#: ACC69 Number of References: 45
Title: CA-2', CALMODULIN-DEPENDENT REGULATION OF MICROTUBULE FORMATION VIA %%%PHOSPHORYLATION%% OF MICROTUBULE-ASSOCIATED PROTEIN-2, %%%TAU%%

-FACTOR, AND TUBULIN, AND COMPARISON WITH THE CYCLIC
AMP-DEPENDENT

%%PHOSPHORYLATION%%

Author(s): YAMAMOTO H; FUKUNAGA K; GOTO S; TANAKA E;
MIYAMOTO E

Corporate Source: KUMAMOTO UNIV, SCH MED, DEPT
PHARMACOL/KUMAMOTO 860//JAPAN/

Journal: JOURNAL OF NEUROCHEMISTRY, %1985%, V44, N3,
P759-768

Language: ENGLISH Document Type: ARTICLE

4/7/111 (Item 7 from file: 434)

DIALOG(R)File 434:SciSearch(R) Cited Ref Sci

(c) 1998 Inst for Sci Info. All rts. reserv.

05749895 Genuine Article#: SP385 Number of References: 34
Title: %%PHOSPHORYLATION%% AFFECTS THE ABILITY OF
%%TAU%%-PROTEIN TO

PROMOTE MICROTUBULE ASSEMBLY

Author(s): LINDWALL G; COLE RD

Corporate Source: UNIV CALIF BERKELEY, DEPT
BIOCHEM/BERKELEY//CA/94720

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, %1984%, V259,
N8, P5301-5305

Language: ENGLISH Document Type: ARTICLE

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Set Items Description

S1 1305 TAU AND PHOSPHORYL? AND (MONOCLONAL OR MAB)

S2 599 RD S1 (unique items)

S3 304 S2 AND PY:1996

S4 111 S3 AND PY:1993

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Ref Items Index-term

E1 2 AU=MERCKEN LOY

E2 15 AU=MERCKEN LUC

E3 137 *AU=MERCKEN M

E4 60 AU=MERCKEN M.

E5 2 AU=MERCKEN M.M.

E6 31 AU=MERCKEN MARC

E7 1 AU=MERCKEN MARC M

E8 2 AU=MERCKEN MARK

E9 1 AU=MERCKEN MM

E10 1 AU=MERCKEN, ARC

E11 1 AU=MERCKEN, H. P. F.

E12 40 AU=MERCKEN, L.

Enter P or PAGE for more

? s e3-e9

137 AU=MERCKEN M

60 AU=MERCKEN M.

2 AU=MERCKEN M.M.

31 AU=MERCKEN MARC

1 AU=MERCKEN MARC M

2 AU=MERCKEN MARK

1 AU=MERCKEN MM

S5 234 E3-E9

? e au=mandeldow e m

Ref Items Index-term

E1 4 AU=MANDELCORN, M.

E2 2 AU=MANDELCORN, M.S.

E3 0 *AU=MANDELDOW E M

E4 1 AU=MANDELEKAR S

E5 1 AU=MANDELEKORN R M

E6 1 AU=MANDELENAKI-LAMBROU K

E7 1 AU=MANDELERT

E8 1 AU=MANDELERT N

E9 1 AU=MANDELERT, N.

E10 30 AU=MANDELES S

E11 2 AU=MANDELES S.

E12 1 AU=MANDELES, M. D.

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? e au=mandelkow e m

Ref Items Index-term

E1 1 AU=MANDELKOW E -M

E2 167 *AU=MANDELKOW E M

E3 151 AU=MANDELKOW E.

E4 4 AU=MANDELKOW E.- M.

E5 113 AU=MANDELKOW E.-M.

E6 13 AU=MANDELKOW E.M.

E7 185 AU=MANDELKOW E-M

E8 59 AU=MANDELKOW ECKHARD

E9 192 AU=MANDELKOW EM

E10 49 AU=MANDELKOW EVA-MARIA

E11 2 AU=MANDELKOW EVA-MARIE

E12 42 AU=MANDELKOW H

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? s e1-e11

1 AU=MANDELKOW E -M

167 AU=MANDELKOW E M

151 AU=MANDELKOW E.

4 AU=MANDELKOW E.- M.

113 AU=MANDELKOW E.-M.

13 AU=MANDELKOW E.M.

185 AU=MANDELKOW E-M

59 AU=MANDELKOW ECKHARD

192 AU=MANDELKOW EM

49 AU=MANDELKOW EVA-MARIA

2 AU=MANDELKOW EVA-MARIE

S6 805 E1-E11

? e au=vandermeeren m

Ref Items Index-term

E1 4 AU=VANDERMEEREN L

E2 1 AU=VANDERMEEREN L A

E3 83 *AU=VANDERMEEREN M

E4 5 AU=VANDERMEEREN M A

E5 3 AU=VANDERMEEREN M M

E6 6 AU=VANDERMEEREN M M P P

E7 26 AU=VANDERMEEREN M.

E8 1 AU=VANDERMEEREN M.A.

E9 4 AU=VANDERMEEREN M.M.P.P.

E10 3 AU=VANDERMEEREN MA

E11 17 AU=VANDERMEEREN MARC

E12 3 AU=VANDERMEEREN MAPP

Enter P or PAGE for more

? s e3-e11

83 AU=VANDERMEEREN M

5 AU=VANDERMEEREN M A

3 AU=VANDERMEEREN M M

6 AU=VANDERMEEREN M M P P

26 AU=VANDERMEEREN M.

1 AU=VANDERMEEREN M.A.

4 AU=VANDERMEEREN M.M.P.P.

3 AU=VANDERMEEREN MA

17 AU=VANDERMEEREN MARC

S7 148 E3-E11

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Set Items Description

S1 1305 TAU AND PHOSPHORYL? AND (MONOCLONAL OR MAB)

S2 599 RD S1 (unique items)

S3 304 S2 AND PY:1996

S4 111 S3 AND PY:1993

S5 234 E3-E9

S6 805 E1-E11

S7 148 E3-E11

? s s5 or s6 or s7

234 S5

805 S6

148 S7

S8 1128 S5 OR S6 OR S7

? s s8 and tau and (monoclonal or mab)

1128 S8

127081 TAU

959154 MONOCLONAL

131828 MAB

S9 77 S8 AND TAU AND (MONOCLONAL OR MAB)

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...completed examining records

S10 33 RD S9 (unique items)

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>>>Format 7 is not valid in file 143

10/7/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

13327015 BIOSIS NO.: 200100534164

%%Monoclonal%% antibodies directed against the
microtubule-associated
protein %%tau%%.

AUTHOR: %%Mercken Marc%%; %%Mandelkow Eva-Maria%%(a);
%%Vandermeeren%%

%%Marc%%; Vanmechelen Eugene; Van De Voorde Andre

AUTHOR ADDRESS: (a)Hamburg**Germany

JOURNAL: Official Gazette of the United States Patent and Trademark
Office

Patents 1246 (5):pNo Pagination May 29, 2001

MEDIUM: e-file

ISSN: 0098-1133

DOCUMENT TYPE: Patent

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: A %%monoclonal%% antibody which forms an immunological
complex

with a phosphorylated epitope of an antigen belonging to human abnormally
phosphorylated %%tau%% protein. The %%tau%% protein ca be
obtained

from a brain homogenate, itself isolated from the cerebral cortex of a
patient having Alzheimer's disease.

10/7/2 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

13301244 BIOSIS NO.: 200100508393

Isolated human %%tau%% peptide epitope which specifically binds
%%monoclonal%% antibody AT120.

AUTHOR: %%Vandermeeren Marc%%(a); Vanmechelen Eugene;
%%Mercken Marc%%;

Van de Voorde Andre

AUTHOR ADDRESS: (a)Geel**Belgium

JOURNAL: Official Gazette of the United States Patent and Trademark
Office

Patents 1246 (3):pNo Pagination May 15, 2001

MEDIUM: e-file

ISSN: 0098-1133

DOCUMENT TYPE: Patent

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: An isolated human %%tau%% peptide epitope which
specifically

binds %%monoclonal%% antibody AT120 consisting of the amino acid
sequence selected from the group consisting of SEQ ID Nos. 2, 3, 4, 15,
16, 17, 18, 19 and 20.

10/7/3 (Item 3 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

12551157 BIOSIS NO.: 200000304659

Isolated human %%tau%% peptide.

AUTHOR: %%Vandermeeren Marc%%(a); %%Mercken Marc%%;

Vanmechelen Eugene;

Van De Voorde Andre

AUTHOR ADDRESS: (a)Geel**Belgium

JOURNAL: Official Gazette of the United States Patent and Trademark
Office

Patents 1230 (1):pNo pagination Jan. 4, 2000

MEDIUM: e-file

ISSN: 0098-1133

DOCUMENT TYPE: Patent

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The invention deals with isolated human %%tau%% peptide
epitopes of SEQ ID Nos: 1 to 4, 7 and 15 to 20 which have the capability
of binding AT120 %%monoclonal%% antibody.

10/7/4 (Item 4 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

12545308 BIOSIS NO.: 200000298810

%%Monoclonal%% antibodies specific for PHF-%%tau%%, hybridomas
secreting them, antigen recognition by these antibodies and their
applications.

AUTHOR: %%Vandermeeren Marc%%(a); Vanmechelen Eugene; Van De
Voorde Andre

AUTHOR ADDRESS: (a)Geel**Belgium

JOURNAL: Official Gazette of the United States Patent and Trademark
Office

Patents 1229 (4):pNo pagination Dec. 28, 1999

MEDIUM: e-file

ISSN: 0098-1133

DOCUMENT TYPE: Patent

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: %%Monoclonal%% antibody AT180 secreted by the
hybridoma

deposited at ECACC on Dec. 22, 1992 under No. 92122204, and
%%monoclonal%% antibody AT270 secreted by the hybridoma
deposited at

ECACC on Jul. 7, 1993 under 93070774, each of which forms an
immunological complex with a phosphorylated epitope of an antigen
belonging to abnormally phosphorylated %%tau%% protein
(PHF-%%tau%%)

residing in the region spanning positions 143-254 with the following
amino acid sequence: 143 150 NH2 - Lys Gly Ala Asp Gly
Lys Thr Lys Ile - 160 Ala Thr Pro Arg Gly Ala Ala Pro Pro
Gly - 170 Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile -
180 Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr - 190 Pro Pro
Ser Ser Gly Glu Pro Pro Lys Ser - 200 Gly Asp Arg Ser Gly
Tyr Ser Ser Pro Gly - 210 Ser Pro Gly Thr Pro Gly Ser Arg
Ser Arg - 220 Thr Pro Ser Leu Pro Thr Pro Thr Arg -
230 Glu Pro Lys Lys Val Ala Val Val Arg Thr - 240 Pro Pro
Lys Ser Pro Ser Ser Ala Lys Ser - 250 Arg Leu Gln Thr Ala
Pro Val Pro Met Pro - Asp Leu Lys COOH with each %%monoclonal%%
antibody specifically detecting abnormally phosphorylated %%tau%%
protein (PHF-%%tau%%) in cerebrospinal fluid (CSF).

10/7/5 (Item 5 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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11850901 BIOSIS NO.: 199900097010

%%Monoclonal%% antibodies directed against the

microtubule-associated

protein %%tau%%, hybridomas secreting these antibodies, antigen
recognition by these %%monoclonal%% antibodies and their
applications.

AUTHOR: %%Vandermeeren M%%; %%Mercken M%%; Vanmechelen
E; Van De Voorde

A

AUTHOR ADDRESS: Geel**Belgium

JOURNAL: Official Gazette of the United States Patent and Trademark
Office

Patents 1218 (3):p2174 Jan. 19, 1999

ISSN: 0098-1133
RECORD TYPE: Citation
LANGUAGE: English

10/7/6 (Item 6 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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11825253 BIOSIS NO.: 199900071362
%%Monoclonal%% antibodies directed against the
microtubule-associated
protein %%Tau%%, and hybridomas secreting these antibodies.
AUTHOR: %%Vandermeeren M%%; %%Mercken M%%; Vanmechelen
E; De Voorde A
AUTHOR ADDRESS: Geel**Belgium
JOURNAL: Official Gazette of the United States Patent and Trademark
Office
Patents 1217 (1):p493 Dec. 1, 1998
ISSN: 0098-1133
RECORD TYPE: Citation
LANGUAGE: English

10/7/7 (Item 7 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

11824334 BIOSIS NO.: 199900070443
Sequential phosphorylation of %%Tau%%-protein by GSK-3beta and PKA
at
Thr212 and Ser214 generates the Alzheimer-specific epitope of antibody
AT100 and requires a paired helical filament-like conformation.
AUTHOR: Zheng-Fischhofer Q; Biernat J; %%Mandelkow E-M%%;
Illenberger S;
Godemann R; Mandelkow E
AUTHOR ADDRESS: Max-Planck-Unit Structural Mol. Biol., Notkestr. 85,
D-22607 Hamburg**Germany
JOURNAL: Society for Neuroscience Abstracts 24 (1-2):p1267 1998
CONFERENCE/MEETING: 28th Annual Meeting of the Society for
Neuroscience,
Part 2 Los Angeles, California, USA November 7-12, 1998
ISSN: 0190-5295
RECORD TYPE: Citation
LANGUAGE: English

10/7/8 (Item 8 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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11394110 BIOSIS NO.: 199800175442
Sequential phosphorylation of %%Tau%% by glycogen synthase
kinase-3beta
and protein kinase A at Thr212 and Ser214 generates the
Alzheimer-specific epitope of antibody AT100 and requires a
paired-helical-filament-like conformation.
AUTHOR: Zheng-Fischhofer Qingyi; Biernat Jacek; Mandelkow Eva-Maria;
Illenberger Susanne; Godemann Robert; %%Mandelkow Eckhard%%(a
AUTHOR ADDRESS: (a)Max-Planck-Unit Structural Mol. Biol., Notkestr. 85,
D-22607 Hamburg**Germany
JOURNAL: European Journal of Biochemistry 252 (3):p542-552 March,
1998
ISSN: 0014-2956
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: AT100, is a %%monoclonal%% antibody highly specific for
phosphorylated %%Tau%% in Alzheimer paired helical filaments. Here
we
show that the epitope is generated by a complex sequence of sequential
phosphorylation, first of Ser199, Ser202 and Thr205 (around the epitope
of antibody AT8), next of Thr212 by glycogen synthase kinase (GSK)-3beta
(a proline-directed kinase), then of Ser214 by protein kinase A (PKA).
Conversely, if Ser214 is phosphorylated first it protects Thr212 and the

Ser-Pro motifs around the AT8 site against phosphorylation, and the
AT100
epitope is not formed. The generation of the AT100 epitope requires a
conformation of %%tau%% induced by polyanions such as heparin, RNA
or
poly(Glu), conditions which also favor the formation of paired helical
filaments. The Alzheimer-like phosphorylation can be induced by brain
extracts. In the extract, the kinases responsible for generating the
AT100 epitope are GSK-3beta and PKA, which can be inhibited by their
specific inhibitors LiCl and RII, respectively. A cellular model
displaying the reaction with AT100 is presented by Sf9 insect cells
transfected with %%Tau%%. Knowledge of the events and kinases
generating the AT100 epitope in cells might allow us to study the
degeneration of the cytoskeleton in Alzheimer's disease.

10/7/9 (Item 9 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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10182315 BIOSIS NO.: 199698637233
Three distinct axonal transport rates for %%tau%%, tubulin, and other
microtubule-associated proteins: Evidence for dynamic interactions of
%%tau%% with microtubules in vivo.
AUTHOR: %%Mercken M%%; Fischer I; Kosik K S; Nixon R A(a
AUTHOR ADDRESS: (a)Lab. Molecular Neuroscience, Mailman Res. Cent.,
McLean
Hosp., 115 Mill Street, Belmont, MA 0217**USA
JOURNAL: Journal of Neuroscience 15 (12):p8259-8267 1995
ISSN: 0270-6474
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Microtubule-associated proteins (MAPs), such as %%tau%%,
modulate neuronal shape and process outgrowth by influencing the
stability and organization of microtubules. The dynamic nature of
MAP-microtubule interactions in vivo, however, is poorly understood.
Here, we have assessed the stability of these interactions by
investigating the synthesis and axoplasmic transport of %%tau%% in
relation to that of tubulin and other MAPs within retinal ganglion cells
of normal adult mice in vivo. Using immunoprecipitation and Western blot
analysis with anti-%%tau%% %%monoclonal%% and polyclonal
antibodies,
we unequivocally identified in optic axons a family of 50-60 kDa
%%tau%% isoforms and a second 90-95 kDa %%tau%% family, the
members
of which were shown to contain the domain of %%tau%% encoded by
exon
4A. To measure the rates of translocation of %%tau%% proteins in vivo,
we injected mice with 35S-methionine intravitreally and, after 6-30 d,
quantitated the radiolabeled %%tau%% isoforms immunoprecipitated
from
eight consecutive 1.1 mm segments of the nerve and optic tract and
separated by electrophoresis. Linear regression analysis of protein
transport along optic axons showed that the %%tau%% isoforms
advanced
at a rate of 0.2-0.4 mm/d, and other radiolabeled MAPs, identified by
their association with taxol-stabilized microtubules, moved three- to
fivefold more rapidly. By contrast, tubulins advanced at 0.1-0.2 mm/d,
significantly more slowly than %%tau%% or other MAPs. These studies
establish that %%tau%% is not cotransported with tubulin or
microtubules, indicating that associations of %%tau%% with
microtubules
within axons are not as stable as previously believed. Our findings also
reveal differences among various MAPs in their interactions with
microtubules and provide evidence that assembly and reorganization of the
microtubule network is an active process even after axons establish
connections and fully mature.

10/7/10 (Item 10 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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09413384 BIOSIS NO.: 199497421754

Epitope mapping of monoclonal antibodies to the paired helical filaments of Alzheimer's disease: Identification of phosphorylation sites in tau protein.

AUTHOR: Goedert Michel(a); Jakes Ross; Crowther R Anthony; Cohen Philip; Vanmechelen Eugene; Vandermeeren Marc%; Cras Patrick
AUTHOR ADDRESS: (a)MRC Lab. Mol. Biol., Cambridge CB2 2QH**UK
JOURNAL: Biochemical Journal 301 (3):p871-877 1994
ISSN: 0264-6021
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Tau is a neuronal phosphoprotein the expression of which is developmentally regulated. A single tau isoform is expressed in fetal human brain but six isoforms are expressed in adult human brain, with the fetal isoform corresponding to the shortest adult isoform. Phosphorylation is also developmentally regulated, as fetal tau is phosphorylated at more sites than adult tau. In Alzheimer's disease, the six adult tau isoforms become hyperphosphorylated and form the paired helical filament (PHF), the major fibrous component of the neurofibrillary lesions. One way to identify phosphorylated sites in tau is to use antibodies that recognize phosphorylated residues within a specific amino acid sequence. We here characterize the two novel phosphorylation-independent anti-tau antibodies AT270 and AT180 and identify their epitopes as containing phosphorylated Thr-181 and Thr-231 respectively. With these antibodies we show that these two threonine residues are partially phosphorylated in fetal and adult tau and almost fully phosphorylated in PHF tau. This result contrasts with previous studies of Ser-202 and Ser-396 which are partially phosphorylated in fetal tau, unphosphorylated in adult tau but almost fully phosphorylated in PHF tau.

10/7/11 (Item 11 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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09002362 BIOSIS NO.: 199497010732

Detection of tau proteins in normal and Alzheimer's disease cerebrospinal fluid with a sensitive sandwich enzyme-linked immunosorbent assay.

AUTHOR: Vandermeeren Marc%; Mercken Marc%; Vanmechelen Eugene;
Six Jan; Van De Voorde Andre; Martin Jean-Jacques; Cras Patrick(a)
AUTHOR ADDRESS: (a)Lab. Neurobiol., Born-Bunge Foundation, Univ. Antwerp,
UIA Build. T., Universiteitplein 1, B-2611 Belgium
JOURNAL: Journal of Neurochemistry 61 (5):p1828-1834 1993
ISSN: 0022-3042
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Alzheimer's disease is a progressive degenerative dementia characterized by the abundant presence of neurofibrillary tangles in neurons. This study was designed to test whether the microtubule-associated protein tau a major component of neurofibrillary tangles, could be detected in CSF. Additionally, we investigated whether CSF tau levels were abnormal in Alzheimer's disease as compared with a large group of control patients. We developed a sensitive sandwich enzyme-linked immunosorbent assay using AT120, a monoclonal antibody directed to human tau, as a capturing antibody. With this technique, the detection limit for tau was less than 5 pg/ml of CSF. Using AT8, which recognizes abnormally phosphorylated serines 199-202 in tau, the detection limit was below 20 pg/ml of CSF. However, with AT8, we found no immunoreactivity in CSF, suggesting that only a small fraction of CSF tau contains the abnormally phosphorylated AT8 epitope. Our results indicate that CSF tau

levels are significantly increased in Alzheimer's disease. Also, CSF tau levels in a large group of patients with a diversity of neurological diseases showed overlap with CSF T levels in Alzheimer's disease.

10/7/12 (Item 12 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

08855919 BIOSIS NO.: 199396007420

The phosphatase inhibitor okadaic acid induces a phosphorylated paired helical filament tau epitope in human LA-N-5 neuroblastoma cells.

AUTHOR: Vandermeeren Marc%; Lubke Ursula; Six Jan; Cras Patrick(a)
AUTHOR ADDRESS: (a)Lab. Neurobiology, Born-Bunge Foundation, Univ. Antwerp,
Univ. 1, B-2610 Wilrijk**Belgium
JOURNAL: Neuroscience Letters 153 (1):p57-60 1993
ISSN: 0304-3940
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Recently, a mitogen activated protein kinase has been implicated in the generation of a phosphorylated paired helical filament (PHF) epitope recognized by the monoclonal antibody AT8. This epitope consists of phosphorylated serines 199 and/or 202 of the human microtubule associated protein tau. Theoretically, aside from abnormal kinase activity, inhibition of phosphatase activity could also be involved in the abnormal phosphorylation status of the microtubule associated protein tau. To investigate this, we incubated LA-N-5 neuroblastoma cells with okadaic acid, a specific inhibitor of phosphatase 2A. We found that incubating neuroblastoma cells with okadaic acid induces the abnormally phosphorylated AT8 epitope. The effect of okadaic acid is time and dose dependent and is reversible. Our findings suggest that phosphatase activity is important in the regulation of the phosphorylation state of tau. Phosphatases may act directly on tau or may influence the activity of mitogen activated protein kinase. Incubation of LA-N-5 neuroblastoma cells with okadaic acid provides a cellular model in which the generation of a well-defined PHF-tau epitope can be investigated.

10/7/13 (Item 13 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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08427296 BIOSIS NO.: 000094134500

MONOCLONAL ANTIBODIES WITH SELECTIVE SPECIFICITY FOR ALZHEIMER

TAU ARE DIRECTED AGAINST PHOSPHATASE-SENSITIVE EPITOPES

AUTHOR: MERCKEN M%; VANDERMEEREN M%; LUEBKE U; SIX J; BOONS J;
VAN DE VOORDE A; MARTIN J-J; GHEUENS J
AUTHOR ADDRESS: LABORATORY MOLECULAR NEUROSCIENCE AGING RESEARCH, MAILMAN
RESEARCH CENTER, MCLEAN HOSPITAL, BELMONT, MASS. 02178, USA.
JOURNAL: ACTA NEUROPATHOL 84 (3). 1992. 265-272. 1992
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A modified form of the microtubule-associated protein tau is the major component of the paired helical filaments (PHF) found in Alzheimer's disease. The characterization of these posttranslational tau modifications is hindered by the lack of sufficient PHF-tau-specific markers. Here we describe several monoclonal

antibodies, prepared by immunization with PHF, two of which showed a selective specificity for PHF- τ without cross-reactivity with normal τ . Epitope recognition by these two monoclonals was sensitive to alkaline phosphatase treatment. In Western blotting these τ monoclonal antibodies reacted specifically with the abnormally phosphorylated epitopes on Alzheimer's disease-associated PHF- τ .

One of the new antibodies can be used for the construction of a sandwich enzyme-linked immunosorbent assay for the specific detection of PHF- τ without cross-reactivity to normal τ proteins.

10/7/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08293779 BIOSIS NO.: 000094065077
PHOSPHORYLATION-DEPENDENT EPITOPES OF NEUROFILAMENT
ANTIBODIES ON τ
PROTEIN AND RELATIONSHIP WITH ALZHEIMER τ
AUTHOR: LICHTENBERG-KRAAG B; τ MANDELKOW E-M%;
BIERNAT J; STEINER B;
SCHROETER C; GUSTKE N; MEYER H E; MANDELKOW E
AUTHOR ADDRESS: MAX-PLANCK-UNIT FOR STRUCTURAL MOLECULAR
BIOL., C/O DESY,
NOTKESTRASSE 85, D-2000 HAMBURG 52, WEST GERMANY.
JOURNAL: PROC NATL ACAD SCI U S A 89 (12). 1992. 5384-5388. 1992
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences
of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have studied the phosphorylation of τ protein from
Alzheimer paired helical filaments, of τ from normal human
brain,
and of recombinant τ isoforms. As a tool we used
 τ monoclonal
antibodies against neurofilament protein that crossreact with
 τ
in a phosphorylation-dependent manner. This allowed us to deduce the
state of phosphorylation in normal and pathological τ , as well
as

antibody epitopes. The epitope of antibody SMI33 is at the first
Lys-Ser-Pro sequence motif (residues 234-236) and requires an
unphosphorylated Ser-235. Antibody SMI31 binds between Ser-396 (in
the
second Lys-Ser-Pro motif) and Ser-404, both of which must be
phosphorylated. SMI34 has a conformational epitope that depends on the
interaction between regions on either side of the microtubule-binding
region; it also requires phosphorylation. The phosphorylatable serines
detected by the SMI antibodies are part of Ser-Pro motifs and can be
phosphorylated by a protein kinase activity that can be used to induce a
paired helical filament-like state in human brain τ in vitro. The
phosphates are incorporated in several stages that can be identified by
antibody reactivity and gel shift. This suggests a role for the
phosphorylation sites in Alzheimer disease, as well as the involvement of
a Ser-Pro-directed protein kinase.

10/7/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08224951 BIOSIS NO.: 000094025915
THE JUVENILE MICROTUBULE-ASSOCIATED PROTEIN MAP2C IS A
ROD-LIKE MOLECULE
THAT FORMS ANTIPARALLEL DIMERS
AUTHOR: WILLE H; τ MANDELKOW E-M%; MANDELKOW E
AUTHOR ADDRESS: MAX-PLANCK-UNIT STRUCTURAL MOLECULAR
BIOLOGY, DEUTSCHES
ELEKTRONEN SYNCHROTRON, NOTKESTRASSE 85, D-2000 HAMBURG
52, GER.
JOURNAL: J BIOL CHEM 267 (15). 1992. 10737-10742. 1992

FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have developed a procedure to isolate the
microtubule-associated protein 2c (MAP2c), a juvenile form of MAP2
occurring in mammalian brain. The shape, size, self-association, and
antibody interactions of MAP2c were studied. Monomeric MAP2c is an
elongated molecule with a length approximately 48 nm, considerably
shorter than the higher molecular weight forms MAP2a or b of adult brain.
Two τ monoclonal antibodies whose epitopes are near the N or C
terminus, respectively, are located close to the opposite ends of the
MAP2c rods. This places constraints on the types of internal folding of
the molecule. MAP2c self-associates into dimers and fibrous aggregates.
The dimers are predominantly antiparallel and nearly in register, as
judged by antibody labeling.

10/7/16 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08183925 BIOSIS NO.: 000094007698
THE SWITCH OF τ PROTEIN TO AN ALZHEIMER-LIKE
STATE INCLUDES THE
PHOSPHORYLATION OF TWO SERINE PROLINE MOTIFS UPSTREAM
OF THE MICROTUBULE
BINDING REGION
AUTHOR: BIERNAT J; τ MANDELKOW E-M%; SCHROETER C;
LICHTENBERG-KRAAG B;
STEINER B; BERLING B; MEYER H; τ MERCKEN M%;
VANDERMEEREN A; GOEDERT M
; MANDELKOW E
AUTHOR ADDRESS: MAX-PLANCK-UNIT STRUCTURAL MOL. BIOL., C/O
DESY,
NOTKESTRASSE 85, D-2000 HAMBURG 52, GER.
JOURNAL: EMBO (EUR MOL BIOL ORGAN) J 11 (4). 1992. 1593-1597.
1992
FULL JOURNAL NAME: EMBO (European Molecular Biology Organization)
Journal
CODEN: EMJOD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The paired helical filaments (PHFs) of Alzheimer's disease
consist mainly of the microtubule-associated protein τ . PHF
 τ differs from normal human brain τ in that it has
a
higher Mr and a special state of phosphorylation. However, the protein
kinase(s) involved, the phosphorylation sites on τ and the
resulting conformational changes are only poorly understood. Here we show
that a new τ monoclonal antibody, AT8, records the PHF-like state
of
 τ in vitro, and we describe a kinase activity that turns normal
 τ into a PHF-like state. The epitope of AT8 is around residue
200, outside the region of internal repeats and requires the
phosphorylation of serines 199 and/or 202. Both of these are followed by
a proline, suggesting that the kinase activity belongs to the family of
proline-directed kinases. The epitope of AT8 is nearly coincident with
that of another phosphorylation-dependent antibody, TAU1 [Binder, L.I.,
Frankfurter, A. and Rebhun, L. (1985) J. Cell Biol., 101, 1371-1378], but
the two are complementary since TAU1 requires a dephosphorylated
epitope.

10/7/17 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08046168 BIOSIS NO.: 000093079516
AFFINITY PURIFICATION OF HUMAN τ PROTEINS AND
THE CONSTRUCTION OF A
SENSITIVE SANDWICH ENZYME-LINKED IMMUNOSORBENT ASSAY
FOR HUMAN τ
DETECTION

AUTHOR: %%%MERCKEN M%%: %%%VANDERMEEREN M%%: LUBKE U: SIX J: BOONS J:
 VANMECHELEN E: VAN DE VOORDE A: GHEUENS J
 AUTHOR ADDRESS: LABORATORY NEUROBIOLOGY, BORN BUNGE FOUNDATION, UNIVERSITY
 ANTWERP, UTA, UNIVERSITEITSPLEIN 1, B-2610 WILRIJK, BELGIUM.
 JOURNAL: J NEUROCHEM 58 (2). 1992. 548-553. 1992
 FULL JOURNAL NAME: Journal of Neurochemistry
 CODEN: JONRA
 RECORD TYPE: Abstract
 LANGUAGE: ENGLISH

ABSTRACT: Immunoaffinity chromatography with a %%%monoclonal%% antibody
 produced against bovine %%%tau%% protein was used to purify %%%tau%%
 . proteins from human brain. Fifty grams of brain tissue yielded approx.
 2 mg of pure %%%tau%% proteins. The affinity-purified human %%%tau%%
 . was used to produce a high-titered rabbit anti-human %%%tau%% serum.
 The %%%monoclonal%% anti- %%%tau%% antibody and the polyclonal rabbit
 anti- %%%tau%% serum were then used to construct a sandwich enzyme-linked immunosorbent assay for detection of human %%%tau%% proteins, with sensitivity of 1 ng/ml.

10/7/18 (Item 18 from file: 5)
 DIALOG(R)File 5: Biosis Previews(R)
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07844834 BIOSIS NO.: 000092115000
 DEMONSTRATION OF A NOVEL NEUROFILAMENT ASSOCIATED ANTIGEN WITH THE
 NEUROFIBRILLARY PATHOLOGY OF ALZHEIMER AND RELATED DISEASES
 AUTHOR: GHEUENS J; CRAS P; PERRY G; BOONS J; CEUTERICK-DE GROOTE C; LUBKE U
 : %%%MERCKEN M%%: TABATON M; GAMBETTI P L: ET AL
 AUTHOR ADDRESS: DIV. NEUROPATHOL., CASE WESTERN RESERVE UNIVERSITY, 2085
 ADELBERT RD., CLEVELAND, OHIO 44106-4901.
 JOURNAL: BRAIN RES 558 (1). 1991. 43-52. 1991
 FULL JOURNAL NAME: Brain Research
 CODEN: BRREA
 RECORD TYPE: Abstract
 LANGUAGE: ENGLISH

ABSTRACT: A %%%monoclonal%% antibody, termed NFT200, was raised after in
 vitro immunization with sonicated neurofibrillary tangle (NFT)-enriched fractions prepared from Alzheimer brain. The antigen to which NFT200 is directed was expressed in the paired helical filaments of NFT in sporadic and familial Alzheimer disease (AD), in the straight filaments of NFT in AD, progressive supranuclear palsy and of Pick bodies, and the NFT in several other conditions such as Parkinson-dementia complex of Guam and subacute sclerosing panencephalitis. Granulovacuolar degeneration of AD was also labeled with NFT200. Hirano bodies and amyloid deposits in AD, as well as Lewy bodies of idiopathic Parkinson disease lacked in the antigen. The NFT200-antigen was also expressed as a phosphatase-insensitive antigen in normal neurofilaments found in spinal cord and peripheral nerve axons but was absent from the perikaryal accumulation of neurofilaments induced by aluminum intoxication. Nevertheless, immunoblot studies failed to detect the NFT200 in isolated preparations of the neurofilament proteins, MAP-2, %%%tau%%, ubiquitin or A4-amyloid peptide. The results indicate that the NFT200 %%%monoclonal%% antibody is directed against a phosphatase-insensitive epitope of an axonal protein associated with neurofilaments but is labile to isolation and expressed as a stable epitope of a 200 kDa component of NFT.

10/7/19 (Item 1 from file: 34)

DIALOG(R)File 34: SciSearch(R) Cited Ref Sci
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10285496 Genuine Article#: 510AY Number of References: 59
 Title: Specific %%%tau%% phosphorylation sites correlate with severity of neuronal cytopathology in Alzheimer's disease
 Author(s): Augustinack JC; Schneider A: %%%Mandelkow EM%%: Hyman BT
 (REPRINT)
 Corporate Source: Harvard Univ, Sch Med, Massachusetts Gen Hosp, Alzheimers
 Res Unit, 114 16th St, Rm 2009/Charlestown//MA/02129 (REPRINT); Harvard
 Univ, Sch Med, Massachusetts Gen Hosp, Dept Neurol, Alzheimers Unit, Charlestown//MA/02129; Max Planck Unit Struct Mol Biol, D-22607 Hamburg//Germany/
 Journal: ACTA NEUROPATHOLOGICA, 2002, V103, N1 (JAN), P26-35
 ISSN: 0001-6322 Publication date: 20020100
 Publisher: SPRINGER-VERLAG, 175 FIFTH AVE, NEW YORK, NY 10010 USA

Language: English Document Type: ARTICLE
 Abstract: Microtubule associated protein %%%tau%% is abnormally phosphorylated in Alzheimer's disease (AD) and aggregates as paired helical filaments (PHFs) in neurofibrillary tangles (NFTs). We show here that the pattern of %%%tau%% phosphorylation correlates with the loss of neuronal integrity. Studies using 11 phosphorylation dependent %%%tau%% antibodies and a panel of AD cases of varying severity were evaluated in terms of three stages of neurofibrillary tangle development: (1) pre-neurofibrillary tangle, (2) intra-, and (3) extra-neuronal neurofibrillary tangles. The pretangle state, in which neurons display nonfibrillar, punctate regions in the cytoplasm, dendrites, somas, and nuclei, was observed especially with phosphotau antibodies T63 (pT231), pS262, and pT153. Intraneuronal neurofibrillary tangles are homogeneously stained with fibrillar %%%tau%% structures, which were most prominently stained with pT175/181, 12E8 (pS262/pS356), pS422, pS46, pS214 antibodies. Extracellular NFTs, which contain substantial filamentous %%%tau%%, are most prominently stained with AT8 (pS199/pS202/pT205), AT100 (pT212/pS214), and PHF-1 (pS396/pS404) antibodies, which also stain intracellular NFT. The sequence of early %%%tau%% phosphorylation suggests that there are events prior to filament formation that are specific to particular phosphorylated %%%tau%% epitopes, leading to conformational changes and cytopathological alterations.

10/7/20 (Item 2 from file: 34)
 DIALOG(R)File 34: SciSearch(R) Cited Ref Sci
 (c) 2002 Inst for Sci Info. All rts. reserv.

09278691 Genuine Article#: 3876J Number of References: 81
 Title: Glycogen synthase kinase-3 beta phosphorylates protein %%%tau%% and rescues the axonopathy in the central nervous system of human four-repeat %%%tau%% transgenic mice
 Author(s): Spittaels K; Van den Haute C; Van Dorpe J; Geerts H; %%%Mercken%%
 %%%M%%: Bruynseels K; Lasrado R; Vandezande K; Laenen I; Boon T; Van Lint
 J; Vandenheede J; Moechars D; Loos R; Van Leuven F (REPRINT)
 Corporate Source: Katholieke Univ Leuven, Ctr Human Genet, Flemish Inst Biotechnol, Expt Genet Grp, Campus Gasthuisberg O&N 06/B-3000 Leuven//Belgium/ (REPRINT); Katholieke Univ Leuven, Ctr Human Genet, Flemish Inst Biotechnol, Expt Genet Grp, B-3000 Leuven//Belgium/
 Janssen Res Fdn, B-2340 Beerse//Belgium/; Katholieke Univ Leuven, Fac Med
 , Dept Biochem, B-3000 Leuven//Belgium/; Katholieke Univ Leuven, Dept Genet Epidemiol, B-3000 Leuven//Belgium/
 Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 2000, V275, N52 (DEC 29), P
 41340-41349
 ISSN: 0021-9258 Publication date: 20001229
 Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650

ROCKVILLE

PIKE, BETHESDA, MD 20814 USA

Language: English Document Type: ARTICLE

Abstract: Protein %tau% filaments in brain of patients suffering from

Alzheimer's disease, frontotemporal dementia, and other tauopathies consist of protein %tau% that is hyperphosphorylated. The responsible kinases operating in vivo in neurons still need to be identified. Here we demonstrate that glycogen synthase kinase-3 beta (GSK-3 beta) is an effective kinase for protein %tau% in cerebral neurons in vivo in adult GSK-3 beta and GSK-3 beta x human tau40 transgenic mice; Phosphorylated protein %tau% migrates slower during electrophoretic separation and is revealed by phosphorylation-dependent anti-%tau% antibodies in Western blot analysis. In addition, its capacity to bind to re-assembled paclitaxel (Taxol(R))-stabilized microtubules is reduced, compared with protein %tau% isolated from mice not overexpressing GSK-3 beta. Co-expression of GSK-3 beta reduces the number of axonal dilations and alleviates the motoric impairment that was typical for single tau40 transgenic animals (Spittaels, K., Van den Haute, C., Van Dorpe, J., Bruynseels, K., Vandezande, K., Laenen, I., Geerts, H., Mercken, M., Sciot, R., Van Lommel, A., Loos, R., and Van Leuven, F. (1999) *Am. J. Pathol.* 155, 2153-2165). Although more hyperphosphorylated protein %tau% is available, neither an increase in insoluble protein %tau% aggregates nor the presence of paired helical filaments or tangles was observed. These findings could have therapeutic implications in the field of neurodegeneration, as discussed.

10/7/21 (Item 3 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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08251686 Genuine Article#: 262XD Number of References: 68

Title: Prominent axonopathy in the brain and spinal cord of transgenic mice overexpressing four-repeat human %tau% protein

Author(s): Spittaels K; VandenHaute C; VanDorpe J; Bruynseels K; Vandezande

K; Laenen I; Geerts H; %Mercken M%; Sciot R; VanLommel A; Loos R;

VanLeuven F (REPRINT)

Corporate Source: KATHOLIEKE UNIV LEUVEN,CTR HUMAN GENET, VLAAMS INST

BIOTECHNOL, EXPT GENET GRP/B-3000 LOUVAIN//BELGIUM/ (REPRINT);

KATHOLIEKE UNIV LEUVEN,CTR HUMAN GENET, VLAAMS INST BIOTECHNOL, EXPT

GENET GRP/B-3000 LOUVAIN//BELGIUM/; JANSSEN RES FDN/B-2340

BEERSE//BELGIUM/; KATHOLIEKE UNIV LEUVEN HOSP,DEPT PATHOL/LOUVAIN//BELGIUM/; KATHOLIEKE UNIV LEUVEN,DEPT GENET

EPIDEMIOLOG/LOUVAIN//BELGIUM/

Journal: AMERICAN JOURNAL OF PATHOLOGY, 1999, V155, N6 (DEC), P2153-2165

ISSN: 0002-9440 Publication date: 19991200

Publisher: AMER SOC INVESTIGATIVE PATHOLOGY, INC, 428 EAST PRESTON ST,

BALTIMORE, MD 21202-3993

Language: English Document Type: ARTICLE

Abstract: Mutations in the human %tau% gene cause frontotemporal dementia and parkinsonism linked to chromosome 17. Some mutations, including mutations in intron 10, induce increased levels of the functionally normal four-repeat %tau% protein isoform, leading to neurodegeneration. We generated transgenic mice that overexpress the four-repeat human %tau% protein isoform specifically in neurons. The transgenic mice developed axonal degeneration in brain and spinal cord. In the model, axonal dilations with accumulation of neurofilaments, mitochondria, and vesicles were documented. The axonopathy and the accompanying dysfunctional sensorimotor capacities were transgene-dosage related. These findings proved that merely increasing the concentration of the four-repeat %tau% protein isoform is sufficient to injure neurons in the central nervous system, without formation of intraneuronal neurofibrillary tangles. Evidence for astrogliosis and ubiquitination of accumulated proteins in the dilated part of the axon supported this conclusion. This transgenic

model, overexpressing the longest isoform of human %tau% protein,

recapitulates features of known neurodegenerative diseases, including Alzheimer's disease and other tauopathies. The model makes it possible to study the interaction with additional factors, to be incorporated genetically, or with other biological triggers that are implicated in neurodegeneration.

10/7/22 (Item 4 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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06936898 Genuine Article#: 105MY Number of References: 82

Title: Mitotic phosphorylation of %tau% protein in neuronal cell lines resembles phosphorylation in Alzheimer's disease

Author(s): Preuss U (REPRINT); %Mandelkow EM%;

Corporate Source: UNIV BONN,INST GENET, MOL GENET SECT, ROMERSTR

164/D-53117 BONN//GERMANY/ (REPRINT); DESY,MAX PLANCK UNIT STRUCT MOL

BIOL/D-2000 HAMBURG//GERMANY/

Journal: EUROPEAN JOURNAL OF CELL BIOLOGY, 1998, V76, N3 (JUL), P176-184

ISSN: 0171-9335 Publication date: 19980700

Publisher: GUSTAV FISCHER VERLAG, VILLENANG 2, D-07745 JENA, GERMANY

Language: English Document Type: ARTICLE

Abstract: %Tau% protein, a neuronal microtubule-associated protein is

phosphorylated on several sites when extracted from brain tissue and is a substrate for many protein kinases in vitro. In Alzheimer's disease it becomes hyperphosphorylated, notably at Ser-Pro or Thr-Pro motifs, and forms the paired helical filaments (PHFs). The increased phosphorylation can be detected by several antibodies raised against Alzheimer %tau%. We show here that a similar type of phosphorylation can be observed in cells of neuronal origin during mitosis. Murine neuroblastoma cells (N2a) were stably transfected with tau40, the largest of the six human %tau% isoforms in the brain. We used several antibodies reporting on the state of phosphorylation of %tau% (%Tau%-1, AT8, AT180, PHF-1, and T46) and the antibody

MPM-2 that recognizes phosphorylated mitotic proteins. The results show that %tau% is in a state of low phosphorylation in interphase cells, whereas during mitosis it becomes highly phosphorylated. This behavior was also found for endogenous tau protein in human neuroblastoma cells (LAN-5). The similarity between %tau% phosphorylation in dividing neuronal cells and Alzheimer degenerating neurons may indicate that aging neurons exposed to inappropriate signals respond by an attempt to activate their machinery for regeneration.

10/7/23 (Item 5 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

(c) 2002 Inst for Sci Info. All rts. reserv.

06805166 Genuine Article#: ZT687 Number of References: 102

Title: The endogenous and cell cycle-dependent phosphorylation of %tau%

protein in living cells: Implications for Alzheimer's disease

Author(s): Illenberger S; ZhengFischhofer QY; Preuss U; Stamer K; Baumann K

; Trinczek B; Biernat J; Godemann R; %Mandelkow EM%;

Mandelkow E

(REPRINT)

Corporate Source: MAX PLANCK UNIT STRUCT MOL BIOL/D-22603

HAMBURG//GERMANY/ (REPRINT); MAX PLANCK UNIT STRUCT MOL BIOL/D-22603

HAMBURG//GERMANY/

Journal: MOLECULAR BIOLOGY OF THE CELL, 1998, V9, N6 (JUN), P1495-1512

ISSN: 1059-1524 Publication date: 19980600

Publisher: AMER SOC CELL BIOLOGY, PUBL OFFICE, 9650 ROCKVILLE PIKE,

BETHESDA, MD 20814

Language: English Document Type: REVIEW

Abstract: In Alzheimer's disease the neuronal microtubule-associated protein τ becomes highly phosphorylated, loses its binding properties, and aggregates into paired helical filaments. There is increasing evidence that the events leading to this hyperphosphorylation are related to mitotic mechanisms. Hence, we have analyzed the physiological phosphorylation of endogenous τ protein in metabolically labeled human neuroblastoma cells and in Chinese hamster ovary cells stably transfected with τ . In nonsynchronous cultures the phosphorylation pattern was remarkably similar in both cell lines, suggesting a similar balance of kinases and phosphatases with respect to τ . Using phosphopeptide mapping

and sequencing we identified 17 phosphorylation sites comprising 80-90% of the total phosphate incorporated. Most of these are in SP or TP motifs, except S214 and S262. Since phosphorylation of microtubule-associated proteins increases during mitosis, concomitant with increased microtubule dynamics, we analyzed cells mitotically arrested with nocodazole. This revealed that S214 is a prominent phosphorylation site in metaphase, but not in interphase. Phosphorylation of this residue strongly decreases the τ -microtubule interaction in vitro, suppresses microtubule assembly, and may be a key factor in the observed detachment of τ from microtubules during mitosis. Since S214 is also phosphorylated in Alzheimer's disease τ , our results support the view that reactivation of the cell cycle machinery is involved in τ hyperphosphorylation.

10/7/24 (Item 6 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04163215 Genuine Article#: RJ792 Number of References: 41

Title: DIFFERENTIAL SENSITIVITY PROTEOLYSIS BY BRAIN CALPAIN OF ADULT

HUMAN- τ , FETAL HUMAN- τ AND PHF- τ

Author(s): MERCKEN M; GRYNSPAN F; NIXON RA

Corporate Source: MCLEAN HOSP,MAILMAN RES CTR,MOLEC NEUROSCI LABS,115 MILL

ST/BELMONT//MA/02178; HARVARD UNIV,SCH MED,DEPT

PSYCHIAT/BELMONT//MA/02178; HARVARD UNIV,SCH

MED,PROGRAM

NEUROSCI/BELMONT//MA/02178

Journal: FEB5 LETTERS, 1995, V368, N1 (JUL 10), P10-14

ISSN: 0014-5793

Language: ENGLISH Document Type: ARTICLE

Abstract: Reduced turn-over of τ by calpains is a possible mechanism to facilitate the incorporation into paired helical filaments (PHFs) in Alzheimer's disease. The present study shows that the differently phosphorylated fetal τ isoforms are all rapidly proteolysed to an equal extent by human brain m-calpain. This result argues against the hypothesis that this type of fetal phosphorylation is involved in reducing τ turn-over by calpain in Alzheimer's disease. Adult and fetal τ fragments in vitro generated by m-calpain, but not trypsin, cathepsin D or chymotrypsin resemble the post-mortem in situ degradation patterns, suggesting a possible role for calpains in τ metabolism in vivo. τ incorporated into PHFs was considerably more resistant to proteolysis by calpain which can help to explain the persistence of these structures in Alzheimer's disease.

10/7/25 (Item 7 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03321197 Genuine Article#: NV430 Number of References: 66

Title: PHOSPHORYLATION OF MICROTUBULE-ASSOCIATED PROTEINS MAP2A,B AND MAP2C

AT SER136 BY PROLINE-DIRECTED KINASES IN-VIVO AND IN-VITRO

Author(s): BERLING B; WILLE H; ROLL B; MANDELKOW EM; GARNER C;

MANDELKOW E

Corporate Source: DESY,MAX PLANCK GESELL,STRUCT MOLEC BIOL RES UNIT,NOTKESTR 85/D-22603 HAMBURG//GERMANY/; DESY,MAX PLANCK

GESELL,STRUCT MOLEC BIOL RES UNIT/D-22603

HAMBURG//GERMANY/; UNIV

HAMBURG,CTR MOLEC NEUROBIOL/W-2000 HAMBURG//GERMANY/

Journal: EUROPEAN JOURNAL OF CELL BIOLOGY, 1994, V64, N1 (JUN), P120-130

ISSN: 0171-9335

Language: ENGLISH Document Type: ARTICLE

Abstract: The microtubule-associated protein 2 (MAP2) and its juvenile splicing variant MAP2c contain a phosphorylation site at Ser136 which is part of a Ser-Pro motif. This site lies within the N-terminal region common to MAP2b and MAP2c. It has been mapped by site-directed mutagenesis of recombinant MAP2c and by a τ monoclonal antibody

AP18 whose epitope contains the phosphorylated Ser136. In vitro this site is phosphorylated by proline-directed kinases such as MAP kinase, GSK-3, or members of the cdk family, but not by other kinases such as PKA, PKC, or CaMK-II. MAP2a,b or MAP2c isolated from brain is found to be endogenously phosphorylated at Ser136. After microinjection into several cell lines dephosphorylated MAP2 isoforms or recombinant MAP2c become also phosphorylated at Ser136 in vivo. Injection of MAP2a,b or MAP2c into living cells causes reorganization of microtubules, including bundle formation. This effect is independent of the phosphorylation at Ser136. The specificity of the phosphorylation reaction provides a tool for analyzing the role and posttranslational processing of MAP2 in nerve cell development.

10/7/26 (Item 8 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03314124 Genuine Article#: NV861 Number of References: 71

Title: MICROTUBULE-ASSOCIATED PROTEIN- τ EPITOPES ARE PRESENT IN

FIBER LESIONS IN DIVERSE MUSCLE DISORDERS

Author(s): LUBKE U; SIX J; VILLANOVA M; BOONS J;

τ VANDERMEEREN M;

CEUTERICK C; CRAS P; MARTIN JJ

Corporate Source: UNIV INSTELLING ANTWERP,BORN BUNGE

FDN,NEUROBIOL LAB,UNIV

PL 1/B-2610 WILRIJK//BELGIUM/; UNIV INSTELLING

ANTWERP,BORN BUNGE

FDN,NEUROBIOL LAB/B-2610 WILRIJK//BELGIUM/; UNIV

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ANTWERP,BORN BUNGE FDN,NEUROPATHOL LAB/B-2610

WILRIJK//BELGIUM/;

INNOGENET/GHENT//BELGIUM/; UNIV SIENA,NEUROPATHOL LAB/I-53100

SIENA//ITALY/

Journal: AMERICAN JOURNAL OF PATHOLOGY, 1994, V145, N1 (JUL), P175-188

ISSN: 0002-9440

Language: ENGLISH Document Type: ARTICLE

Abstract: The microtubule-associated protein τ is a major cytoskeletal protein involved in the neurofibrillary tangles of Alzheimer's disease. Although τ is predominantly a neuronal protein, it has been demonstrated in glia and other nonneuronal cells. We describe the presence of microtubule-associated protein τ

epitopes in various muscle fiber lesions in oculopharyngeal and Becker muscular dystrophy, dermatomyositis, central core disease, neurogenic atrophy, and in the recovery phase of an attack of malignant hyperthermia. Western blot demonstrated a 100- to 110-kd τ -immunoreactive protein probably corresponding to 'big τ ' as described in peripheral nerves. τ immunoreactivity in muscle fiber lesions usually co-localized with tubulin, although electron microscopy failed to show an increase in microtubules. τ and tubulin reactivity also correlated with the presence of desmin and vimentin epitopes. Possible explanations for the presence of τ are briefly discussed.

10/7/27 (Item 9 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03225554 Genuine Article#: NN763 Number of References: 63
Title: A SEQUENCE OF CYTOSKELETON CHANGES RELATED TO THE FORMATION OF

NEUROFIBRILLARY TANGLES AND NEUROPIL THREADS
Author(s): BRAAK E; BRAAK H; %%%MANDELKOW EM%%
Corporate Source: UNIV FRANKFURT,ZENTRUM MORPHOL,THEODAR STERN KAI

7/D-60590 FRANKFURT//GERMANY/: DESY,MAX PLANCK

GESELL,ARBEITSGRP

STRUKTURELLE MOLEK BIOL/D-22607 HAMBURG//GERMANY/

Journal: ACTA NEUROPATHOLOGICA, 1994, V87, N6 (JUN), P554-567
ISSN: 0001-6322

Language: ENGLISH Document Type: ARTICLE

Abstract: Frontal sections of the temporal lobe including the transentorhinal/entorhinal region, amygdala, and/or hippocampus from human adult brains are studied for cytoskeleton changes using immunostaining with the antibodies AT8 and Alz-50 and selective silver impregnation methods for neurofibrillary changes of the Alzheimer type. For the purpose of correlation, the two methods are carried out one after the other on the same section. Layer pre-alpha in the transentorhinal/entorhinal region harbours nerve cells which are among the first nerve cells in the entire brain to show the development of neurofibrillary changes. This presents the opportunity for study of both early events in the destruction of the cytoskeleton in individual neurons, and to relate changes which occur in the neuronal processes in the absence of alterations in their immediate surroundings to those happening in the soma. Immunoreactions with the AT8 antibody in particular reveal a clear sequence of changes in the neuronal cytoskeleton. Group 1 neurons present initial cytoskeleton changes in that the soma, dendrites, and axon are completely marked by granular AT8 immunoreactive material. These neurons appear quite normal and turn out to be devoid of argyrophilic material when observed in silver-stained sections. Group 2 neurons show changes in the cellular processes. The terminal tuft of the apical dendrite is replaced by tortuous varicose fibres and coarse granules. The distal portions of the dendrites are curved and show appendages and thickened portions. Intensely homogeneously immunostained rod-like inclusions are encountered in these thickened portions and in the soma. A number of these rod-like inclusions are visible after silver staining, as well. Group 3 neurons display even more pronounced alterations of their distal - most dendritic portions. The intermediate dendritic parts lose immunoreactivity, but the soma is homogeneously immunostained. Silver staining reveals in most of the distal dendritic parts neuropil threads, and in the soma a classic neurofibrillary tangle. Group 4 structures are marked by accumulations of coarse AT8-immunoreactive granules. Silver staining provides evidence that the fibrillary material has become an extraneuronal, "early" ghost tangle. Finally, group 5 structures present "late" ghost tangles in silver-stained sections but fail to demonstrate AT8 immunoreactivity. It is suggested that the altered %%%tau%%% protein shown by the antibody AT8 represents an early cytoskeleton change which eventually leads to the formation of argyrophilic neurofibrillary tangles and neuropil threads.

10/7/28 (Item 10 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

01462227 Genuine Article#: HA732 Number of References: 52
Title: SPECIFIC %%%MONOCLONAL%%%-ANTIBODIES AGAINST NORMAL

MICROTUBULE-ASSOCIATED PROTEIN-2 (MAP2) EPITOPES PRESENT IN ALZHEIMER

PATHOLOGICAL STRUCTURES DO NOT RECOGNIZE PAIRED HELICAL FILAMENTS

Author(s): SIX J; LUBKE U; %%%MERCKEN M%%%; %%%VANDERMEEREN M%%%; CEUTERICK

C; VANDEVOORDE A; BOONS J; GHEUENS J

Corporate Source: UNIV INSTELLING ANTWERP,BORN BUNGE FBN,NEUROBIOL

LAB,UNIVERSITEITSPLEIN 1/B-2610 WILRIJK//BELGIUM/: UNIV INSTELLING

ANTWERP,NEUROPATHOL LABS/B-2610WILRIJK//BELGIUM/: INNOGENETICS/GHENT//BELGIUM/

Journal: ACTA NEUROPATHOLOGICA, 1992, V83, N2 (JAN), P179-189

Language: ENGLISH Document Type: ARTICLE

Abstract: We have developed %%%monoclonal%%% antibodies that detect normal

microtubule-associated protein-2 (MAP2) epitopes in routinely fixed, paraffin-embedded tissue. The somatodendritic distribution of MAP2 in bovine and human nervous tissue was confirmed with several of these antibodies. Furthermore, some of these antibodies immunohistochemically labeled certain pathological structures in Alzheimer brain, especially neurites in senile plaques. Electron microscopic observations, however, indicate that these MAP2 epitopes are not located in the Alzheimer paired helical filaments themselves, but in amorphous granular structures coexistent with them. While the pathological nature of these structures is undetermined, they may represent artefactual modifications of normal cytoskeletal components.

10/7/29 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE
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07742031 EMBASE No: 1999224250

Phosphorylation of %%%tau%%% protein by recombinant GSK-3beta: Pronounced

phosphorylation at select Ser/Thr-Pro motifs but no phosphorylation at Ser262 in the repeat domain

Godemann R.; Biernat J.; %%%Mandelkow E.%%%; %%%Mandelkow E.M.%%%

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FEBS Letters (FEBS LETT.) (Netherlands) 1999, 454/1-2 (157-164)

CODEN: FEBLA ISSN: 0014-5793

PUBLISHER ITEM IDENTIFIER: S0014579399007413

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 60

Glycogen synthase kinase-3beta (GSK-3beta) has been described as a proline-directed kinase which phosphorylates %%%tau%%% protein at several sites that are elevated in Alzheimer paired helical filaments. However, it has been claimed that GSK-3beta can also phosphorylate the non-proline-directed KXGS motifs in the presence of heparin, including Ser262 in the repeat domain of %%%tau%%%, which could induce the detachment of %%%tau%%% from microtubules. We have analyzed the activity of recombinant GSK-3beta and of GSK-3beta preparations purified from tissue, using two-dimensional phosphopeptide mapping, immunoblotting with phosphorylation-sensitive antibodies, and phosphopeptide sequencing. The most prominent phosphorylation sites on %%%tau%%% are Ser396 and Ser404 (PHF-1 epitope), Ser46 and Thr50 in the first insert, followed by a less efficient phosphorylation of other Alzheimer phosphopeptides (antibodies AT-8, AT-270, etc). We also show that the non-proline-directed activity at KXGS motifs is not due to GSK-3beta itself, but to kinase contaminations in common GSK-3beta preparations from tissues which are activated upon addition of heparin. Copyright (C) 1999 Federation of European Biochemical Societies.

10/7/30 (Item 2 from file: 73)
DIALOG(R)File 73:EMBASE
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06229171 EMBASE No: 1995265576

Alteration in %%%tau%%% antigenicity and electrophoretic migration by PKCalpha under cell-free conditions

Cressman C.M.; %%%Mercken M.M.%%%; Shea T.B.

Gen Cell Neurobiol Neurodegen Res, Department of Biological Sciences, University of Massachusetts Lowell, MA 01854 United States

Neuroscience Research Communications (NEUROSCI. RES. COMMUN.) (United

Kingdom) 1995, 17/2 (61-64)
CODEN: NRCOE ISSN: 0893-6609
DOCUMENT TYPE: Journal: Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Previous studies have demonstrated that PKC is capable of phosphorylating τ under cell-free conditions. However, PKC did not induce the 'AD-like' alterations in τ antigenicity and electrophoretic migration that have been reported for several other kinases. In the present study, we observed that short-term (30 min) incubation of purified human brain τ with PKC α indeed did not induce significant alterations in τ antigenicity or electrophoretic migration. By contrast, extended (20 hr) incubation with PKC α altered τ migration to produce a form that migrated at 68 kDa on SDS-gels, significantly increased its reactivity with ALZ-50, and induced the de novo appearance of the PHF-1 epitope. These findings, taken together with previous studies, underscore the potential involvement of PKC in modulation of τ function, especially during neuronal development and neurodegeneration.

10/7/31 (Item 3 from file: 73)
DIALOG(R)File 73:EMBASE
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05414892 EMBASE No: 1993182991

The abnormal phosphorylation of τ protein at Ser-202 in Alzheimer disease recapitulates phosphorylation during development
Goedert M.; Jakes R.; Crowther R.A.; Six J.; Lubke U.;
 τ Vandermeeren
 τ M.; Cras P.; Trojanowski J.Q.; Lee V.M.-Y.
MRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH
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Proceedings of the National Academy of Sciences of the United States of America (PROC. NATL. ACAD. SCI. U. S. A.) (United States) 1993, 90/11 (5066-5070)
CODEN: PNAS ISSN: 0027-8424
DOCUMENT TYPE: Journal: Conference Paper
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

τ is a neuronal phosphoprotein whose expression is developmentally regulated. A single τ isoform is expressed in fetal human brain but six isoforms are expressed in adult brain, with the fetal isoform corresponding to the shortest of the adult isoforms. Phosphorylation of τ is also developmentally regulated, as fetal τ is phosphorylated at more sites than adult τ . In Alzheimer disease, the six adult τ isoforms become abnormally phosphorylated and form the paired helical filament, the major fibrous component of the characteristic neurofibrillary lesions. We show here that Ser-202 (in the numbering of the longest human brain τ isoform) is a phosphorylation site that distinguishes fetal from adult τ and we identify it as one of the abnormal phosphorylation sites in Alzheimer disease. The abnormal phosphorylation of τ at Ser-202 in Alzheimer disease thus recapitulates normal phosphorylation during development.

10/7/32 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
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12183691 PASCAL No.: 95-0398612

Neuronal kinase stimulation leads to aberrant τ phosphorylation and neurotoxicity. Commentaries
The cytoskeleton and Alzheimer's disease
NUYDENS R; DE JONG M; NUYENS R; CORNELISSEN F; GEERTS H;
AVILA J comment;
 τ MANDELKOW E M comment
Janssen res. foundation, dep. cellular physiology life sci., 2340 Beerse,

Belgium

Schmitt symposium (Rochester NY USA) 1994-05-21
Journal: Neurobiology of aging, 1995, 16 (3) 465-477
ISSN: 0197-4580 CODEN: NEA6DO Availability: INIST-20387;
354000051039660210

No. of Refs.: 49 ref.
Document Type: P (Serial); C (Conference Proceedings); A (Analytic)
Country of Publication: USA
Language: English
NUYDENS, R., M. DE JONG, R. NUYENS, F. CORNELISSEN AND H. GEERTS.

Neuronal kinase stimulation leads to aberrant τ phosphorylation and neurotoxicity. NEUROBIOL AGING 16(3) 465-477, 1995.-
Neurofibrillary tangles in Alzheimer's disease brain consist mainly of abnormally phosphorylated τ proteins organised in paired helical filaments.

Induction of τ phosphorylation in living neurons by hyperstimulation is monitored by specific τ monoclonal antibodies, such as AT-8 and PHF-1. By quantitative immunocytochemistry, we show that aberrant phosphorylation at the Ser199/Ser202 epitope (AT-8) and at the Ser

396 epitope (PHF-1) are moderately induced, proportionally to the degree of kinase stimulation. Whereas AT8 expression is prominent after 48 h, cell death becomes significant at 72 h and is related to the degree of stimulation and the expression level of aberrant τ phosphorylation.

Time-lapse videomicroscopy of individual neuroblastoma cells suggest that hyperstimulation leads to a form of morphological over-differentiation. Immediately before cell death, some cells tend to display some features of mitosis. The data suggest a strong correlation between the expression of specific PHF-epitopes and subsequent cell death. The extended time scale of toxicity in this model may be appropriate to study in more detail the steps leading to aberrant phosphorylation associated neurotoxicity.

10/7/33 (Item 1 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

09735631 Genuine Article#: AT454 Number of References: 37
Title: τ -PROTEIN BECOMES LONG AND STIFF UPON PHOSPHORYLATION -

CORRELATION BETWEEN PARACRYSTALLINE STRUCTURE AND DEGREE OF PHOSPHORYLATION

Author(s): HAGESTEDT T; LICHTENBERG B; WILLE H; MANDELKOW EM;

MANDELKOW E
Corporate Source: MAX PLANCK UNIT STRUCT MOLEC BIOL/D-2000 HAMBURG 52//FED
REP GER/

Journal: JOURNAL OF CELL BIOLOGY, 1989, V109, N4, P1643-1651
Language: ENGLISH Document Type: ARTICLE

